

SEARCH REQUEST FORM

Requestor's
Name: Liu S

Serial
Number: 101757745

Date: 03-15-06

Phone: _____

Art Unit: 1653

REM 3A64/3C70

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Seq ID 2 : 115-121
54-140
145-153

EST dB 1000 Summary Listing
200 hits displayed

Extended Search

STAFF USE ONLY

Date completed: _____

Searcher: Beverly e 2528

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

____ STIC

____ CM-1

____ Pre-S

Type of Search

____ N.A. Sequence

____ A.A. Sequence

____ Structure

____ Bibliographic

Vendors

____ IG

____ STN

____ Dialog

____ APS

____ Geninfo

____ SDC

____ DARC/Questel

☒ Other CGN

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 16, 2006, 00:29:49 ; Search time 706.806 Seconds
(without alignments)
595.756 Million cell updates/sec

Title: US-10-757-745-2_COPY_145_153
Perfect score: 45
Sequence: 1 FDVIFLQEV 9

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delep 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-O=/abs/ABSSMB.spool/US1075745/runat.15032006.165652.3610/app.query.fasta_1
-DB=EST -QFMT=fastaop -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=bl0sum62 -TRANS=human0.cct -LIST=1000
-DOCALIGN=200 -THR.SCOR=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=200 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US1075745 @CN1.1 8148 @runat.15032006.165652.3610 -NCPU=6 -ICPU=3
-NO MAP -NEG.SCOR=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV.TIMEOUT=120
-NARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_esc3:*
4: gb_esc4:*
5: gb_esc5:*
6: gb_esc6:*
7: gb_esc7:*
8: gb_esc8:*
9: gb_esc9:*
10: gb_esc10:*
11: gb_esc11:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	149	3	BQ363306 PM1-MT014
2	45	100.0	156	3	BQ331200 MR4-ET014
3	45	100.0	247	2	BF768814 PM0-IT001
4	45	100.0	252	1	AA325145 EST28102
5	45	100.0	296	2	BF992136 OV3-GN020
6	45	100.0	313	2	BF992133 OV3-GN020
7	45	100.0	368	2	BE694706 PM0-BT075

8	45	100.0	388	1	AV659558	AV659558
9	45	100.0	394	1	AV661333	AV661333
10	45	100.0	413	3	BQ332322	BQ332322
11	45	100.0	419	2	BF853399	BF853399
12	45	100.0	422	2	BG982044	BG982044
13	45	100.0	429	5	BQ582059	BQ582059
14	45	100.0	435	3	BQ332331	BQ332331
15	45	100.0	437	2	BF768820	BF768820
16	45	100.0	440	2	BG982029	BG982029
17	45	100.0	441	2	BG982036	BG982036
18	45	100.0	441	2	BF992415	BF992415
19	45	100.0	441	2	BF893925	BF893925
20	45	100.0	444	2	BF893187	BF893187
21	45	100.0	447	2	BF891509	BF891509
22	45	100.0	453	3	BF773259	BF773259
23	45	100.0	453	3	BQ315535	BQ315535
24	45	100.0	454	2	BG982031	BG982031
25	45	100.0	456	2	BF996980	BF996980
26	45	100.0	456	3	BQ332321	BQ332321
27	45	100.0	458	3	BQ366782	BQ366782
28	45	100.0	459	2	BG982034	BG982034
29	45	100.0	460	2	BF893150	BF893150
30	45	100.0	461	2	BG982012	BG982012
31	45	100.0	463	2	BF852788	BF852788
32	45	100.0	463	2	BF893919	BF893919
33	45	100.0	463	2	BF893919	BF893919
34	45	100.0	471	2	BF893924	BF893924
35	45	100.0	471	7	CR543841	CR543841
36	45	100.0	473	6	CB120234	CB120234
37	45	100.0	480	1	AT750554	AT750554
38	45	100.0	485	1	AA486032	AA486032
39	45	100.0	491	1	AU681912	AU681912
40	45	100.0	491	2	B1016235	B1016235
41	45	100.0	530	3	BM846221	BM846221
42	45	100.0	534	7	CN289921	CN289921
43	45	100.0	546	2	BG541031	BG541031
44	45	100.0	549	1	AM669835	AM669835
45	45	100.0	554	3	BP220985	BP220985
46	45	100.0	565	3	BP226620	BP226620
47	45	100.0	566	3	BP226508	BP226508
48	45	100.0	568	3	BP257211	BP257211
49	45	100.0	570	3	BM172060	BM172060
50	45	100.0	570	3	BP221518	BP221518
51	45	100.0	570	3	BP258309	BP258309
52	45	100.0	572	3	BP262485	BP262485
53	45	100.0	573	1	AU279894	AU279894
54	45	100.0	573	3	BP221260	BP221260
55	45	100.0	573	3	BP261500	BP261500
56	45	100.0	576	3	BP262542	BP262542
57	45	100.0	577	7	CN289919	CN289919
58	45	100.0	580	3	BP261787	BP261787
59	45	100.0	580	3	BP274368	BP274368
60	45	100.0	581	1	AV171253	AV171253
61	45	100.0	581	3	BP207751	BP207751
62	45	100.0	581	3	BP225088	BP225088
63	45	100.0	581	3	BP262101	BP262101
64	45	100.0	581	3	BP262638	BP262638
65	45	100.0	581	3	BP270744	BP270744
66	45	100.0	581	3	BP349936	BP349936
67	45	100.0	581	3	BP379659	BP379659
68	45	100.0	581	6	CB286391	CB286391
69	45	100.0	582	3	BM507091	BM507091
70	45	100.0	582	3	BP219740	BP219740
71	45	100.0	582	3	BP233592	BP233592
72	45	100.0	582	3	BP234218	BP234218
73	45	100.0	582	3	BP261141	BP261141
74	45	100.0	582	3	BP261789	BP261789
75	45	100.0	582	3	BP263516	BP263516
76	45	100.0	582	3	BP270415	BP270415
77	45	100.0	582	3	BP275810	BP275810
78	45	100.0	583	3	BP195721	BP195721
79	45	100.0	583	3	BP262103	BP262103
80	45	100.0	583	3	BP262741	BP262741

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81	45	100.0	583	3	BP319548	BP319548	154	45	100.0	1087	7	CN642527	CN642527
82	45	100.0	583	3	BP319548	BP319548	155	45	100.0	1089	11	DO049205	DO049205
83	45	100.0	584	3	BP263059	BP263059	156	45	100.0	1089	11	DO049206	DO049206
84	45	100.0	584	3	BP348623	BP348623	157	45	100.0	1090	7	DO049207	DO049207
85	45	100.0	588	3	BP236074	BP236074	158	45	100.0	1103	3	BM551041	BM551041
86	45	100.0	588	3	BP348796	BP348796	159	45	100.0	1103	3	BM551042	BM551042
87	45	100.0	602	1	AL703449	AL703449	160	45	100.0	1128	4	BM551043	BM551043
88	45	100.0	621	6	CB069952	CB069952	161	45	100.0	1132	4	BM551044	BM551044
89	45	100.0	626	2	CB069952	CB069952	162	45	100.0	1132	4	BM551045	BM551045
90	45	100.0	634	6	CB157906	CB157906	163	45	100.0	1132	4	BM551046	BM551046
91	45	100.0	634	7	CB023369	CB023369	164	45	100.0	1132	4	BM551047	BM551047
92	45	100.0	644	7	CB133830	CB133830	165	45	100.0	1132	4	BM551048	BM551048
93	45	100.0	648	6	CB764797	CB764797	166	45	100.0	1132	4	BM551049	BM551049
94	45	100.0	650	2	CB431303	CB431303	167	45	100.0	1132	4	BM551050	BM551050
95	45	100.0	657	7	CN298920	CN298920	168	45	100.0	1132	4	BM551051	BM551051
96	45	100.0	674	2	CN791432	CN791432	169	45	100.0	1132	4	BM551052	BM551052
97	45	100.0	678	2	CK952220	CK952220	170	45	100.0	1132	4	BM551053	BM551053
98	45	100.0	680	7	CK981492	CK981492	171	45	100.0	1132	4	BM551054	BM551054
99	45	100.0	683	7	CK981492	CK981492	172	45	100.0	1132	4	BM551055	BM551055
100	45	100.0	701	7	CK767236	CK767236	173	45	100.0	1132	4	BM551056	BM551056
101	45	100.0	704	3	BI334820	BI334820	174	45	100.0	1132	4	BM551057	BM551057
102	45	100.0	710	5	BU661472	BU661472	175	45	100.0	1132	4	BM551058	BM551058
103	45	100.0	710	5	BU661472	BU661472	176	45	100.0	1132	4	BM551059	BM551059
104	45	100.0	711	7	CN298922	CN298922	177	45	100.0	1132	4	BM551060	BM551060
105	45	100.0	729	7	CN298922	CN298922	178	45	100.0	1132	4	BM551061	BM551061
106	45	100.0	729	7	CN298922	CN298922	179	45	100.0	1132	4	BM551062	BM551062
107	45	100.0	731	8	CK760857	CK760857	180	45	100.0	1132	4	BM551063	BM551063
108	45	100.0	739	7	CR791801	CR791801	181	45	100.0	1132	4	BM551064	BM551064
109	45	100.0	749	7	CR767800	CR767800	182	45	100.0	1132	4	BM551065	BM551065
110	45	100.0	750	2	BI181461	BI181461	183	45	100.0	1132	4	BM551066	BM551066
111	45	100.0	751	2	BP243927	BP243927	184	45	100.0	1132	4	BM551067	BM551067
112	45	100.0	752	1	AUI39147	AUI39147	185	45	100.0	1132	4	BM551068	BM551068
113	45	100.0	757	3	BI760756	BI760756	186	45	100.0	1132	4	BM551069	BM551069
114	45	100.0	767	2	BI258848	BI258848	187	45	100.0	1132	4	BM551070	BM551070
115	45	100.0	770	2	BI258848	BI258848	188	45	100.0	1132	4	BM551071	BM551071
116	45	100.0	770	2	BI258848	BI258848	189	45	100.0	1132	4	BM551072	BM551072
117	45	100.0	774	3	BI258848	BI258848	190	45	100.0	1132	4	BM551073	BM551073
118	45	100.0	780	5	BI258848	BI258848	191	45	100.0	1132	4	BM551074	BM551074
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121	45	100.0	793	2	BI258848	BI258848	194	45	100.0	1132	4	BM551077	BM551077
122	45	100.0	798	8	BI258848	BI258848	195	45	100.0	1132	4	BM551078	BM551078
123	45	100.0	799	8	BI258848	BI258848	196	45	100.0	1132	4	BM551079	BM551079
124	45	100.0	838	8	BI258848	BI258848	197	45	100.0	1132	4	BM551080	BM551080
125	45	100.0	846	2	BI258848	BI258848	198	45	100.0	1132	4	BM551081	BM551081
126	45	100.0	852	7	BI258848	BI258848	199	45	100.0	1132	4	BM551082	BM551082
127	45	100.0	858	3	BI258848	BI258848	200	45	100.0	1132	4	BM551083	BM551083
128	45	100.0	870	5	BI258848	BI258848	201	45	100.0	1132	4	BM551084	BM551084
129	45	100.0	870	5	BI258848	BI258848	202	45	100.0	1132	4	BM551085	BM551085
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131	45	100.0	883	5	BI258848	BI258848	204	45	100.0	1132	4	BM551087	BM551087
132	45	100.0	883	5	BI258848	BI258848	205	45	100.0	1132	4	BM551088	BM551088
133	45	100.0	904	6	BI258848	BI258848	206	45	100.0	1132	4	BM551089	BM551089
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138	45	100.0	932	2	BI258848	BI258848	211	45	100.0	1132	4	BM551094	BM551094
139	45	100.0	932	2	BI258848	BI258848	212	45	100.0	1132	4	BM551095	BM551095
140	45	100.0	942	5	BI258848	BI258848	213	45	100.0	1132	4	BM551096	BM551096
141	45	100.0	942	5	BI258848	BI258848	214	45	100.0	1132	4	BM551097	BM551097
142	45	100.0	942	5	BI258848	BI258848	215	45	100.0	1132	4	BM551098	BM551098
143	45	100.0	952	2	BI258848	BI258848	216	45	100.0	1132	4	BM551099	BM551099
144	45	100.0	952	2	BI258848	BI258848	217	45	100.0	1132	4	BM551100	BM551100
145	45	100.0	952	2	BI258848	BI258848	218	45	100.0	1132	4	BM551101	BM551101
146	45	100.0	952	2	BI258848	BI258848	219	45	100.0	1132	4	BM551102	BM551102
147	45	100.0	952	2	BI258848	BI258848	220	45	100.0	1132	4	BM551103	BM551103
148	45	100.0	952	2	BI258848	BI258848	221	45	100.0	1132	4	BM551104	BM551104
149	45	100.0	952	2	BI258848	BI258848	222	45	100.0	1132	4	BM551105	BM551105
150	45	100.0	952	2	BI258848	BI258848	223	45	100.0	1132	4	BM551106	BM551106
151	45	100.0	952	2	BI258848	BI258848	224	45	100.0	1132	4	BM551107	BM551107
152	45	100.0	952	2	BI258848	BI258848	225	45	100.0	1132	4	BM551108	BM551108
153	45	100.0	952	2	BI258848	BI258848	226	45	100.0	1132	4	BM551109	BM551109

227	44	97.8	847	8	DR667246	JGI CABG9	C 300	39	86.7	478	3	BP702326
228	44	97.8	850	6	CR378639	AGENCOURT	C 301	39	86.7	509	5	BP068432
229	44	97.8	860	8	CA358090	JGI CAAX9	C 302	39	86.7	519	2	BP997052
230	44	97.8	866	8	CX843565	JGI CAAX1	C 303	39	86.7	522	1	AI532142
231	44	97.8	876	7	CK798287	AGENCOURT	C 304	39	86.7	625	6	CB190353
232	44	97.8	879	7	CK797649	AGENCOURT	C 305	39	86.7	632	7	CK974856
233	44	97.8	879	8	CX824886	JGI CAK4	C 306	39	86.7	636	5	BY177844
234	44	97.8	891	1	AL879624	AL879624	C 307	39	86.7	677	10	EX157564
235	44	97.8	894	1	BX776016	BX776016	C 308	39	86.7	743	10	AG015268
236	44	97.8	896	6	CA971409	AGENCOURT	C 309	39	86.7	751	10	AG015292
237	44	97.8	900	6	CA980929	AGENCOURT	C 310	39	86.7	754	10	AG015267
238	44	97.8	909	5	BX780455	BX780455	C 311	39	86.7	789	5	BX885044
239	44	97.8	909	6	CA982823	AGENCOURT	C 312	39	86.7	805	10	BX153274
240	44	97.8	919	6	CA973596	CA973596	C 313	39	86.7	811	5	BP907830
241	44	97.8	927	6	CA972288	AGENCOURT	C 314	39	86.7	985	10	CNS0143T
242	44	97.8	927	6	CA972607	AGENCOURT	C 315	38	84.4	347	7	BM590472
243	44	97.8	942	2	BG298330	BG298330	C 316	38	84.4	371	8	DN134037
244	44	97.8	946	5	BU468774	BU468774	C 317	38	84.4	375	1	ADJ52626
245	44	97.8	961	2	BU150788	BU150788	C 318	38	84.4	405	10	CL450896
246	44	97.8	963	3	B1556151	B1556151	C 319	38	84.4	464	7	CV395524
247	44	97.8	984	3	BX846715	BX846715	C 320	38	84.4	464	7	CV395537
248	44	97.8	1077	5	BU131072	BU131072	C 321	38	84.4	504	5	BM576902
249	44	97.8	1289	4	AK009089	AK009089	C 322	38	84.4	509	10	CG890538
250	42	93.3	467	3	BO329405	BO329405	C 323	38	84.4	515	5	BO533034
251	42	93.3	523	7	CK993108	CK993108	C 324	38	84.4	532	7	CK689578
252	42	93.3	532	6	CB387482	CB387482	C 325	38	84.4	532	10	BX652342
253	42	93.3	544	3	BQ142674	BQ142674	C 326	38	84.4	537	6	CF341430
254	42	93.3	711	8	DR407274	DR407274	C 327	38	84.4	537	6	BI747771
255	41	91.1	378	10	CG698498	CG698498	C 328	38	84.4	572	6	CF341423
256	41	91.1	385	1	AV655175	AV655175	C 329	38	84.4	575	6	CF244882
257	41	91.1	426	1	AL830731	AL830731	C 330	38	84.4	588	9	CG852793
258	41	91.1	517	11	DE122996	DE122996	C 331	38	84.4	593	6	CF248804
259	41	91.1	556	3	BM036121	BM036121	C 332	38	84.4	595	6	CF248904
260	41	91.1	581	3	AL727624	AL727624	C 333	38	84.4	604	6	CG800090
261	41	91.1	581	3	BP199948	BP199948	C 334	38	84.4	614	2	CG375256
262	41	91.1	628	1	BZ446884	BZ446884	C 335	38	84.4	725	5	BM7556081
263	41	91.1	633	1	AL725543	AL725543	C 336	38	84.4	752	9	CC533352
264	41	91.1	640	6	CB505136	CB505136	C 337	38	84.4	754	5	BU312770
265	41	91.1	644	3	BM660342	BM660342	C 338	38	84.4	760	7	CO137205
266	41	91.1	672	11	DE094838	DE094838	C 339	38	84.4	772	10	CL638755
267	41	91.1	675	1	AL722584	AL722584	C 340	38	84.4	784	9	CG844908
268	41	91.1	699	1	AL722490	AL722490	C 341	38	84.4	824	11	CR196544
269	41	91.1	718	4	CNS08551	CR639168	C 342	38	84.4	826	7	CO461752
270	41	91.1	735	9	BZ507313	BZ507313	C 343	38	84.4	856	9	BP376374
271	41	91.1	735	7	CV480860	CV480860	C 344	38	84.4	856	9	CR233535
272	41	91.1	736	5	BX306203	BX306203	C 345	38	84.4	881	9	CG2076268
273	41	91.1	811	7	CK693033	CK693033	C 346	38	84.4	926	9	CC138405
274	41	91.1	834	7	CO795546	CO795546	C 347	38	84.4	945	9	CC8664782
275	41	91.1	838	7	CV482470	CV482470	C 348	38	84.4	2580	10	CL947132
276	41	91.1	839	5	BX911124	BX911124	C 349	37	82.2	137	1	AL811593
277	41	91.1	842	8	DN597142	DN597142	C 350	37	82.2	151	9	AO666559
278	41	91.1	846	7	CN175478	CN175478	C 351	37	82.2	188	5	BP756411
279	41	91.1	857	7	CN017421	CN017421	C 352	37	82.2	203	6	CA926684
280	41	91.1	860	7	CO918949	CO918949	C 353	37	82.2	204	2	BI127808
281	41	91.1	1236	8	DN716145	DN716145	C 354	37	82.2	220	5	BU824493
282	40	88.9	266	5	C27290	C27290	C 355	37	82.2	222	6	CB803754
283	40	88.9	399	6	CD851570	CD851570	C 356	37	82.2	229	2	BU827440
284	40	88.9	409	8	CX104493	CX104493	C 357	37	82.2	256	5	BU827440
285	40	88.9	425	6	CB696073	CB696073	C 358	37	82.2	260	7	CO340036
286	40	88.9	514	7	CO652817	CO652817	C 359	37	82.2	261	5	BU888707
287	40	88.9	556	3	BP243301	BP243301	C 360	37	82.2	275	1	AA283964
288	40	88.9	577	1	AM664871	AM664871	C 361	37	82.2	301	1	AI165352
289	40	88.9	618	3	BU011279	BU011279	C 362	37	82.2	312	1	AI1488987
290	40	88.9	703	5	BY719852	BY719852	C 363	37	82.2	347	8	CK654106
291	40	88.9	706	8	CV995337	CV995337	C 364	37	82.2	355	2	BG130680
292	40	88.9	832	9	BH494823	BH494823	C 365	37	82.2	358	6	CF799956
293	40	88.9	847	9	BZ469664	BZ469664	C 366	37	82.2	377	5	BU834187
294	40	88.9	852	10	CL969573	CL969573	C 367	37	82.2	384	5	BU824338
295	40	88.9	853	11	CNS0335C	AL225705	C 368	37	82.2	402	5	BU823987
296	40	88.9	892	2	BE212652	BE212652	C 369	37	82.2	411	7	CO292885
297	40	88.9	932	10	CL482642	CL482642	C 370	37	82.2	411	7	CO292885
298	39	86.7	356	1	AI087839	AI087839	C 371	37	82.2	417	8	DN493640
299	39	86.7	473	9	BH752266	BH752266	C 372	37	82.2	421	7	CV251839

C 373	82.2	431	2	BQ353285	saB89601.	C 446	82.2	662	2	BF261175	BF261175	HVSMFE002
C 374	82.2	433	3	BQ253828	saB67509.	C 447	82.2	664	2	BF215618	BF215618	EST471464
C 375	82.2	445	8	H56475	YF87211.r1	C 448	82.2	676	1	AJ774552	AJ774552	EST4714552
C 376	82.2	444	5	BQ091671	BT575h1.y	C 449	82.2	675	7	CV704309	CV704309	URCPN01.0
C 377	82.2	451	8	DN350074	LIR3579-y0	C 450	82.2	679	11	DR33012T	DR33012T	Damo.Te
C 378	82.2	456	9	BQ216680	AZ916680	C 451	82.2	685	5	BF129483	BF129483	EST4751329
C 379	82.2	460	2	BQ350528	BT130528	C 452	82.2	694	8	DN692037	DN692037	P058B09
C 380	82.2	466	7	CN563757	LAf94P10.	C 453	82.2	695	5	DN692636	DN692636	ACAD-aa2b0
C 381	82.2	469	2	BT129291	BT129291	C 454	82.2	698	8	DN167342	DN167342	LTf.BM01F
C 382	82.2	477	5	BQ090431	BT129291	C 455	82.2	698	2	BE039444	BE039444	AC03P1.A
C 383	82.2	480	2	BQ315603	BT129291	C 456	82.2	700	7	CO085240	CO085240	GR.BM02E
C 384	82.2	481	3	BP892753	BP892753	C 457	82.2	703	8	CX169196	CX169196	AO5_69-59
C 385	82.2	483	3	BP878616	BP878616	C 458	82.2	712	2	BP124431	BP124431	EST470077
C 386	82.2	487	3	BP8789510	BP8789510	C 459	82.2	712	8	BR609556	BR609556	BB609556
C 387	82.2	488	3	BP891917	BP891917	C 460	82.2	714	10	CW346414	CW346414	104.849
C 388	82.2	489	8	CN878734	CN878734	C 461	82.2	717	10	CW369604	CW369604	f4B5001F
C 389	82.2	490	8	AL830794	AL830794	C 462	82.2	718	5	CE512714	CE512714	saB1001F
C 390	82.2	490	2	BT135001	BT135001	C 463	82.2	720	5	BQ126451	BQ126451	EST472097
C 391	82.2	494	2	BT135001	BT135001	C 464	82.2	720	5	BQ126451	BQ126451	EST472097
C 392	82.2	503	1	AVS550020	AVS550020	C 465	82.2	724	5	BQ126451	BQ126451	EST472097
C 393	82.2	503	1	AVS550020	AVS550020	C 466	82.2	724	5	BQ126451	BQ126451	EST472097
C 394	82.2	508	9	Z26047	Z26047	C 467	82.2	724	5	BQ126451	BQ126451	EST472097
C 395	82.2	512	7	CK117597	CK117597	C 468	82.2	724	9	CE1811437	CE1811437	LTfgr-gB8-
C 396	82.2	519	7	CO146735	CO146735	C 469	82.2	725	2	BQ129546	BQ129546	EST475132
C 397	82.2	522	1	AD259329	AD259329	C 470	82.2	726	2	BQ129546	BQ129546	EST475132
C 398	82.2	535	9	AD251495	AD251495	C 471	82.2	727	2	CE103084	CE103084	CSU-K34.1
C 399	82.2	536	6	CD570498	CD570498	C 472	82.2	731	2	BQ132750	BQ132750	EST465642
C 400	82.2	556	5	BU868577	BU868577	C 473	82.2	733	8	CX534651	CX534651	URCPN01.5
C 401	82.2	559	2	BU849836	BU849836	C 474	82.2	733	8	CX534651	CX534651	URCPN01.5
C 402	82.2	561	3	BQ233835	BQ233835	C 475	82.2	733	10	CV659563	CV659563	LTfgr-gB8-
C 403	82.2	562	1	AM282506	AM282506	C 476	82.2	736	7	CV659563	CV659563	LTfgr-gB8-
C 404	82.2	563	3	BT101646	BT101646	C 477	82.2	737	7	CF869745	CF869745	LTfgr-gB8-

C 373	82.2	43.1	2	BQ353285	saB89601.	C 446	82.2	66.2	2	BF261175		
C 374	82.2	43.3	3	BQ255828	saB67509.	C 447	82.2	66.4	2	BF215618		
C 375	82.2	44.5	8	H56475	YF87211.r1	C 448	82.2	67.6	1	AV774552		
C 376	82.2	44.4	5	BQ091671	BT75h10.Y	C 449	82.2	67.5	7	CUT704309		
C 377	82.2	45.1	8	DN350074	LIR3579-Y0	C 450	82.2	67.9	11	DR33D12T		
C 378	82.2	45.6	9	A2316680	4911.fd63	C 451	82.2	68.2	695	5	BU892037	
C 379	82.2	46.0	2	B1305028	G106P81Y	C 452	82.2	69.4	8	DN167342		
C 380	82.2	46.6	7	CN563757	LaF94P10.	C 453	82.2	69.5	8	DN162626		
C 381	82.2	46.9	2	BI129291	BI129291.G088P61Y	C 454	82.2	69.8	2	BE032522		
C 382	82.2	47.5	5	BQ090431	srT1c10.Y	C 455	82.2	69.8	2	BE032522		
C 383	82.2	48.0	2	BQ315603	saB82402.	C 456	82.2	70.0	7	CO085244		
C 384	82.2	48.1	3	BP892753	BP892753.BP893049	C 457	82.2	70.3	8	CX161916		
C 385	82.2	48.3	3	BP878616	BP878616.BP878616	C 458	82.2	71.2	2	CG124431		
C 386	82.2	48.7	3	BP891917	BP891917.saa64501.	C 459	82.2	71.2	2	BR609556		
C 387	82.2	48.8	3	BP891917	BP891917.BP891917	C 460	82.2	71.2	10	CM346414		
C 388	82.2	48.9	8	CN878734	LaF84006.	C 461	82.2	71.7	10	CM346414		
C 389	82.2	49.0	1	AI2830794	AI2830794.	C 462	82.2	71.8	5	CM322714		
C 390	82.2	49.4	2	BP315001	BP315001.saaB8401.	C 463	82.2	72.0	5	BM216451		
C 391	82.2	50.3	1	AY555002	AY555002.	C 464	82.2	72.0	5	BM216451		
C 392	82.2	50.3	1	AY555002	AY555002.	C 465	82.2	72.4	5	BM216451		
C 393	82.2	50.8	9	Z26047	Z26047.A11TTS319.Gr	C 466	82.2	72.4	5	BM216451		
C 394	82.2	51.2	7	CK117597	CK117597.215K03.PI	C 467	82.2	72.4	9	CE1811437		
C 395	82.2	51.9	3	CO146735	LaF94501.	C 468	82.2	72.5	2	BM216451		
C 396	82.2	52.1	1	AD259329	AD259329.BA7938117	C 469	82.2	72.6	2	BM216451		
C 397	82.2	53.5	9	AD2512495	AD2512495.LM0358105	C 470	82.2	72.7	2	BM216451		
C 398	82.2	53.6	6	CD5704998	CD5704998.kD68907.Y	C 471	82.2	73.1	2	CG130364		
C 399	82.2	55.6	5	BU868577	R033C04.P	C 472	82.2	73.2	2	CG132750		
C 400	82.2	55.9	2	BM449636	BM449636.BST361274	C 473	82.2	73.3	8	CX343651		
C 401	82.2	56.1	3	BQ233835	BQ233835.saaB1508.	C 474	82.2	73.7	7	CM359563		
C 402	82.2	56.2	1	AM228506	AM228506.BST337294	C 475	82.2	73.7	10	CM359563		
C 403	82.2	56.3	3	BI701646	BI701646.saaB18605.	C 476	82.2	73.6	7	CM359563		
C 404	82.2	56.5	7	CM366460	LaF93C09.	C 477	82.2	73.8	7	CF869745		
C 405	82.2	56.9	6	CG336144	CG336144.saaB58C07.	C 478	82.2	74.1	2	BG110831		
C 406	82.2	57.0	3	CG336144	CG336144.saaB58C07.	C 479	82.2	75.0	2	BG110831		
C 407	82.2	57.2	1	AM093325	AM093325.BST287105	C 480	82.2	75.4	6	CF228812		
C 408	82.2	57.2	7	COB31168	COB31168.LM.GB5..01	C 481	82.2	75.5	10	CL635161		
C 409	82.2	57.2	8	DN249274	ACAE-saa5	C 482	82.2	75.6	5	BX852008		
C 410	82.2	58.0	3	BM503555	BM503555.lh33e07.Y	C 483	82.2	77.2	8	DN168831		
C 411	82.2	58.0	4	AC0647578	ArabiIdophs	C 484	82.2	77.6	7	DN168831		
C 412	82.2	58.2	5	BM503555	BM503555.lh33e07.Y	C 485	82.2	77.6	7	DN168831		
C 413	82.2	58.2	5	BM503555	BM503555.lh33e07.Y	C 486	82.2	77.6	7	DN168831		
C 414	82.2	58.3	8	CX560482	YdP41H03.	C 487	82.2	77.8	11	CR039405		
C 415	82.2	58.3	8	CX560482	YdP41H03.	C 488	82.2	79.3	8	DN168830		
C 416	82.2	59.0	3	BQ252684	saB795C10.	C 489	82.2	79.4	8	DR191652		
C 417	82.2	59.3	3	BQ252684	saB795C10.	C 490	82.2	79.5	6	CB899892		
C 418	82.2	59.6	7	CK118498	216017.PI	C 491	82.2	80.1	8	DN859228		
C 419	82.2	59.8	2	BF114159	EST741749	C 492	82.2	80.4	8	BZ806951		
C 420	82.2	59.9	10	CZ363904	ZNM8P0142	C 493	82.2	81.4	3	B1956553		
C 421	82.2	60.3	3	BM585349	BM585349	C 494	82.2	81.6	10	BX245167		
C 422	82.2	60.3	8	DN241671	ACAD-saa9	C 495	82.2	81.7	2	BF268078		
C 423	82.2	60.3	9	CC099748	CSU-K34.1	C 496	82.2	81.7	9	CC100686		
C 424	82.2	60.5	2	BG129668	EST475344	C 497	82.2	82.2	881	6	DN302362	
C 425	82.2	60.7	7	CK119198	213123.PI	C 498	82.2	82.2	891	6	DN300419	
C 426	82.2	60.8	5	BU825269	UKI05TG08	C 499	82.2	82.2	897	6	CD302839	
C 427	82.2	61.0	8	DN248317	ACAE-saa3	C 500	82.2	82.2	897	10	CZ499474	
C 428	82.2	61.5	3	BI435551	EST538312	C 501	82.2	92.4	6	CA974929		
C 429	82.2	61.5	5	BM589974	BM589974	C 502	82.2	92.5	9	CC094149		
C 430	82.2	61.9	3	BQ297857	saB94d08.	C 503	82.2	93.6	5	BY708937		
C 431	82.2	62.0	5	BM578161	BM578161	C 504	82.2	93.8	4	CNS0A4KZ		
C 432	82.2	62.0	10	CM140305	104.530.1	C 505	82.2	93.8	4	CM1071941		
C 433	82.2	62.2	3	BI204065	EST522105	C 506	82.2	99.8	10	CL0719168		
C 434	82.2	62.2	3	BI292946	EST549135	C 507	82.2	104.6	6	CA976386		
C 435	82.2	62.3	3	BP561437	BP561437	C 508	82.2	104.6	6	CA976386		
C 436	82.2	62.6	8	CX634728	LaJ43EF09.	C 509	82.2	104.6	6	CA976386		
C 437	82.2	62.6	10	CX634728	LaJ43EF09.	C 510	82.2	104.6	6	CA976386		
C 438	82.2	62.8	1	AI782798	EST63677	C 511	82.2	104.6	6	CA976386		
C 439	82.2	62.8	1	AI782798	EST63677	C 512	82.2	104.6	6	CA976386		
C 440	82.2	63.1	3	BU066897	KS07019D1	C 513	82.2	104.6	6	CA976386		
C 441	82.2	64.0	5	BU068585	ML17F12.P	C 514	82.2	104.6	6	CA976386		
C 442	82.2	64.7	3	BU003259	BU003259	C 515	82.2	104.6	6	CA976386		
C 443	82.2	65.8	1	AM219075	EST301557	C 516	82.2	104.6	6	CA976386		
C 444	82.2	65.8	9	ACQ43484	Sheared.D	C 517	82.2	104.6	6	CA976386		
C 445	82.2	65.9	8	DR121694	49189910	C 518	82.2	104.6	6	CA976386		
C 446	82.2	65.9	8	DR121694	49189910	C 519	82.2	104.6	6	CA976386		
C 447	82.2	65.9	8	DR121694	49189910	C 520	82.2	104.6	6	CA976386		
C 448	82.2	65.9	8	DR121694	49189910	C 521	82.2	104.6	6	CA976386		
C 449	82.2	65.9	8	DR121694	49189910	C 522	82.2	104.6	6	CA976386		
C 450	82.2	65.9	8	DR121694	49189910	C 523	82.2	104.6	6	CA976386		
C 451	82.2	65.9	8	DR121694	49189910	C 524	82.2	104.6	6	CA976386		
C 452	82.2	65.9	8	DR121694	49189910	C 525	82.2	104.6	6	CA976386		
C 453	82.2	65.9	8	DR121694	49189910	C 526	82.2	104.6	6	CA976386		
C 454	82.2	65.9	8	DR121694	49189910	C 527	82.2	104.6	6	CA976386		
C 455	82.2	65.9	8	DR121694	49189910	C 528	82.2	104.6	6	CA976386		
C 456	82.2	65.9	8	DR121694	49189910	C 529	82.2	104.6	6	CA976386		
C 457	82.2	65.9	8	DR121694	49189910	C 530	82.2	104.6	6	CA976386		
C 458	82.2	65.9	8	DR121694	49189910	C 531	82.2	104.6	6	CA976386		
C 459	82.2	65.9	8	DR121694	49189910	C 532	82.2	104.6	6	CA976386		
C 460	82.2	65.9	8	DR121694	49189910	C 533	82.2	104.6	6	CA976386		
C 461	82.2	65.9	8	DR121694	49189910	C 534	82.2	104.6	6	CA976386		
C 462	82.2	65.9	8	DR121694	49189910	C 535	82.2	104.6	6	CA976386		
C 463	82.2	65.9	8	DR121694	49189910	C 536	82.2	104.6	6	CA976386		
C 464	82.2	65.9	8	DR121694	49189910	C 537	82.2	104.6	6	CA976386		
C 465	82.2	65.9	8	DR121694	49189910	C 538	82.2	104.6	6	CA976386		
C 466	82.2	65.9	8	DR121694	49189910	C 539	82.2	104.6	6	CA976386		
C 467	82.2	65.9	8	DR121694	49189910	C 540	82.2	104.6	6	CA976386		
C 468	82.2	65.9	8	DR121694	49189910	C 541	82.2	104.6	6	CA976386		
C 469	82.2	65.9	8	DR121694	49189910	C 542	82.2	104.6	6	CA976386		
C 470	82.2	65.9	8	DR121694	49189910	C 543	82.2	104.6	6	CA976386		
C 471	82.2	65.9	8	DR121694	49189910	C 544	82.2	104.6	6	CA976386		
C 472	82.2	65.9	8	DR121694	49189910	C 545	82.2	104.6	6	CA976386		
C 473	82.2	65.9	8	DR121694	49189910	C 546	82.2	104.6	6	CA976386		
C 474	82.2	65.9	8	DR121694	49189910	C 547	82.2	104.6	6	CA976386		
C 475	82.2	65.9	8	DR121694	49189910	C 548	82.2	104.6	6	CA976386		
C 476	82.2	65.9	8	DR121694	49189910	C 549	82.2	104.6	6	CA976386		
C 477	82.2	65.9	8	DR121694	49189910	C 550	82.2	104.6	6	CA976386		
C 478	82.2	65.9	8	DR121694	49189910	C 551	82.2	104.6	6	CA976386		
C 479	82.2	65.9	8	DR121694	49189910	C 552	82.2	104.6	6	CA976386		
C 480	82.2	65.9	8	DR121694	49189910	C 553	82.2	104.6	6	CA976386		
C 481	82.2	65.9	8	DR121694	49189910	C 554	82.2	104.6	6	CA976386		
C 482	82.2	65.9	8	DR121694	49189910	C 555	82.2	1				

C 519	36	80.0	351	5	BU431751	BU431751	UT-HF-BNO	592	36	80.0	519	7	CN114991	CN114991
C 520	36	80.0	354	7	CO270062	CO270062	EK097260	593	36	80.0	519	9	A2433235	A2433235
C 521	36	80.0	356	8	CM603106	CM603106	CT02034B1	594	36	80.0	520	7	CR744847	CR744847
C 522	36	80.0	369	7	CN108604	CN108604	EC2CA32B	595	36	80.0	521	7	CN101773	CN101773
C 523	36	80.0	370	9	AO243158	AO243158	HS 2055 B	522	36	80.0	522	7	CN119290	EC0CA001
C 524	36	80.0	370	7	CN106316	CN106316	EC2CA25B	596	36	80.0	522	7	CV245242	CV245242
C 525	36	80.0	370	7	CN110426	CN110426	EC2CA35B	598	36	80.0	523	7	CN101772	CN101772
C 526	36	80.0	376	9	CC082877	CC082877	CSU-K331	599	36	80.0	525	2	BE882216	BE882216
C 527	36	80.0	381	3	BP735561	BP735561	BP735561	600	36	80.0	526	2	BE458767	BE458767
C 528	36	80.0	382	7	CN105590	CN105590	EC2CA27D	601	36	80.0	527	2	BE458767	EC2CA4059
C 529	36	80.0	383	7	CN088799	CN088799	EC2BBA30C	602	36	80.0	527	2	CN120477	CN120477
C 530	36	80.0	387	3	BM141271	BM141271	ZFT134 Zg	603	36	80.0	527	8	DNS00268	UK127G02
C 531	36	80.0	390	7	BC405082	BC405082	sac41h10	604	36	80.0	528	1	A1545991	A1545991
C 532	36	80.0	391	7	CO994884	CO994884	UWC-Pd12	605	36	80.0	531	7	CN106089	CN106089
C 533	36	80.0	398	6	CB707016	CB707016	AMGNNUC:S	606	36	80.0	532	7	CN104368	EC2CA25D
C 534	36	80.0	401	1	AA213791	AA213791	zr1D02.s	607	36	80.0	532	8	DN487008	P081D05.3
C 535	36	80.0	401	9	AO830829	AO830829	HS 5497 A	608	36	80.0	533	7	CN105095	CN105095
C 536	36	80.0	401	9	AO904317	AO904317	G8STC010	609	36	80.0	534	5	BU827139	BU827139
C 537	36	80.0	401	9	AZ050607	AZ050607	G8STC1145	610	36	80.0	536	7	CN114422	CN114422
C 538	36	80.0	405	7	CN109181	CN109181	EC2CA33B	611	36	80.0	537	9	CE016806	CE016806
C 539	36	80.0	406	6	CB807515	CB807515	AMGNNUC:N	612	36	80.0	538	1	AL927623	AL927623
C 540	36	80.0	407	7	CN115490	CN115490	EC2CA42D	613	36	80.0	538	7	CN114292	EC2CA40D
C 541	36	80.0	408	3	BP925500	BP925500	BP925500	614	36	80.0	538	7	CN118309	CN118309
C 542	36	80.0	409	7	CO270066	CO270066	EK097304	615	36	80.0	539	7	CR928469	CR928469
C 543	36	80.0	412	5	BO618684	BO618684	fah06f08	616	36	80.0	540	9	AO877860	HS 2152 B
C 544	36	80.0	412	6	CB801707	CB801707	AMGNNUC:S	617	36	80.0	544	7	CN181810	CN181810
C 545	36	80.0	414	5	BO617903	BO617903	Ia81912	618	36	80.0	545	7	CN087170	EC2BBA28B
C 546	36	80.0	416	1	A1779915	A1779915	EST260794	619	36	80.0	549	1	AM621780	AM621780
C 547	36	80.0	416	6	CB767746	CB767746	AMGNNUC:N	620	36	80.0	549	7	CN095858	CN095858
C 548	36	80.0	423	1	A1190894	A1190894	q661e06.x	621	36	80.0	550	3	BM529016	BM529016
C 549	36	80.0	423	7	CN115491	CN115491	EC2CA44D	622	36	80.0	550	7	CN119801	CN119801
C 550	36	80.0	425	1	A1497291	A1497291	fb63f11.y	623	36	80.0	550	7	CN119858	EC0CA002
C 551	36	80.0	425	3	BI809535	BI809535	F01P09 O	624	36	80.0	552	6	CA953478	CA953478
C 552	36	80.0	426	9	AO444341	AO444341	G8STC0321	625	36	80.0	552	8	DT055486	AGENCOURT
C 553	36	80.0	429	3	BI433060	BI433060	EST535821	626	36	80.0	554	2	BE995683	EST41406
C 554	36	80.0	431	2	BG135185	BG135185	EST468077	627	36	80.0	554	7	CN095872	EC2CA10C
C 555	36	80.0	432	9	AO458488	AO458488	HS 5061 A	628	36	80.0	557	7	CR432620	CR432620
C 556	36	80.0	433	6	CB759611	CB759611	AMGNNUC:N	629	36	80.0	558	2	BE354465	EST355808
C 557	36	80.0	435	1	AW811331	AW811331	IL3-ST014	630	36	80.0	558	8	BO597729	MI-P-A2-a
C 558	36	80.0	439	1	AL915855	AL915855	AL915855	631	36	80.0	558	8	CX388765	JGI X2T37
C 559	36	80.0	446	8	DN492103	DN492103	V046H08.3	632	36	80.0	559	5	BK706546	BK706546
C 560	36	80.0	447	3	BI882955	BI882955	fn01c06.x	633	36	80.0	559	7	CN108095	EC2CA31B
C 561	36	80.0	447	7	CN074221	CN074221	EC0CBA004	634	36	80.0	560	1	A1497360	A1497360
C 562	36	80.0	449	8	T96423	T96423	ye34g05.sl	635	36	80.0	560	7	BU525099	BU525099
C 563	36	80.0	451	1	A1023586	A1023586	CV80a02.s	636	36	80.0	560	3	CN082174	EC2BBA20C
C 564	36	80.0	453	8	DR875341	DR875341	JGI CABH1	637	36	80.0	561	1	AL965676	AL965676
C 565	36	80.0	454	11	DE037146	DE037146	Branchios	638	36	80.0	564	7	CN074222	EC0CBA004
C 566	36	80.0	460	6	CB737454	CB737454	AMGNNUC:N	639	36	80.0	564	8	DT093242	JGI ANNN5
C 567	36	80.0	463	11	DE136921	DE136921	Oryziab1	640	36	80.0	564	8	DX925854	DX925854
C 568	36	80.0	465	9	CC841879	CC841879	NDL.17N12	641	36	80.0	566	5	BE354465	BE354465
C 569	36	80.0	470	7	CN106425	CN106425	EC2CA23C	642	36	80.0	566	8	DR896168	DR896168
C 570	36	80.0	471	8	DR875342	DR875342	JGI CABH1	643	36	80.0	567	7	CN105157	EC2CA27A
C 571	36	80.0	475	2	BE558057	BE558057	fl1Be02.y	644	36	80.0	567	7	CN105307	EC2CA27B
C 572	36	80.0	476	5	BO858578	BO858578	OGC10K08	645	36	80.0	568	3	BM529516	BM529516
C 573	36	80.0	477	1	BP903498	BP903498	BP903498	646	36	80.0	570	6	CE188859	CE188859
C 574	36	80.0	479	1	AJ457525	AJ457525	V046H08 P	647	36	80.0	571	3	BU002196	BU002196
C 575	36	80.0	479	5	BU878410	BU878410	EC2CA42A	648	36	80.0	571	6	CD015852	hac23c06
C 576	36	80.0	483	2	CN114992	CN114992	fd53a08.y	649	36	80.0	572	6	BU529214	BU529214
C 577	36	80.0	491	2	BF717871	BF717871	MI-P-A2-a	650	36	80.0	573	7	CN099377	EC2CA16A
C 578	36	80.0	491	5	BO597720	BO597720	T095E10 P	651	36	80.0	575	7	CN082175	EC2BBA20C
C 579	36	80.0	491	5	BU837167	BU837167	UK11TG02	652	36	80.0	576	7	CR432621	CR432621
C 580	36	80.0	492	8	DN490285	DN490285	EST300711	653	36	80.0	577	8	CX780714	AGENCOURT
C 581	36	80.0	495	1	AM223900	AM223900	EC2CA25D	654	36	80.0	577	7	CN106426	EC2CA29C
C 582	36	80.0	497	7	CN104369	CN104369	EC2CA25D	655	36	80.0	580	3	BM532980	BM532980
C 583	36	80.0	500	5	BM116268	BM116268	EC2CA27B	656	36	80.0	580	7	CN104227	CN104227
C 584	36	80.0	500	5	CN105306	CN105306	EST618009	657	36	80.0	581	6	CE102943	hac39f08
C 585	36	80.0	503	5	BO510594	BO510594	z848a07.s	658	36	80.0	581	6	CN093672	CN093672
C 586	36	80.0	504	1	AA290567	AA290567	EX114109	659	36	80.0	583	1	AM595479	AM595479
C 587	36	80.0	511	7	CO274429	CO274429	OSTF173E1	660	36	80.0	584	1	CN099878	EC2CA16D
C 588	36	80.0	512	6	CB400312	CB400312	HS 5358 A	661	36	80.0	585	1	AJ656696	AJ656696
C 589	36	80.0	516	9	AO691311	AO691311	EC2CA16A	662	36	80.0	585	7	CN084599	EC2BBA24B
C 590	36	80.0	519	7	CN099376	CN099376	EC2CA16A	663	36	80.0	585	7	CN084599	EC2BBA24B
C 591	36	80.0	519	7	CN105156	CN105156	EC2CA27A	664	36	80.0	585	7	CN084599	EC2BBA24B

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665	36	80.0	586	8	CX694439	CX694439	YdC9aMOc.	C 738	36	80.0	663	5	BM318781	BM318781
C 666	36	80.0	587	1	AI781459	AI781459	EST262338	C 739	36	80.0	665	5	BM213645	BM213645
C 667	36	80.0	587	1	BM112051	BM112051	EST559587	C 740	36	80.0	665	5	BM213965	BM213965
C 668	36	80.0	588	9	CN087111	CN087111	EC2BBA28B	C 741	36	80.0	667	2	AV264817	AV264817
C 669	36	80.0	589	9	BH656435	BH656435	BOMWV377F	C 742	36	80.0	669	2	BE205098	BE205098
C 670	36	80.0	589	10	CE8442861	CE8442861	C1gr-988-	C 743	36	80.0	671	10	AG127133	AG127133
C 671	36	80.0	590	10	CN091358	CN091358	EC2BBA34D	C 744	36	80.0	672	7	CN83757	CN83757
C 672	36	80.0	592	3	BP362058	BP362058	BP362058	C 745	36	80.0	674	5	BOC03230	BOC03230
C 673	36	80.0	594	7	CN106317	CN106317	EC2CA29B	C 746	36	80.0	675	5	BM240966	BM240966
C 674	36	80.0	595	1	AV957991	AV957991	AV957991	C 747	36	80.0	676	5	BM244963	BM244963
C 675	36	80.0	595	7	CN108605	CN108605	EC2CA32B	C 748	36	80.0	678	3	BU001063	BU001063
C 676	36	80.0	596	9	BZ206854	BZ206854	CH230-526	C 749	36	80.0	680	7	CK116164	CK116164
C 677	36	80.0	597	1	AL630355	AL630355	AL630355	C 750	36	80.0	684	5	BM213933	BM213933
C 678	36	80.0	597	5	BO615424	BO615424	1aB26c08.	C 751	36	80.0	685	9	BZ000604	BZ000604
C 679	36	80.0	598	6	CA779231	CA779231	CA779231	C 752	36	80.0	686	9	CC958715	CC958715
C 680	36	80.0	598	6	CB582935	CB582935	CB582935	C 753	36	80.0	688	1	AM256622	AM256622
C 681	36	80.0	598	10	CZ188860	CZ188860	OA_BBA011	C 754	36	80.0	688	5	BM266391	BM266391
C 682	36	80.0	599	1	AM594942	AM594942	IK26F12.Y	C 755	36	80.0	688	7	CO132929	CO132929
C 683	36	80.0	600	3	BI990895	BI990895	4082-64.M	C 756	36	80.0	690	8	CK643472	CK643472
C 684	36	80.0	600	6	CB582552	CB582552	AMGNNUC:N	C 757	36	80.0	690	8	DN899099	DN899099
C 685	36	80.0	600	7	CN118939	CN118939	EC2CA9BG	C 758	36	80.0	690	8	BZ006739	BZ006739
C 686	36	80.0	601	1	AL676115	AL676115	AL676115	C 759	36	80.0	692	5	BM689563	BM689563
C 687	36	80.0	602	9	BZ459560	BZ459560	BONPU68TF	C 760	36	80.0	692	10	CL441074	CL441074
C 688	36	80.0	604	5	BX706547	BX706547	EC2CA32D	C 761	36	80.0	694	8	BZ519703	BZ519703
C 689	36	80.0	604	9	BZ428721	BZ428721	BONEB60TR	C 762	36	80.0	696	8	DT059997	DT059997
C 690	36	80.0	605	2	BE942386	BE942386	EST421965	C 763	36	80.0	696	9	BH755521	BH755521
C 691	36	80.0	605	6	CB581627	CB581627	AMGNNUC:N	C 764	36	80.0	697	9	AZ098153	AZ098153
C 692	36	80.0	606	6	CB581271	CB581271	AMGNNUC:N	C 765	36	80.0	698	10	CM546663	CM546663
C 693	36	80.0	606	6	CF102947	CF102947	hac39f12.	C 766	36	80.0	701	1	AM584642	AM584642
C 694	36	80.0	606	6	CV990651	CV990651	IPCGFrl.4	C 767	36	80.0	702	3	BM213466	BM213466
C 695	36	80.0	606	9	AO670292	AO670292	HS_5389.B	C 768	36	80.0	703	5	BZ519418	BZ519418
C 696	36	80.0	607	9	BH439596	BH439596	BOGQ32TR	C 769	36	80.0	704	8	CK358689	CK358689
C 697	36	80.0	608	8	CX780443	CX780443	AGENCOURT	C 770	36	80.0	704	9	DR403106	DR403106
C 698	36	80.0	608	10	CE327594	CE327594	C1gr-988-	C 771	36	80.0	704	9	BH793753	BH793753
C 699	36	80.0	609	3	BI206117	BI206117	EST524157	C 772	36	80.0	704	9	BH119975	BH119975
C 700	36	80.0	609	3	BZ518923	BZ518923	BM284683	C 773	36	80.0	706	8	DR398845	DR398845
C 701	36	80.0	610	5	BM284683	BM284683	EC2CA10C	C 774	36	80.0	711	9	BM460979	BM460979
C 702	36	80.0	611	7	CN058589	CN058589	EC2CA10C	C 775	36	80.0	711	10	CE344241	CE344241
C 703	36	80.0	612	6	CB472985	CB472985	rm63.B02.	C 776	36	80.0	713	1	AM687479	AM687479
C 704	36	80.0	613	7	CN0585873	CN0585873	EC2CA10C	C 777	36	80.0	714	9	BZ017165	BZ017165
C 705	36	80.0	613	7	CN109182	CN109182	EC2CA33B	C 778	36	80.0	715	2	BG127881	BG127881
C 706	36	80.0	615	10	CG158686	CG158686	FUIBQ78TB	C 779	36	80.0	719	9	CC087525	CC087525
C 707	36	80.0	617	7	CN076601	CN076601	EC2BBA12A	C 780	36	80.0	729	3	BM407961	BM407961
C 708	36	80.0	617	7	CN118310	CN118310	EC2CA5BB	C 781	36	80.0	730	6	CB230219	CB230219
C 709	36	80.0	621	9	AZ964314	AZ964314	2M02330C3	C 782	36	80.0	730	6	CK142645	CK142645
C 710	36	80.0	622	7	CN053673	CN053673	EC2BBA8CB	C 783	36	80.0	730	11	DE106380	DE106380
C 711	36	80.0	625	3	BZ523935	BZ523935	EC2BBA24B	C 784	36	80.0	732	5	BU357601	BU357601
C 712	36	80.0	625	3	CN084600	CN084600	Oryziae	C 785	36	80.0	732	7	CK029504	CK029504
C 713	36	80.0	625	11	DE077612	DE077612	Oryziae	C 786	36	80.0	732	7	CK029504	CK029504
C 714	36	80.0	626	8	DN649064	DN649064	G6709..69	C 787	36	80.0	740	8	DN172096	DN172096
C 715	36	80.0	627	8	CN082302	CN082302	EC2BBA20D	C 788	36	80.0	744	7	CKR69681	CKR69681
C 716	36	80.0	629	7	CN102763	CN102763	EC2CA20B	C 789	36	80.0	745	8	DN633827	DN633827
C 717	36	80.0	630	7	CN108096	CN108096	EC2CA31B	C 790	36	80.0	752	5	BU345436	BU345436
C 718	36	80.0	630	7	CN100544	CN100544	EC2CA17D	C 791	36	80.0	752	9	BM334733	BM334733
C 719	36	80.0	633	3	BZ520612	BZ520612	CN118295	C 792	36	80.0	752	10	AG484711	AG484711
C 720	36	80.0	634	3	CR284334	CR284334	CR284334	C 793	36	80.0	754	7	CK025268	CK025268
C 721	36	80.0	635	7	CX362343	CX362343	JGI_XZT42	C 794	36	80.0	754	10	CM546932	CM546932
C 722	36	80.0	637	8	BM341041	BM341041	Oryziae	C 795	36	80.0	756	7	CV239322	CV239322
C 723	36	80.0	641	5	DE084868	DE084868	Oryziae	C 796	36	80.0	756	7	AG591785	AG591785
C 724	36	80.0	644	11	AM128739	AM128739	f636h01.Y	C 797	36	80.0	757	10	BM452545	BM452545
C 725	36	80.0	644	11	BM655036	BM655036	BO1BM18TF	C 798	36	80.0	763	8	DN632536	DN632536
C 726	36	80.0	650	2	CC943865	CC943865	NDL.131H1	C 799	36	80.0	765	10	AG536094	AG536094
C 727	36	80.0	650	2	CC874266	CC874266	NDL.131H1	C 800	36	80.0	765	10	CJ179586	CJ179586
C 728	36	80.0	651	9	AL899320	AL899320	AI899320	C 801	36	80.0	766	7	CO927591	CO927591
C 729	36	80.0	652	1	CR755214	CR755214	DMFZ468T	C 802	36	80.0	766	7	BM668902	BM668902
C 730	36	80.0	655	1	AM686411	AM686411	NFO37FI2N	C 803	36	80.0	767	9	CK970326	CK970326
C 731	36	80.0	655	1	BM406368	BM406368	EST580791	C 804	36	80.0	767	9	BZ520070	BZ520070
C 732	36	80.0	659	3	BM0598198	BM0598198	MT-P-E3-a	C 805	36	80.0	769	8	DN769703	DN769703
C 733	36	80.0	660	7	CO080078	CO080078	GR_BA43E	C 806	36	80.0	770	8	DN635674	DN635674
C 734	36	80.0	663	5	BM214540	BM214540		C 807	36	80.0	771	8	DN771972	DN771972
C 735	36	80.0						C 808	36	80.0	771	8	DN771972	DN771972
C 736	36	80.0						C 809	36	80.0	772	3	BI691494	BI691494
C 737	36	80.0						C 810	36	80.0	772	3	BI691494	BI691494

C 811	36	80.0	774	4	CN6093XT	CR708901 Tetradon	C 884	36	80.0	892	9	CC003651	CC003651 PUD633TD
C 812	36	80.0	774	9	B2061928	B2061928 1Jq72905	C 885	36	80.0	895	10	CG958396	CG958396 MBEDJ02TR
C 813	36	80.0	775	8	DN834001	DN834001 AGENCOURT	C 886	36	80.0	896	2	BG179307	BG179307 602331027
C 814	36	80.0	776	8	DN766133	DN766133 AGENCOURT	C 887	36	80.0	896	7	CO915165	CO915165 AGENCOURT
C 815	36	80.0	778	3	BH557483	BH557483 BOGJUT58TR	C 888	36	80.0	897	7	CN832588	CN832588 AGENCOURT
C 816	36	80.0	780	3	BI908127	BI908127 603067423	C 889	36	80.0	917	10	CG205672	CG205672 PUFUF74TD
C 817	36	80.0	780	7	CV486862	CV486862 AGENCOURT	C 890	36	80.0	918	10	C2939052	C2939052 259193 To
C 818	36	80.0	782	8	DN765964	DN765964 AGENCOURT	C 891	36	80.0	924	7	CK176696	CK176696 EST766016
C 819	36	80.0	782	8	DN767167	DN767167 AGENCOURT	C 892	36	80.0	924	8	DN836260	DN836260 AGENCOURT
C 820	36	80.0	783	8	DN764812	DN764812 AGENCOURT	C 893	36	80.0	930	6	CF265987	CF265987 AGENCOURT
C 821	36	80.0	783	8	DN833932	DN833932 AGENCOURT	C 894	36	80.0	932	7	CK865572	CK865572 AGENCOURT
C 822	36	80.0	784	1	AM004353	AM004353 AGENCOURT	C 895	36	80.0	934	7	CK285610	CK285610 EST748332
C 823	36	80.0	785	2	BG588660	BG588660 EST490469	C 896	36	80.0	934	7	CK870860	CK870860 AGENCOURT
C 824	36	80.0	786	8	DN956036	DN956036 AGENCOURT	C 897	36	80.0	940	7	CK866313	CK866313 AGENCOURT
C 825	36	80.0	787	8	DN768395	DN768395 AGENCOURT	C 898	36	80.0	941	7	CK869539	CK869539 AGENCOURT
C 826	36	80.0	788	8	DN768957	DN768957 AGENCOURT	C 899	36	80.0	942	7	CN024895	CN024895 AGENCOURT
C 827	36	80.0	788	8	DN770073	DN770073 AGENCOURT	C 900	36	80.0	942	9	CC123294	CC123294 ND1.81F18
C 828	36	80.0	789	8	DN771600	DN771600 AGENCOURT	C 901	36	80.0	944	5	BU162006	BU162006 AGENCOURT
C 829	36	80.0	790	8	DN770937	DN770937 AGENCOURT	C 902	36	80.0	947	7	CK865531	CK865531 AGENCOURT
C 830	36	80.0	791	8	DN860832	DN860832 Tab15a08	C 903	36	80.0	949	10	CK929232	CK929232 EDCBV70TR
C 831	36	80.0	792	8	DN832561	DN832561 AGENCOURT	C 904	36	80.0	952	7	CK284495	CK284495 EST747217
C 832	36	80.0	793	2	BG581983	BG581983 EST483720	C 905	36	80.0	982	11	CNS05561	AL351442 Tetradon
C 833	36	80.0	797	8	CV480774	CV480774 AGENCOURT	C 906	36	80.0	1004	3	BM802261	BM802261 AGENCOURT
C 834	36	80.0	797	8	DN765186	DN765186 AGENCOURT	C 907	36	80.0	1028	10	CNS0272R	AL184140 Tetradon
C 835	36	80.0	798	8	CK428111	CK428111 JGI XZG18	C 908	36	80.0	1039	11	CNS078KL	AL184107 T3 end of
C 836	36	80.0	801	8	DN770486	DN770486 AGENCOURT	C 909	36	80.0	1050	11	CNS079YX	AL13519 T7 end of
C 837	36	80.0	803	8	DN766957	DN766957 AGENCOURT	C 910	36	80.0	1052	10	CG698922	CG698922 ZMMBC011
C 838	36	80.0	810	9	BH489742	BH489742 BOGL284TR	C 911	36	80.0	1092	3	BM464240	BM464240 AGENCOURT
C 839	36	80.0	811	9	BH681250	BH681250 BOHT20TR	C 912	36	80.0	1101	3	CK025645	CK025645 AGENCOURT
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C 841	36	80.0	814	9	CK705054	CK705054 ZF101-P00	C 914	36	80.0	1249	8	DN654269	DN654269 CEC10-B09
C 842	36	80.0	814	9	BH583793	BH583793 BOGSA46TR	C 915	36	80.0	1376	8	DN674916	DN674916 CFW83-DO1
C 843	36	80.0	816	8	DN772216	DN772216 AGENCOURT	C 916	36	80.0	1464	8	DN712479	DN712479 CNB02-F02
C 844	36	80.0	818	11	CNS040X1	AL294094 Tetradon	C 917	36	80.0	1467	10	CL483710	CL483710 SAIL 386
C 845	36	80.0	820	7	CK289667	CK289667 EST752389	C 918	36	80.0	1508	8	DN722763	AK044557 Mus muscu
C 846	36	80.0	823	5	BX709893	BX709893 ZF201-P00	C 919	36	80.0	2678	4	AK044557	AK044557 Mus muscu
C 847	36	80.0	824	9	CK714119	CK714119 ZF201-P00	C 920	36	80.0	3146	4	AK035902	AK035902 Mus muscu
C 848	36	80.0	824	9	BZ973974	BZ973974 PUCAR75TD	C 921	36	80.0	3159	4	AK045634	AK045634 Mus muscu
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C 850	36	80.0	829	6	CAS82815	CAS82815 EST002490	C 923	35	77.8	213	3	BJ518712	BJ518712
C 851	36	80.0	832	1	AM944027	AM944027 LP03982.3	C 924	35	77.8	217	1	AA447954	AA447954 xz11f08. x
C 852	36	80.0	833	7	CK872711	CK872711 AGENCOURT	C 925	35	77.8	245	1	AA686381	AA686381 EST110082
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C 854	36	80.0	835	6	CA475101	CA475101 AGENCOURT	C 927	35	77.8	255	9	CE121975	CE121975 tigr-g88
C 855	36	80.0	836	3	BI596769	BI596769 603242853	C 928	35	77.8	261	7	CO597815	CO597815 DGH-15312
C 856	36	80.0	837	8	DN980449	DN980449 SV6 26A12	C 929	35	77.8	264	6	BF566417	BF566417 UI-R-BT1-
C 857	36	80.0	838	7	CK127453	CK127453 AGENCOURT	C 930	35	77.8	275	9	CC447990	CC447990 ZMMBC032
C 858	36	80.0	838	7	CK698680	CK698680 ZF101-P00	C 931	35	77.8	277	8	WB80043	WB80043 mF67h04. r1
C 859	36	80.0	847	10	CG442399	CG442399 OGTVH88TV	C 932	35	77.8	280	1	AM834949	AM834949 RCL-LT000
C 860	36	80.0	851	7	CN832906	CN832906 AGENCOURT	C 933	35	77.8	285	1	AV074251	AV074251
C 861	36	80.0	851	7	CV488243	CV488243 AGENCOURT	C 934	35	77.8	290	7	CV084603	CV084603 MdItC3075
C 862	36	80.0	852	7	CK710088	CK710088 ZF201-P00	C 935	35	77.8	293	7	CO596794	CO596794 DGH-13561
C 863	36	80.0	855	8	CK440126	CK440126 JGI XZG59	C 936	35	77.8	302	10	AY413662	AY413662 Pan. trogl
C 864	36	80.0	859	6	CA472064	CA472064 AGENCOURT	C 937	35	77.8	304	7	CK755582	CK755582 1tu01-2ms
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C 866	36	80.0	859	9	BZ791322	BZ791322 PUFARI7TB	C 939	35	77.8	309	1	BB138183	BB138183
C 867	36	80.0	859	9	CC398589	CC398589 PUDU84TD	C 940	35	77.8	311	1	AF090128	AF090128 AF090128
C 868	36	80.0	862	6	CA975491	CA975491 AGENCOURT	C 941	35	77.8	311	3	BM060318	BM060318 KS0101340
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C 870	36	80.0	863	3	BI661315	BI661315 UCRPT02.6	C 943	35	77.8	327	6	CF082930	CF082930 OHL18N07.
C 871	36	80.0	863	3	BI661279	BI661279 603304253	C 944	35	77.8	328	1	AA980766	AA980766 ua4505.8
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C 875	36	80.0	868	6	CD460974	CD460974 EG09.0301	C 948	35	77.8	339	9	AQ081824	AQ081824 RPI11-55
C 876	36	80.0	870	7	CN159101	CN159101 948133 MA	C 949	35	77.8	341	2	BF414768	BF414768 UI-R-BJ2-
C 877	36	80.0	870	7	CN319582	CN319582 AGENCOURT	C 950	35	77.8	346	6	CD527357	CD527357 3529.1.12
C 878	36	80.0	870	7	CO248883	CO248883 AGENCOURT	C 951	35	77.8	347	1	AJ692750	AJ692750 AJ692750
C 879	36	80.0	870	7	CK877247	CK877247 SV5 41C11	C 952	35	77.8	352	2	BP752461	BP752461 UI-R-DC0-
C 880	36	80.0	872	7	CK872059	CK872059 AGENCOURT	C 953	35	77.8	352	3	BP752461	BP752461
C 881	36	80.0	876	9	CC353764	CC353764 PUPH35TB	C 954	35	77.8	360	10	AY413661	AY413661 Homo sapi
C 882	36	80.0	878	10	AG885893	AG885893 Oryza sat	C 955	35	77.8	360	10	AY413663	AY413663 Mus muscu
C 883	36	80.0	886	2	BG283688	BG283688 602407456	C 956	35	77.8	363	7	CR473038	CR473038

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C 957 35 77.8 365 10 AG978275 AG978275 Drosophila
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961 35 77.8 373 5 BR333312 BR333312
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963 35 77.8 381 5 BR333312 BR333312
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965 35 77.8 385 5 BR333312 BR333312
966 35 77.8 387 5 BR333312 BR333312
967 35 77.8 390 7 CG645654 CG645654
968 35 77.8 392 1 AM872311 AM872311
969 35 77.8 394 1 AM872311 AM872311
970 35 77.8 396 1 AM872311 AM872311
971 35 77.8 396 6 BR333312 BR333312
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ALIGNMENTS

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RESULT 1 149 bp mRNA linear EST 20-MAY-2002
LOCUS BQ336306
DEFINITION BQ336306
ACCESSION BQ336306
VERSION BQ336306.1
KEYWORDS GI:20992407
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 149)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagai,M.A., da Silva,W.J., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.U., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.J.
Shogun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
```

```

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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PMID2=PM1-MT0143-
100701-007-e12&t=2001-07-10&t=4=1)
Seq primer: puc 18 forward
High quality sequence start: 22
High quality sequence stop: 148.
Location/Qualifiers
1. 149
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/notes="Organ: marrow; Vector: puc18; Site: 1; Sma1; Site 2;
Sma1; A mini-library was made by cloning products derived
from ORFESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
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FEATURES
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1. 149
/organism="Homo sapiens"
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/notes="Organ: marrow; Vector: puc18; Site: 1; Sma1; Site 2;
Sma1; A mini-library was made by cloning products derived
from ORFESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
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ORIGIN
Alignment Scores:
Pred. No.: 5.86 Length: 149
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3
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US-10-757-745-2_COPY_145_153 (1-9) x BQ336306 (1-149)
OR 1 Procaspal1lePheLeuGingJuval 9
DB 91 CCAGATGATATTTCTACAGAAATT 117
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RESULT 2
LOCUS BQ331200/c 156 bp mRNA linear EST 17-MAY-2002
DEFINITION BQ331200
ACCESSION BQ331200
VERSION BQ331200.1
KEYWORDS GI:20972241
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 156)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagai,M.A., da Silva,W.J., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.U., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.J.
Shogun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.J.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
```

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&c2=MR4-ET0140-220101-004-h09_1c1c3-2001-01-22&c4=1)

Seq primer: puc 18 forward.

FEATURES

source

Location/Qualifiers

1..156

/organism="Homo sapiens"

/mol_type="mRNA"

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/dev_stage="Adult"

/clone_1lb="ET0140"

/note="Organ: lung; tumor; Vector: puc18; Site 1: SmaI;

Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	6.17	Length:	156
Score:	45.00	Matches:	9
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DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BQ331200 (1-156)

Qy 1 ProaPValIIlePheLeuGInGluVal 9

Db 76 CCAGATGTCATATTTCTACAGAGATT 50

RESULT 3

LOCUS

BF768814 247 bp mRNA linear EST 12-JAN-2001

DEFINITION PM0-IT0018-091100-001-d12 IT0018 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF768814

VERSION BF768814.1 GI:12116818

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

1 (bases 1 to 247)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM0-IT0018-091100-001-d12&c3=2000-11-09&c4=1)
Seq primer: puc 18 forward

FEATURES

source

High quality sequence start: 9

High quality sequence stop: 246.

Location/Qualifiers

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/dev_stage="Adult"

/clone_1lb="IT0018"

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Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	10.4	Length:	247
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
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Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF768814 (1-247)

Qy 1 ProaPValIIlePheLeuGInGluVal 9

Db 110 CCAGATGTCATATTTCTACAGAGATT 136

RESULT 4

LOCUS

AA325145 252 bp mRNA linear EST 20-APR-1997

DEFINITION EST28102 Cerebellum II Homo sapiens cDNA 5' end, mRNA sequence.

ACCESSION AA325145

VERSION AA325145.1 GI:1977400

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

1 (bases 1 to 252)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weissbrock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wei, C., Clayton, R.A., Cline, T.R., Corcoran, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marzanos, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Uterbeck, T.R., Weidman, J.F., Li, Y., Bedarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dinke, D., Feng, D.-F., Ferris, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meisner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavage@igf.org

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/cdb/hgi/hgi.html>)

Seq primer: M13 Reverse:

FEATURES

source

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/note="Organ: brain; Vector: pBluescript SK-; Site_1:
EcorI; Site_2: XhoI"

ORIGIN

Alignment Scores:

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Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AA325145 (1-252)

QY 1 Proaspvalli11epheleungingluva1 9
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DB 2 CCAGATGTGATATTCTACGAGAGTT 28

RESULT 5
BF992136 296 bp mRNA linear EST 23-JAN-2001
LOCUS QV3-GN0201-301000-454-b08 GN0201 Homo sapiens cDNA, mRNA sequence.
DEFINITION
VERSION BF992136.1 GI:12398459
KEYWORDS
SOURCE EST
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

JOURNAL

PUBLISHED

COMMENT

1 (bases 1 to 296)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Contact: Simpson A.J.G.
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV3&t2=QV3-GN0201-301000-454-b08&t3=2000-10-30&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 296.
Location/Qualifiers
1..296
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES

source

/dev_stage="Adult"
/clone_lib="GN0201"
/note="Organ: placenta normal; Vector: puc18; Site_1:
SmaI; Site_2: SmaI; A mini-library was made by cloning
products derived from ORBSTES PCR (U.S. letters patent
application No. 196,116) into the pUC18 vector. Reverse
transcription product of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	12.8	Length:	296
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF992136 (1-296)

QY 1 Proaspvalli11epheleungingluva1 9
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DB 99 CCAGATGTGATATTCTACGAGAGTT 125

RESULT 6
BF992133 313 bp mRNA linear EST 23-JAN-2001
LOCUS QV3-GN0201-301000-454-g09 GN0201 Homo sapiens cDNA, mRNA sequence.
DEFINITION
VERSION BF992133.1 GI:12398456
KEYWORDS
SOURCE EST
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

AUTHORS

JOURNAL

PUBLISHED

COMMENT

1 (bases 1 to 313)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Brazil
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=QV3&t2=QV3-GN0201-301000-454-g09&t3=2000-10-30&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 45
High quality sequence stop: 311.
Location/Qualifiers
1..313
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="GN0201"
/note="Organ: placenta normal; Vector: puc18; Site_1:
SmaI; Site_2: SmaI; A mini-library was made by cloning
products derived from ORBSTES PCR (U.S. letters patent

Application No. 196, 716 - Ludwig Institute for Cancer Research profiles into the pUC18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ALIGNMENT SCORES:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	13.6	9	9	0	0	0
Percent Similarity:	45.00					
Best Local Similarity:	100.0%					
Query Match:	100.0%					
DB:	2					

US-10-757-745-2_COPY_145_153 (1-9) x BE694706 (1-368)

Qy 1 ProaPvAl1lePheLeuGInGluVal 9
 Db 99 CCAGATGATATTTCTACAGAGATT 125

RESULT 7

LOCUS BE694706 368 bp mRNA linear EST 11-SHP-2000
 DEFINITION PMO-BT0757-140800-006-d10 BT0757 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BE694706
 VERSION BE694706.1 GI:10081866
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo

REFERENCE

1 (bases 1 to 368)
 Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Bioness, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.G.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

PUBMED

COMMENT

10737800
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 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PMO-BT0757-140800-006-d10&ct=2000-08-14&f4=1)
 Seq primer: puc18 forward
 High quality sequence start: 37
 High quality sequence stop: 368.
 Location/Qualifiers

FEATURES

source

1..368
 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_11b="BT0757"
 /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	16.4	368	9	0	0	0
Percent Similarity:	45.00					
Best Local Similarity:	100.0%					
Query Match:	100.0%					
DB:	2					

US-10-757-745-2_COPY_145_153 (1-9) x BE694706 (1-368)

Qy 1 ProaPvAl1lePheLeuGInGluVal 9
 Db 176 CCAGATGATATTTCTACAGAGATT 150

RESULT 8

LOCUS AV659558 368 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV659558 GLC Homo sapiens cDNA clone GLCFYD04 3', mRNA sequence.
 ACCESSION AV659558
 VERSION AV659558.1 GI:9880572
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo

REFERENCE

1 (bases 1 to 368)
 Xiao, H., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, O., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, W., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.
 Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL

PUBMED

COMMENT

11752456
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 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China
 Tel: 86-21-50801919(ex.45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn
 This clone is available at CHGC in Shanghai.
 Location/Qualifiers

FEATURES

source

1..368
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCFYD04"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SQR"
 /clone_11b="GLC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	17.4	368	9	0	0	0
Percent Similarity:	45.00					
Best Local Similarity:	100.0%					
Query Match:	100.0%					
DB:	1					

US-10-757-745-2_COPY_145_153 (1-9) x AV659558 (1-368)

Qy 1 ProaPvAl1lePheLeuGInGluVal 9
 Db 315 CCAGATGATATTTCTACAGAGATT 341

ORIGIN

```

RESULT 9
LOCUS      AV661333
DEFINITION AV661333 GLC Homo sapiens cDNA clone GICGRD01 3', mRNA sequence.
ACCESSION  AV661333
VERSION     AV661333.1 GI:9882347
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 394)
            Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
            Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
            Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
            Hu,G., Gu,J., Chen,Z. and Han,Z.
            Insight into hepatocellular carcinogenesis at transcriptome level
            by comparing gene expression profiles of hepatocellular carcinoma
            with those of corresponding noncancerous liver
            Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
            11752456
JOURNAL     PubMed
COMMENT      Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919 (ex.45)
            Fax: 86-21-50801922
            Email: hanzg@hgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES
source      Location/Qualifiers
            1..394
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            /db_xref="taxon:9606"
            /clone="GICGRD01"
            /issue_type="corresponding non cancerous liver tissue"
            /dev_stage="Adult"
            /lab_host="SOLR"
            /clone_1fb="GLC"
            /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
            XhoI"
ORIGIN
Alignment Scores:
Pred. No.:      17.7      Length:      394
Score:          45.00     Matches:      9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    100.0%   Indels:      0
DB:             1        Gaps:        0
US-10-757-745-2_COPY_145_153 (1-9) x AV661333 (1-394)
QY          1 Proaapvalllpheleuglnluva1 9
DB          221 CCNAGTGTATTTCTACAGAGATT 247
RESULT 10
LOCUS      BQ332322
DEFINITION MR4-ET0140-240501-015-d11 ET0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BQ332322
VERSION     BQ332322.1 GI:20973745
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 413)
            Dias,Neto,E., Garcia,Correa,R., Verjovskij-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Shotgun sequencing of the human transcriptome with ORF expressed
REFERENCE
AUTHORS      Goldman,G.H., Carvalho,A.F., Metukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            10737800
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            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the PAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR4ct2-mr4-ET0140-
            240501-015-d11ct3=2001-05-24ct4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 413.
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            /clone_1fb="ET0140"
            /note="Organ: lung; tumor; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
ORIGIN
Alignment Scores:
Pred. No.:      18.7      Length:      413
Score:          45.00     Matches:      9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    100.0%   Indels:      0
DB:             3        Gaps:        0
US-10-757-745-2_COPY_145_153 (1-9) x BQ332322 (1-413)
QY          1 Proaapvalllpheleuglnluva1 9
DB          53 CCNAGTGTATTTCTACAGAGATT 79
RESULT 11
LOCUS      BF853399
DEFINITION MR3-EN0087-191200-015-d07 EN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF853399
VERSION     BF853399.1 GI:12241143
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 419)
            Dias,Neto,E., Garcia,Correa,R., Verjovskij-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
REFERENCE
AUTHORS      Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed

```

```

TITLE
AUTHORS
REFERENCE
AUTHORS      Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
            10737800
JOURNAL     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the PAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR4ct2-mr4-ET0140-
            240501-015-d11ct3=2001-05-24ct4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 413.
FEATURES
source      Location/Qualifiers
            1..413
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
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            /clone_1fb="ET0140"
            /note="Organ: lung; tumor; Vector: puc18; Site_1: SmaI;
            Site_2: SmaI; A mini-library was made by cloning products
            derived from ORESTES PCR (U.S. Letters Patent application
            No. 196,716 - Ludwig Institute for Cancer Research)
            profiles into the pUC 18 vector. Reverse transcription of
            tissue mRNA and cDNA amplification were performed under
            low stringency conditions."
ORIGIN
Alignment Scores:
Pred. No.:      18.7      Length:      413
Score:          45.00     Matches:      9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    100.0%   Indels:      0
DB:             3        Gaps:        0
US-10-757-745-2_COPY_145_153 (1-9) x BQ332322 (1-413)
QY          1 Proaapvalllpheleuglnluva1 9
DB          53 CCNAGTGTATTTCTACAGAGATT 79
RESULT 11
LOCUS      BF853399
DEFINITION MR3-EN0087-191200-015-d07 EN0087 Homo sapiens cDNA, mRNA sequence.
ACCESSION  BF853399
VERSION     BF853399.1 GI:12241143
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 419)
            Dias,Neto,E., Garcia,Correa,R., Verjovskij-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
REFERENCE
AUTHORS      Goldman,G.H., Carvalho,A.F., Matukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jorgensen,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed

```

JOURNAL
PUBMED
COMMENT

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&ct2=MR3-EN0087-
1912001-015-a07&ct3=2000-12-19&ct4=1)
Seg primer: puc 18 forward
High quality sequence stop: 419.
Location/Qualifiers
1..419
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1b="EN0087"
/note="Organ: lung_normal; Vector: puc18; Site_1: Smal;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 19 Length: 419
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF653399 (1-419)

Qy 1 ProaepVal11epheugIngluVal 9
DB 59 CCAGATGATATTTCTACAGAGATT 85

RESULT 12
LOCUS BG982044/C 422 bp mRNA linear EST 12-JUN-2001
DEFINITION MR3-CN0147-120201-011-h12 CN0147 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG982044
VERSION BG982044.1 GI:14384779
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 422)

REFERENCE
AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, M. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bale, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
PUBMED
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&ct2=MR3-CN0147-
120201-011-h12&ct3=2001-02-12&ct4=1)
Seg primer: puc 18 forward
High quality sequence stop: 427.
Location/Qualifiers
1..422
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1b="CN0147"
/note="Organ: colon_normal; Vector: puc18; Site_1: Smal;
Site_2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 19.2 Length: 422
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG982044 (1-422)

Qy 1 ProaepVal11epheugIngluVal 9
DB 342 CCAGATGATATTTCTACAGAGATT 316

RESULT 13
LOCUS BQ582059 429 bp mRNA linear EST 20-JUN-2002
DEFINITION 1112c11.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6029589
5' similar to TR:095551 095551 D3J0M3.3 ;, mRNA sequence.
ACCESSION BQ582059
VERSION BQ582059.1 GI:21494955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 429)

REFERENCE
AUTHORS

Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
Lemshka, I., Scarce, M., Bresselli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bistrain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvilli, R.,
Williams, T., Jackson, Y. and Bowers, Y.

TITLE

Unpublished (2000)

JOURNAL

Other ESTs: 1112c11.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

Email: dmellon@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@wustl.edu)
Seq primer: -40RP from Glibco.
Location/Qualifiers

FEATURES
source

1..435
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6029589"
/issue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="human insulinoma"
/note="Organ: Pancreas; Vector: pBluescript SK-; Site: 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZapII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permut
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.: 19.5 Length: 429
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BQ582059 (1-429)

QY 1 ProaapvAlIlePheLeuGInGluVal 9
|||||
DB 376 CCAGATGTGATATTCTACAGGAAGTT 402

RESULT 14

LOCUS BQ32331/c 435 bp mRNA linear EST 17-MAY-2002
DEFINITION MR4-ET0140-240501-015-g10 ET0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ32331
VERSION BQ32331.1 GI:20973758
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 435)

REFERENCE

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coats,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Tel: +55-11-2704922
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fil=MR4et2-MR4-ET0140-
240501-015-g10ct3=2001-05-24et4=1)
Seq primer: puc 18 forward
High quality sequence start: 132
High quality sequence stop: 435.
Location/Qualifiers

FEATURES

source

1..435
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="ET0140"
/note="Organ: Lung tumor; Vector: puc18; Site: 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 19.8 Length: 435
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BQ32331 (1-435)

QY 1 ProaapvAlIlePheLeuGInGluVal 9
|||||
DB 355 CCAGATGTGATATTCTACAGGAAGTT 329

RESULT 15

LOCUS BF768820/c 437 bp mRNA linear EST 12-JAN-2001
DEFINITION PM0-IT0018-091100-001-IT0018 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF768820
VERSION BF768820.1 GI:12116824
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 437)

REFERENCE

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Coats,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?fil=PM0et2-PM0-IT0018-
091100-001-401et3=2000-11-09et4=1)
Seq primer: puc 18 forward

High quality sequence start: 28
High quality sequence stop: 437.
Location/Qualifiers

FEATURES
source

1. .437
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="T0018"
/note="Organ: epid.tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	19.9	Length:	437
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF768820 (1-437)

Qy 1 ProaSpValllePhleuGlnGluVal 9
DB 357 CCAGATGATATTTCTACAGGAGCTT 331

RESULT 16

BG982029/c

LOCUS MR3-CN0147-120201-011-b10 CN0147 Homo sapiens cDNA, mRNA sequence.

DEFINITION

ACCESSION BG982029

VERSION BG982029.1 GI:14384764

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Simpson A.J.G.

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This sequence was derived from the PAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-CN0147-

120201-011-b10&t3=2001-02-12&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 440.

Location/Qualifiers

1. .440

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"
/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Pred. No.:	20.1	Length:	440
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG982029 (1-440)

Qy 1 ProaSpValllePhleuGlnGluVal 9
DB 360 CCAGATGATATTTCTACAGGAGCTT 334

RESULT 17

BG982036/c

LOCUS MR3-CN0147-120201-011-d12 CN0147 Homo sapiens cDNA, mRNA sequence.

DEFINITION

ACCESSION BG982036

VERSION BG982036.1 GI:14384771

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Simpson A.J.G.

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Email: asimpson@ludwig.org.br

This sequence was derived from the PAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-CN0147-

120201-011-d12&t3=2001-02-12&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 440.

Location/Qualifiers

1. .440

/organism="Homo sapiens"

/mol_type="rRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="CN0147"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	20.1	Length:	440
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG982036 (1-440)

QY

1 ProaSpVall1pHeLeuGInGluVal 9
|||
360 CCAGATGATATTCTTACGAGAGTT 334

RESULT 18

BF692415 441 bp mRNA linear EST 18-JAN-2001
LOCUS PM1-MT0143-041100-002-f12 MT0143 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF692415
ACCESSION BF692415.1 GI:12283874
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 441)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t=PM1-MT0143-
041100-002-f12&t=32000-11-04&t=1)
Seq primer: puc 18 forward
High quality sequence stop: 441.

FEATURES

source

1 441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0143"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	20.1	Length:	441
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF692415 (1-441)

QY

1 ProaSpVall1pHeLeuGInGluVal 9
|||
81 CCAGATGATATTCTTACGAGAGTT 107

RESULT 19

BF693925 441 bp mRNA linear EST 18-JAN-2001
LOCUS PM1-MT0143-131100-004-g08 MT0143 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF693925
ACCESSION BF693925.1 GI:12285384
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 441)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t=PM1-MT0143-
131100-004-g08&t=32000-11-13&t=41)
Seq primer: puc 18 forward
High quality sequence stop: 441.

FEATURES

source

1 441
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0143"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 20.1 Length: 441
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893925 (1-441)

Qy 1 ProaepVal11lePheLeuGInG1uVal 9
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 DB 81 CCAGATGATATTTCTACAGAACTT 107

RESULT 20
 BF893187 444 bp mRNA linear EST 18-JAN-2001
 LOCUS PM1-MT0143-101100-003-h07 MT0143 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF893187
 ACCESSION BF893187 GI:12284646
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 444)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 JOURNAL
 PUBMED
 COMMENT
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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 Tel: +55-11-2704922
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 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-MT0143-
 101100-003-h07&c3=2000-11-10&c4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 444.
 Location/Qualifiers
 1..444
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_11b="MT0143"
 /note="Organ: marrow; Vector: puc18; Site 1: Sma1; Site 2:
 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.3 Length: 444
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893187 (1-444)

Qy 1 ProaepVal11lePheLeuGInG1uVal 9
 |||||
 DB 81 CCAGATGATATTTCTACAGAACTT 107

DB 84 CCAGATGATATTTCTACAGAACTT 110

RESULT 21
 BF891509 447 bp mRNA linear EST 18-JAN-2001
 LOCUS PM1-MT0143-281000-001-h02 MT0143 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF891509
 ACCESSION BF891509 GI:12282981
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 447)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
 JOURNAL
 PUBMED
 COMMENT
 10737800
 Contact: Simpson A.J.G.
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 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&c2=PM1-MT0143-
 281000-001-h02&c3=2000-10-28&c4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 27
 High quality sequence stop: 447.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_11b="MT0143"
 /note="Organ: marrow; Vector: puc18; Site 1: Sma1; Site 2:
 Sma1; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.5 Length: 447
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF891509 (1-447)

Qy 1 ProaepVal11lePheLeuGInG1uVal 9
 |||||
 DB 88 CCAGATGATATTTCTACAGAACTT 114

RESULT 22
 BF773259/c 453 bp mRNA linear EST 12-JAN-2001
 LOCUS BF773259

DEFINITION PM0-IT0018-151200-002-d10 IT0018 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF773259
VERSION BF773259.1 GI:12121159
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 453)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
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COMMENT
JOURNAL
PUBMED
CONTACT: Simpson A.J.G.
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Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM0&t2=PM0-IT0018-
151200-002-d10&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 133.
Location/Qualifiers
1..453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="IT0018"
/note="Organ: epid.tumor; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,716 - Ludwig Institute for Cancer Research)
No. files into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Alignment Scores: 20.8 Length: 453
Pred. No.: 9
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 2
US-10-757-745-2_COPY_145_153 (1-9) x BF773259 (1-453)
QY 1 ProApyvAlIlePhelcGInGluVAI 9
Db 373 CCGAGTGTGATATTTCACAGGAAGTT 347
RESULT 23
LOCUS BQ315535/c 453 bp mRNA linear EST 16-MAY-2002
DEFINITION PM0-IT0018-151200-002-d06 IT0018 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ315535
VERSION BQ315535.1 GI:20874720
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 453)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R.,
Nagai,M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
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sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT
JOURNAL
PUBMED
CONTACT: Simpson A.J.G.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM0&t2=PM0-IT0018-
151200-002-d06&t3=2000-12-15&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 20.
Location/Qualifiers
1..453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="IT0018"
/note="Organ: epid.tumor; Vector: puc18; Site:1: SmaI;
Site:2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No.196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Alignment Scores: 20.8 Length: 453
Pred. No.: 9
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3
US-10-757-745-2_COPY_145_153 (1-9) x BQ315535 (1-453)
QY 1 ProApyvAlIlePhelcGInGluVAI 9
Db 373 CCGAGTGTGATATTTCACAGGAAGTT 347
RESULT 24
LOCUS BG982031/c 454 bp mRNA linear EST 12-JUN-2001
DEFINITION MR3-CN0147-120201-011-b12 CN0147 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG982031
VERSION BG982031.1 GI:14384766
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 454)

AUTHORS
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
 10737800

COMMENT
 Contact: Simpson A.J.G.
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 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=MR3&t2=MR3-CN0147-120201-011-b1&t3=2001-02-12&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 15
 High quality sequence stop: 453.
 Location/Qualifiers

FEATURES
 source
 1..454
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="CN0147"
 /note="Organ: colon_normal; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.8 Length: 454
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG982031 (1-454)

Qy
 1 Proaapvallllephleuglngluval 9
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 373 CCAGATGATATTTCTACAGAGGTT 347

Db
 373 CCAGATGATATTTCTACAGAGGTT 347

RESULT 25
 BF996980 456 bp mRNA linear EST 23-JAN-2001
 LOCUS BF996980
 DEFINITION QV3-GN0201-081100-468-c10 GN0201 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF996980
 VERSION BF996980.1 GI:12403303
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 456)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and

REFERENCE
 AUTHORS

TITLE
 Simpson, A. J.

JOURNAL
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

PUBMED
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT
 Contact: Simpson A.J.G.
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 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=QV3&t2=QV3-GN0201-081100-468-c10&t3=2000-11-08&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 456.
 Location/Qualifiers

FEATURES
 source
 1..456
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="GN0201"
 /note="Organ: placenta_normal; Vector: puc18; Site: 1: SmaI; Site: 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Alignment Scores:
 Pred. No.: 20.9 Length: 456
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF996980 (1-456)

Qy
 1 Proaapvallllephleuglngluval 9
 |||||
 376 CCAGATGATATTTCTACAGAGGTT 350

Db
 376 CCAGATGATATTTCTACAGAGGTT 350

RESULT 26
 BQ332321 456 bp mRNA linear EST 17-MAY-2002
 LOCUS BQ332321
 DEFINITION MR4-ET0140-240501-015-d10 ET0140 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BQ332321
 VERSION BQ332321.1 GI:20973744
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 456)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

REFERENCE
 AUTHORS

TITLE
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED
 10737800

COMMENT
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR4&ct2=MR4-ET0140-
240501-015-dl0&ct3=2001-05-24&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 456.
Location/Qualifiers
1..456
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="ET0140"
/note="Organ: lung tumor; Vector: puc18; Site 1: Sma1;
Site 2: Sma1; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent applica-
tion No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 20.9 Length: 456
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BQ323221 (1-456)

QY 1 Proaapvaliilepheelengingluval 9

DB 96 CCAGATGATGATTTCTACAGAGATT 122

RESULT 27

LOCUS BQ36782 458 bp mRNA linear EST 21-MAY-2002
DEFINITION OY3-GN0201-081100-437-c05 GN0201 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ36782
VERSION BQ36782.1 GI:21042296
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
(bases 1 to 459)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
JOURNAL
COMMENT
Contact: Simpson A.J.G.
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=QV3&ct2=QV3-GN0201-
081100-437-c05&ct3=2000-11-08&ct4=1)
Seq primer: puc 18 forward
High quality sequence stop: 12.
Location/Qualifiers
1..458
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="GN0201"
/note="Organ: placenta normal; Vector: puc18; Site 1:
Sma1; Site 2: Sma1; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 21 Length: 458
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BQ36782 (1-458)

QY 1 Proaapvaliilepheelengingluval 9

DB 378 CCAGATGATGATTTCTACAGAGATT 352

RESULT 28

LOCUS BQ982034 459 bp mRNA linear EST 12-JUN-2001
DEFINITION MR3-CN0147-120201-011-C09 CN0147 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ982034
VERSION BQ982034.1 GI:14384769
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
(bases 1 to 459)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.G.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
JOURNAL
COMMENT
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Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&ct2=MR3-CN0147-
120201-011-c09&ct3=2001-02-12&ct4=1)
Seq primer: puc 18 forward

High quality sequence start: 19
High quality sequence stop: 459
Location/Qualifiers

FEATURES
source 1..459
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 21.1 Length: 459
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG982034 (1-459)

QY 1 ProaSpVal11lePhelengIngluVal 9
DB 379 CCAGATGATATTTCTACAGAGATT 353

RESULT 29

BF893150 460 bp mRNA linear EST 18-JUN-2001
LOCUS PM1-MT0143-101100-003-b07 MT0143 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF893150
VERSION BF893150.1 GI:12284609

KEYWORDS

EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.
1 (bases 1 to 460)

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1-MT0143-101100-003-b07&c3=2000-11-10&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 434.

FEATURES

source 1..460
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0143"

/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 21.1 Length: 460
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893150 (1-460)

QY 1 ProaSpVal11lePhelengIngluVal 9
DB 100 CCAGATGATATTTCTACAGAGATT 126

RESULT 30

BG982012 461 bp mRNA linear EST 12-JUN-2001
LOCUS MR3-CN0147-120201-011-b03 CN0147 Homo sapiens cDNA, mRNA sequence.

ACCESSION BG982012
VERSION BG982012.1 GI:14384747

KEYWORDS

EST.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.
1 (bases 1 to 461)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H., Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR3&c2=MR3-CN0147-120201-011-b03&c3=2001-02-12&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 191.

Location/Qualifiers

1..461
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

High quality sequence stop: 191.

Location/Qualifiers

1..461
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

High quality sequence stop: 191.

Location/Qualifiers

1..461
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CN0147"

/note="Organ: colon normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

High quality sequence stop: 191.

derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	21.2	Length:	463
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG982012 (1-461)

QY 1 ProaPVal11epheLeuGIngluVal 9
DB 381 CCAGATGTGATATTCTCGAGGAGGTT 355

RESULT 31

BF852284 463 bp mRNA linear EST 16-JAN-2001
LOCUS MR3-EN0087-121200-007-d01 EN0087 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF852284
ACCESSION BF852284
VERSION BF852284.1 GI:12239655
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 463)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR3&l2=MR3-EN0087-121200-007-d01&l3=2000-12-15&l4=1)
Seq primer: puc 18 forward
High quality sequence stop: 463.
Location/Qualifiers

FEATURES

source

1..463
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0087"

/note="Organ: lung_normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	21.3	Length:	463
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BF852284 (1-463)

QY 1 ProaPVal11epheLeuGIngluVal 9
DB 95 CCAGATGTGATATTCTACGAGAGTT 121

RESULT 32

BF852788 463 bp mRNA linear EST 16-JAN-2001
LOCUS MR3-EN0087-151200-012-a09 EN0087 Homo sapiens cDNA, mRNA sequence.
DEFINITION BF852788
ACCESSION BF852788
VERSION BF852788.1 GI:12240532
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 463)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Britones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=MR3&l2=MR3-EN0087-151200-012-a09&l3=2000-12-15&l4=1)
Seq primer: puc 18 forward
High quality sequence stop: 31
High quality sequence stop: 463.
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0087"

/note="Organ: lung_normal; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	21.3	Length:	463
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0

Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 2
Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF852788 (1-463)

QY 1 Proaspvalli11epheleunglingluyal 9
DB 383 CCAGATGATATTTCTACAGAAAGTT 357

RESULT 33

LOCUS BF893919 463 bp mRNA linear EST 18-JAN-2001
DEFINITION PM1-MT0143-131100-004-e06 MT0143 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF893919
VERSION BF893919.1 GI:12285378
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 463)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, M. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

REFERENCE

AUTHORS

TITLE
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPER/P/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&t2=PM1-MT0143-
131100-004-e06&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 463.
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="MT0143"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 21.3 Length: 463
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893919 (1-463)

QY 1 Proaspvalli11epheleunglingluyal 9
DB 103 CCAGATGATATTTCTACAGAAAGTT 129

RESULT 34

LOCUS BF893924 471 bp mRNA linear EST 18-JAN-2001
DEFINITION PM1-MT0143-131100-004-g07 MT0143 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF893924
VERSION BF893924.1 GI:12285383
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 471)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
Nagai, M. A., da Silva, M. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,
Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V.,
O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

REFERENCE

AUTHORS

TITLE
JOURNAL
PUBMED
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPER/P/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM1&t2=PM1-MT0143-
131100-004-g07&t3=2000-11-13&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 33
High quality sequence stop: 471.
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_11b="MT0143"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 21.7 Length: 471
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF893924 (1-471)

QY 1 Proaspvalli11epheleunglingluyal 9
DB 391 CCAGATGATATTTCTACAGAAAGTT 365

Thu Mar 16 10:39:25 2006

us-10-757-745-2_copy_145_153.rst

Page 24

RESULT	35
CRES43841	
LOCUS	
DEFINITION	CRES43841 471 bp - tRNA } linear EST 07-JUL-2004
ACCESSION	DK29265900742.R1_459 (synonym) Pongo pygmaeus cDNA clone
VERSION	DK29265900742.5, mRNA sequence.
KEYWORDS	CRES43841 GI:49895553
SOURCE	EST.
ORGANISM	Pongo pygmaeus (orangutan)
	Pongo pygmaeus
	Buxartyleta, Melitaea; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Pongo.
REFERENCE	1 (bases 1 to 471)
AUTHORS	Bloecher,H., Boecker,M., Brandt,P., Mewes,H.W., Well,B., Amid,C.,
TITLE	Osainger,A., Fobo,G., Han,W. and Wismann,S.
JOURNAL	Pongo pygmaeus mRNA [Bloecher,H., Boecker,M., Brandt,P., et al.]
COMMENT	Unpublished (2004)
Contact:	MIPS

Ingolstaedter Landstr.1, D-85764 Neuburg, Germany
This is the 5' sequence of the clone insert Cloned from S. Wiemann,
Molecular Genome Analysts, German Cancer Research Center (DKFZ),
Email: s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany).
Within the CDNA sequencing consortium of the German Genome Project.
The CDNA was sequenced by the German Genome Project.
Berlin-Charlottenburg, Germany; Email: clonexpd.de; Further
please contact the RZPD, Ressourcenzentrum "Heidelberg 6, 14059
information about the clone and the sequencing project is available
at <http://mips.gsf.de/projects/cdna/>.

```

FEATURES
source
  location/Qualifiers
  1..471
    /organism="Pongo pygmaeus"
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    /db_xref="DKEY:00074"
    /tissue_type="cortex"
    /dev_stage="adult"
    /lab_host="DH10B"
    /clone_lib="459 (synonym: ppcor1)"
    /notes="Vector: pSPori1.Sfi; Site 1: SfiI; Site 2: SfiII"

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ORIGIN	
Alignment Scores:	
Pred. No.:	21.7
Score:	45.00
Score Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	7
US-10-757-745-2 COPY 145_153 (1-9) x CR543841 (1-471)	
	Length: 471
	Matches: 9
	Mismatched: 0
	Mismatches: 0
	Indels: 0
	Gaps: 0

[illegible]

TITLE	Oh,K.Y., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
JOURNAL	21C Frontier Korean EST Project 2001
COMMENT	Unpublished (2002) Contact: Kim_Y.S Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Boeundong Yuseong-5u, Daejeon 305-353, South Korea Tel.: +82-42-860-4470 Fax: +82-42-860-4403 Email: yongsung@mail.kr.ibm.re.kr Plate: 29 row: F column: 06 High quality sequence stop: 473. Location/Qualifiers 1..473
FEATURES	
source	

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L85CKO-29-F06"
/sex="M"
/cell_line="SCK"
/lab_host="ToploF"
/clone_1ib="L85CKO"
/notes="Organ: Liver; Vector: pRT73-Pac; Site: 1: EcoRI;
Site: 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-906. RNA was prepared from harvested cell
culture."

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ORIGIN	
Alignment Scores:	
Pred. No.:	21.8
Score:	45.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	6
US-10-10-757-745-2_COPY_145_153 (1-9) x CB120234 (1-473)	
QY	1 ProAepYallIephelengInuVal 9
db	382 CCACATGTGATATTTCTACAGAAAGTT 408

RESULT 37
LOCUS
AI750554
DEFINITION
AI750554 480 bp mRNA linear EST 20-JUN-2002
cno4a01.y1 Normal Human Trabecular Bone Cells Homo sapiens CDNA
AI750554
ACCESSION
AI750554.1 GI:5128818
VERSION
AI750554.1
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 480)
Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
Beckerlorn-Sternberg,S.M., Green,E.D., Powell,O.I., Yang,L.M.,
Rodey,F.G., Hochstetler,R.N. and Francantonio,C.A.
SGAP: The Skeletal Genome Anatomy Project
Unpublished, 1974
Contact: Labm Jia
Medical Research Branch
National Heart Genome Research Institute
101001610 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-402-7157
Email: jlbjnb@nih.gov
DNA sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).

Plate: 04 row: a column: 01
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers

FEATURES

source

1..480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NH7BC_cn04a01"
/sex="Female"
/tissue_type="Bone"
/cell_type="Tribecular Bone Cells"
/lab_host="SURE"
/clone_lib="Normal Human Tribecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Robey (NIDCR)"

ORIGIN

Alignment Scores:

Pred. No.:	22.2	Length:	480
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AJ750554 (1-480)

QY 1 ProaPVal11lePheLeuGInGluVal 9

DB 427 CCAGATGATATTTCTACAGAACTT 453

RESULT 38

LOCUS

AA486032 485 bp mRNA linear EST 06-MAR-1998

DEFINITION ab40b10.r1 StrataGene Hela cell s3 937216 Homo sapiens cDNA clone

IMAGE:843259 5', mRNA sequence.

ACCESSION

AA486032.1 GI:2216248

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 485)

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Stepcoe, M., Tan, F.,

Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

Washington University School of Medicine

Unpublished (1997)

Contact: Wilson RK

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1913 Std Error: 0.00

Seq primer: -28m13 rev1 ET from Amerham

High quality sequence Bcop: 444.

Location/Qualifiers

1..485

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:843259"

/sex="Female"

/dev_stage="Hela S3 cell line"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene Hela cell s3 937216"

ORIGIN

Alignment Scores:

Pred. No.:	22.4	Length:	485
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AA486032 (1-485)

QY 1 ProaPVal11lePheLeuGInGluVal 9

DB 423 CCAGATGATATTTCTACAGAACTT 449

RESULT 39

LOCUS

AJ681912 491 bp mRNA linear EST 29-JUN-2004

DEFINITION AJ681912 CSEORAN04 Sus scrofa cDNA clone C0001797_I20, mRNA

sequence.

ACCESSION

AJ681912.1 GI:49414502

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Sus scrofa (pig)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

Sus.

1 (bases 1 to 491)

Anderson, S.I., Finlayson, H.A. and Archibald, A.L.

Development of cDNA and EST resources for studying reproduction and

embryo development in pigs and cattle

Unpublished (2004)

Contact: Anderson SI

Genomics and Bioinformatics

Roslin Institute

Roslin, Midlothian, EH25 9PS, UNITED KINGDOM

Single pass sequencing. Bases called and trimmed with phred

v0.020425.c. Vector identified by cross match with the -minscore 20

and -mismatch 12 options. Vector:pBluescriptII(KS+). R. Site1: EcoRI

R. Site2: NotI 5' Seq Primer M13P Normalised library constructed

from pig uterus. Clones available from UK Centre for Functional

Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,

EH25 9PS, www.arkgenomics.org.

Location/Qualifiers

1..491

/organism="Sus scrofa"

/mol_type="mRNA"

/db_xref="taxon:9823"

/clone="C0001797_I20"

/tissue_type="uterus"

/clone_lib="CSEORAN04"

/note="Vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:

NotI; Single pass sequencing. Normalised library

constructed from pig uterus."

/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Hela S3
epithelioid carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; uni-ZAP XR
Vector. -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'
adaptor sequence: 5' CTCGATGTTTTTTTTTTTTTTT 3'."

ORIGIN

Alignment Scores:

Pred. No.:	22.8	Length:	491
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AJ681912 (1-491)

Thu Mar 16 10:39:26 2006

US-10-757-745-2_copy_145_153.rst

Page 26

QY 1 Proaapvalli1lepheluengluval 9
DB 127 CCAAGTGTGATTTCTACAGAGATT 153

RESULT 40
BI016235/c 491 bp mRNA linear EST 13-JUN-2001
DEFINITION MR4-ET0140-130301-009-a09 ET0140 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI016235
VERSION BI016235.1 GI:14420306
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 491)
Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800

JOURNAL
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MR4&rt2=MR4-ET0140-
130301-009-a09&rt3=2001-03-13&rt4=1
130301-009-a09&rt3=2001-03-13&rt4=1
Hed primer puc 18 forward
High quality sequence start: 7
High quality sequence stop: 232.
Location/Qualifiers
1..491
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_id="ET0140"
/note="Organ: Lung tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESSES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores: 22.8 Length: 491
Pred. No.: 45.00 Matches: 9
Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BI016235 (1-491)

QY 1 Proaapvalli1lepheluengluval 9
DB 410 CCAAGTGTGATTTCTACAGAGATT 384

RESULT 41
LOCUS BM846221 530 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0125204 S13KMS5 Homo sapiens cDNA clone S13KMS5-59-C04 5',
mRNA sequence.
ACCESSION BM846221
VERSION BM846221.1 GI:19202620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 530)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.U., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseungemall.kribb.re.kr
Plate: 59 Row: C Column: 04
High quality sequence stop: 530.
Location/Qualifiers
1..530
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13KMS5-59-C04"
/tissue="myeloma"
/cell_line="RMS-5"
/lab_host="TOP10F"
/clone_id="S13KMS5"
/note="Vector: pCNS; Site 1: EcoRI; Site 2: NotI. The poly
(A) + RNA was dephosphorylated with bacterial alkaline
phosphatase (BAP) and then dephosphorylated with tobacco acid
pyrophosphatase (TAP). The dephosphorylated RNA was
ligated with DNA-RNA linker including EcoRI site by
treatment of T4 RNA ligase and the ligase strand cDNA was
synthesized from oligo dt-selected mRNA by priming with
dt-tailed vector. The dt-tailed vector was digested to
have about 60nt. The cDNA vector was religated with E.
coli DNA ligase after digestion of EcoRI which site is
also included in vector. An RNA strand converted to a DNA
strand by Okayama-Berg method. The obtained cDNA vectors
were used for transformation of competent cells E. coli
TOP10F by electroporation method. The cDNA libraries
constructed by this method are full-length enriched cDNA
library."

ORIGIN
Alignment Scores: 24.8 Length: 530
Pred. No.: 45.00 Matches: 9
Score: 100.0% Conservative: 0
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 100.0% Indels: 0
Query Match: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BM846221 (1-530)

QY 1 Proaapvalli1lepheluengluval 9
DB 437 CCAAGTGTGATTTCTACAGAGATT 463

RESULT 42
LOCUS CN298921 534 bp mRNA linear EST 16-MAY-2004


```

DEFINITION 17000531590248 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN2989921
VERSION CN2989921.1 GI:47315335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1 (bases 1 to 534)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Flisk, G.J.,
            Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
            Lebowitz, J. and Stanton, L.W.
            Transcriptional characterization elucidates signaling networks that
            control human ES cell growth and differentiation
            Nat. Biotechnol. 22 (6), 707-716 (2004)
JOURNAL 15146197
PUBMED Contact: Brandenberger R
COMMENT Regenerative Medicine
            Genon Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@genon.com
FEATURES
    source
        1. 534
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /issue_type="embryonic stem cells, embryoid bodies
        /derived_from="H1, H7 and H9 cells"
        /clone_1lb="GRN_EB"
        /note="oligo dt primed, full-length enriched cDNA library
        from embryoid body outgrowth derived from h9 cell lines
        H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
        conditions."
ORIGIN
Alignment Scores:
Pred. No.: 25 Length: 534
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CN2989921 (1-534)
QY 1 ProAapValIlePheLeuGlnGluVal 9
Db 40 CCAGATGATGATATTCTTCAAGAGAGATT 66
RESULT 43
BG541031 546 bp mRNA linear EST 03-APR-2001
LOCUS 602570130F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694374 5',
DEFINITION mRNA sequence.
ACCESSION BG541031
VERSION BG541031.1 GI:13533264
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE 1 (bases 1 to 546)
AUTHORS NIH-MGC http://imgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.

```

```

cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L16M1518 row: d column: 23
High quality sequence etop: 545.
FEATURES
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        1. 546
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone_1lb="IMAGE:4694374"
        /lab_host="DH10B (T1 phage-resistant)"
        /clone_1lb="NIH MGC 77"
        /note="Organ: Lung; Vector: pMDR-LTR (Clontech); Site 1:
        SfiI (ggcgccctcgcc); Site 2: SfiI (ggccatgatgcc); 5' and
        3' adaptors were used in cloning as follows: 5' adaptor
        sequence: 5'-CACGCCATTATGACC-3' and 3' adaptor sequence:
        5'-ATTCTAGAGCGCGAGCGCGCCGACATG-dt (30)BN-3' (where B = A,
        C, or G and N = A, C, G, or T). Average insert size 1.9
        kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
        by PCR. This library was enriched for full-length clones
        and was constructed by Clontech Laboratories (Palo Alto,
        CA). Note: this is a NIH-MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 25.7 Length: 546
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BG541031 (1-546)
QY 1 ProAapValIlePheLeuGlnGluVal 9
Db 39 CCAGATGATGATATTCTTCAAGAGAGATT 65
RESULT 44
AM669835 549 bp mRNA linear EST 25-APR-2001
LOCUS 113421 MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION AM669835
VERSION AM669835.1 GI:7526349
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 549)
AUTHORS Smith, R.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
            Casab, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
            Bennett, G.L., Heaton, M.P., Jaeger, W.W., Rohrer, G.A.,
            Chitko-McKown, C.G., Pettea, G., Holt, I., Karaymcheva, S., Liang, F.,
            Quackenbush, J. and Keise, J.W.
            Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
            Genome Res. 11 (4), 626-630 (2001)
JOURNAL Contact: Smith TPJ
PUBMED USDA, ARS, US Meat Animal Research Center
COMMENT PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@mail.marc.usda.gov
            Single pass sequencing. Bases called and alt trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -mismatch 12 options.

```

PCR primers
FORWARD: AGGAACAGCATGACCAT
BACKWARD: GTTCCCGACGACG
Plate: 108 row: M column: 18
Seq primer: ATTAGTGACACATAG.

FEATURES
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1..549
/organism="Bos taurus"
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/tissue_type="pooled"
/lab_host="MDH10B"
/clone_lib="MARC 1BOV"
/note="vector: pCMV SPORT6; site 1: NotI; site 2: SalI;
library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

ORIGIN

Alignment Scores:

Pred. No.:	25.9	Length:	549
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AW669835 (1-549)

Ox
1 ProaPvAl11epheleuGInguvAl 9
|||||
498 CCGATGTGATATTCTACGGAAGTC 524

RESULT 45
BP220985 554 bp mRNA linear EST 15-SEP-2004
LOCUS BP220985 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION COL06450, mRNA sequence.
ACCESSION BP220985.1 GI:52093890
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 554)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
Source
1..554
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="COL06450"
/tissue_type="colon"
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ORIGIN

Alignment Scores:

Pred. No.:	26.1	Length:	554
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP220985 (1-554)

Ox
1 ProaPvAl11epheleuGInguvAl 9
|||||
342 CCGATGTGATATTCTACGGAAGTC 368

RESULT 46
BP226620 565 bp mRNA linear EST 15-SEP-2004
LOCUS BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
DEFINITION clone DMC03190, mRNA sequence.
ACCESSION BP226620.1 GI:52099525
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 565)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
Source
1..565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="DMC03190"
/clone_lib="Sugano cDNA library, dermoid cancer"
/note="dermoid cancer"

ORIGIN

Alignment Scores:

Pred. No.:	26.7	Length:	565
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP226620 (1-565)

Ox
1 ProaPvAl11epheleuGInguvAl 9
|||||
434 CCGATGTGATATTCTACGGAAGTC 460

RESULT 47
BP220508 566 bp mRNA linear EST 15-SEP-2004
LOCUS BP220508 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION COL03160, mRNA sequence.
ACCESSION BP220508.1 GI:52093413
VERSION EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 566)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL03160"
/issue_type="colon"
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ORIGIN

Alignment Scores:

Pred. No.:	26.8	Length:	566
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP220508 (1-566)

Qy 1 Proaapval11ephleuglngu1val 9
|||||
DB 352 CCAGATGATATTTCTACAGAGATT 378

RESULT 48
BP257211 568 bp mRNA linear EST 16-SBP-2004

LOCUS BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone

DEFINITION HRT00430, mRNA sequence.

ACCESSION BP257211

VERSION BP257211.1 GI:52172441

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 568)

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRT00430"
/issue_type="heart"
/clone_1ib="Sugano cDNA library, heart"

ORIGIN

Alignment Scores:

Pred. No.:	26.9	Length:	568
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP257211 (1-568)

Qy 1 Proaapval11ephleuglngu1val 9
|||||
DB 403 CCAGATGATATTTCTACAGAGATT 429

RESULT 49
BM172060 570 bp mRNA linear EST 04-DEC-2001

LOCUS IMAGE:4700059 5', mRNA sequence.

DEFINITION BM172060

ACCESSION BM172060

VERSION BM172060.1 GI:17311623

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 570)

AUTHORS Kale, P. I., Harsch, T. J., Folta, P. A., Nelson, D. O., Sanders, C. G. and Prange, C. K.

TITLE The I.M.A.G.E. Consortium quality control effort: clone resequencing for verification

JOURNAL Unpublished (2001)

COMMENT Other ESTs: BG533717
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the correct orientation), as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact info@image.llnl.gov.
Plate: LBCM1533 row: a column: 20
Seq primer: -21m13
High quality sequence stop: 570.
Location/Qualifiers
1..570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4700059"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NIH MGC 76"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site: 1; SfiI (ggcgccgagc); Site 2: SfiI (ggcgatcgagc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATATGACC-3' and 3' adaptor sequence: 5'-ATCTGAGAGCGGAGCGGCGGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	27	Length:	570
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
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DB:	3	Gaps:	0

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QY 1 ProaPVAL11epheleuglncgluval 9
DB 285 CCAGATGATGATTTCTTACGAGAGATT 311

RESULT 50
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DEFINITION BP221518 Sugano cDNA library, colon Homo sapiens cDNA clone
ACCESSION BP221518
VERSION BP221518.1 GI:52094423
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 570)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,S., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
DB: 3

JOURNAL
PUBMED 1534256
LOCUS BP221485 572 bp mRNA linear EST 16-SEP-2004
DEFINITION BP221485 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS107111, mRNA sequence.
ACCESSION BP221485
VERSION BP221485.1 GI:52177716
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 572)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,S., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
DB: 3

JOURNAL
PUBMED 1534256
LOCUS BP221485 572 bp mRNA linear EST 16-SEP-2004
DEFINITION BP221485 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT03149, mRNA sequence.
ACCESSION BP221485
VERSION BP221485.1 GI:52173539
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 570)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,S., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
```

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JOURNAL
PUBMED 1534256
LOCUS BP221485 572 bp mRNA linear EST 16-SEP-2004
DEFINITION BP221485 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS107111, mRNA sequence.
ACCESSION BP221485
VERSION BP221485.1 GI:52177716
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 572)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,S., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
DB: 3

JOURNAL
PUBMED 1534256
LOCUS BP221485 572 bp mRNA linear EST 16-SEP-2004
DEFINITION BP221485 Sugano cDNA library, heart Homo sapiens cDNA clone
HRT03149, mRNA sequence.
ACCESSION BP221485
VERSION BP221485.1 GI:52173539
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 570)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,S., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
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US-10-757-745-2_COPY_145_153 (1-9) x BP262485 (1-572)

QY 1 ProaapvaliilepHeuGlnGluval 9
DB 389 CCAGATGTGATATTTCTACAGAGATT 415

RESULT 53

LOCUS AU279894 573 bp mRNA linear EST 31-JUL-2003
DEFINITION AU279894 CHONS2 Homo sapiens cDNA clone CHONS2002038 5', mRNA
sequence.

ACCESSION AU279894
VERSION AU279894.1 GI:28299121
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

AUTHORS 1 (bases 1 to 573)
Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R.,
Isogai, T., Hata, J., Tomoya, Y. and Umezawa, A.

TITLE Redifferentiation of dedifferentiated chondrocytes and
chondrogenesis of human bone marrow stromal cells via chondrosphere
formation with expression profiling by large-scale cDNA analysis

JOURNAL Exp. Cell Res. 288 (1), 35-50 (2003)
PUBMED 12878157

COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@ri.co.jp

FEATURES
source 1..573
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/cell_type="chondrocytes"
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/note="Vector: pME18SFL3"

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Alignment Scores:

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Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AU279894 (1-573)

QY 1 ProaapvaliilepHeuGlnGluval 9
DB 470 CCAGATGTGATATTTCTACAGAGATT 496

RESULT 54

LOCUS BP221260

DEFINITION BP221260 Sugano cDNA library, colon Homo sapiens cDNA clone
COL08083, mRNA sequence.

ACCESSION BP221260
VERSION BP221260.1 GI:52094165
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

AUTHORS 1 (bases 1 to 573)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL 15342556
PUBMED

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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ORIGIN

Alignment Scores:

Pred. No.: 27.1 Length: 573
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP221260 (1-573)

QY 1 ProaapvaliilepHeuGlnGluval 9
DB 355 CCAGATGTGATATTTCTACAGAGATT 381

RESULT 55

LOCUS BP261500

DEFINITION BP261500 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS103816, mRNA sequence.

ACCESSION BP261500
VERSION BP261500.1 GI:52176731
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

AUTHORS 1 (bases 1 to 573)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL 15342556
PUBMED

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source 1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS103816"
/tissue_type="small intestine"

ORIGIN /clone_1lb="Sugano cDNA library, small intestine"

Alignment Scores:

Pred. No.: 27.1 Length: 573
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP261500 (1-573)

QY 1 ProaPVal11lePhleuGInGluVal 9

DB 339 CCAAGATGATATTTCTACAGAAAGTT 365

RESULT 56

BP262642 576 bp mRNA linear EST 16-SEP-2004

LOCUS BP262642 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION BP262642.1 GI:52177873

ACCESSION

BP262642

VERSION

BP262642.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 576)

AUTHORS

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

TITLE

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

JOURNAL

Genome Res. 14 (9), 1711-1718 (2004)

COMMENT

Contact: Yutaka Suzuki

FEATURES

Location/Qualifiers

1..576

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_1lb="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.: 27.3 Length: 576
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP262642 (1-576)

QY 1 ProaPVal11lePhleuGInGluVal 9

DB 357 CCAAGATGATATTTCTACAGAAAGTT 363

RESULT 57

BP262642 577 bp mRNA linear EST 16-MAY-2004

LOCUS

BP262642 17000600175228 GRN_PRRHP Homo sapiens cDNA 5', mRNA sequence.

DEFINITION

BP262642.1 GI:47315333

ACCESSION

BP262642

VERSION

BP262642.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 577)

Brandenberger,R., Mei,H., Zheng,S., Lai,S., Murage,J., Fisk,G.J.,

Li,Y., Xu,C., Farg,R., Guegler,R., Rao,M.S., Mandelam,R.,

Lebkowsky,D. and Stanton,L.M.

Transcriptome characterization elucidates signaling networks that

control human ES cell growth and differentiation

Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R

Regenerative Medicine

Genon Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@genon.com

Insert Length: 577, Std Error: 0.00.

Location/Qualifiers

1..577

/organism="Homo sapiens"

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/issue_type="embryonic stem cells, DMSO-treated H9 cell

line

/clone_1lb="GRN_PRRHP"

/note="Oligo GT-primed, full-length enriched cDNA library

from DMSO-treated H9 cell line H9 (p22) maintained in

feeder-free conditions"

ORIGIN

Alignment Scores:

Pred. No.: 27.4 Length: 577
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN298919 (1-577)

QY 1 ProaPVal11lePhleuGInGluVal 9

DB 433 CCAAGATGATATTTCTACAGAAAGTT 459

RESULT 58

BP261787 580 bp mRNA linear EST 16-SEP-2004

LOCUS BP261787 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION BP261787.1 GI:52177018

ACCESSION BP261787

VERSION BP261787.1

KEYWORDS EST.

ORGANISM Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 580)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Department of Medical Science, University of Tokyo

4-6-1, Shirokanebatai, Minato-ku, Tokyo 108-8639, Japan

Email: yusuzuki@ms.u-tokyo.ac.jp.

FEATURES
source
Location/Qualifiers
1. 580
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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ORIGIN
Alignment Scores:
Pred. No.: 27.5 Length: 580
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP261787 (1-580)

OY 1 ProaapVal11lephleugIngluVal 9
DB 368 CCAGATGATATTCTTCTACAGGAAGTT 394

RESULT 59
BP274368 580 bp mRNA linear EST 16-SEP-2004
LOCUS BP274368 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION KDN00894, mRNA sequence.
ACCESSION BP274368
VERSION BP274368.1 GI:52188100
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 580)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
Location/Qualifiers
1. 580
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN
Alignment Scores:
Pred. No.: 27.5 Length: 580
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP274368 (1-580)

OY 1 ProaapVal11lephleugIngluVal 9
DB 453 CCAGATGATATTCTTCTACAGGAAGTT 479

RESULT 60
AV1717253 581 bp mRNA linear EST 16-OCT-2000
LOCUS AV1717253 DCB Homo sapiens cDNA clone DCBMA04 5', mRNA sequence.
DEFINITION AV1717253
ACCESSION AV1717253
VERSION AV1717253.1 GI:10814405
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 581)
Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
Unpublished (2000)
CONTACT Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
Location/Qualifiers
1. 581
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN
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Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AV1717253 (1-581)

OY 1 ProaapVal11lephleugIngluVal 9
DB 276 CCAGATGATATTCTTCTACAGGAAGTT 302

RESULT 61
BP207751 581 bp mRNA linear EST 14-SEP-2004
LOCUS BP207751 Sugano cDNA library, coronary artery smooth muscle cell
DEFINITION BP207751
ACCESSION BP207751
VERSION BP207751.1 GI:52064157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

REFERENCE
AUTHORS
TITLE
JOURNAL

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 34

PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source location/Qualifiers

1..581
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/clone_lib="Sugano CDNA library, coronary artery smooth muscle cell"

ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP207751 (1-581)

QY 1 ProkaryoticPhlebotomus1 9
DB 341 CCAGATGTGATTTCTACAGAGATT 367

RESULT 62
BP225088 581 bp mRNA linear EST 15-SEP-2004
LOCUS BP225088 Sugano CDNA library, lymphocyte Daudi Homo sapiens CDNA
DEFINITION BP225088 DAI05184, mRNA sequence.
BP225088
ACCESSION BP225088.1 GI:52097993
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE
AUTHORS 1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
location/Qualifiers

FEATURES

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1..581
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/cell_line="Daudi"
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/note="Burkitt's lymphoma"

ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP225088 (1-581)

QY 1 ProkaryoticPhlebotomus1 9
DB 454 CCAGATGTGATTTCTACAGAGATT 480

RESULT 63
BP262101 581 bp mRNA linear EST 16-SEP-2004
LOCUS BP262101 Sugano CDNA library, small intestine Homo sapiens CDNA
DEFINITION BP262101 HSI05893, mRNA sequence.
BP262101
ACCESSION BP262101.1 GI:52177332
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE
AUTHORS 1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
location/Qualifiers

FEATURES

source
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSI05893"
/tissue_type="small intestine"
/clone_lib="Sugano CDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP262101 (1-581)

QY 1 ProkaryoticPhlebotomus1 9
DB 61 CCAGATGTGATTTCTACAGAGATT 87

RESULT 64
BP262638 581 bp mRNA linear EST 16-SEP-2004
LOCUS BP262638 Sugano CDNA library, small intestine Homo sapiens CDNA
DEFINITION BP262638 HSI0576, mRNA sequence.
BP262638
ACCESSION BP262638.1 GI:52177869
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE
1 (bases 1 to 581)

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp

FEATURES
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1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS107576"
/issue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 3

US-10-757-745-2_COPY_145_153 (1-9) x BP262638 (1-581)

QY 1 ProaapVal11lephLeugInglVal 9
Db 350 CCAGATGATATTTCTACAGAGATT 376

RESULT 65
BP270744 581 bp mRNA linear EST 17-SEP-2004
LOCUS BP270744
DEFINITION clone KAR05146, mRNA sequence.
ACCESSION BP270744
VERSION BP270744.1 GI:52220093
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp

FEATURES
source
1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAR05146"
/issue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 3

US-10-757-745-2_COPY_145_153 (1-9) x BP349936 (1-581)

QY 1 ProaapVal11lephLeugInglVal 9
Db 210 CCAGATGATATTTCTACAGAGATT 236

RESULT 67
BP379659 581 bp mRNA linear EST 21-SEP-2004
LOCUS BP379659
DEFINITION BP379659 Sugano cDNA library, uterus Homo sapiens cDNA clone
WMD06642, mRNA sequence.
ACCESSION BP379659
VERSION BP379659.1 GI:52412762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 3

US-10-757-745-2_COPY_145_153 (1-9) x BP270744 (1-581)

QY 1 ProaapVal11lephLeugInglVal 9
Db 341 CCAGATGATATTTCTACAGAGATT 367

RESULT 66
BP349936 581 bp mRNA linear EST 17-SEP-2004
LOCUS BP349936
DEFINITION BP349936 Sugano cDNA library, brain Homo sapiens cDNA clone
SZR06923, mRNA sequence.
ACCESSION BP349936
VERSION BP349936.1 GI:52279921
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 581)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ms.u-tokyo.ac.jp

FEATURES
source
1..581
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/mol_type="mRNA"
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/clone="SZR06923"
/issue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:
Pred. No.: 27.6 Length: 581
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 3

US-10-757-745-2_COPY_145_153 (1-9) x BP349936 (1-581)

QY 1 ProaapVal11lephLeugInglVal 9
Db 210 CCAGATGATATTTCTACAGAGATT 236

RESULT 67
BP379659 581 bp mRNA linear EST 21-SEP-2004
LOCUS BP379659
DEFINITION BP379659 Sugano cDNA library, uterus Homo sapiens cDNA clone
WMD06642, mRNA sequence.
ACCESSION BP379659
VERSION BP379659.1 GI:52412762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 581)
 AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: ysuzuki@ims.u-tokyo.ac.jp

FEATURES
 source
 1..581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="WMD06642"
 /issue_type="uteras"
 /clone_lib="Sugano CDNA library, uterus"

ORIGIN
 Alignment Scores:
 Pred. No.: 27.6 Length: 581
 Score: 45.00 Matches: 9
 Percent Similarity: 100.04 Conservative: 0
 Best Local Similarity: 100.04 Mismatches: 0
 Query Match: 100.04 Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP379659 (1-581)
 QY 1 Proapval11epheenglnlval 9
 DB 342 CCAGATGTGATATTCTACAGAGATT 368

RESULT 68
 CB286391 581 bp mRNA linear EST 27-FEB-2003
 LOCUS CB286391
 DEFINITION CMO36_C09_69 UNMMPW3 Sus scrofa cDNA clone PPSUBLIB_21C09 5', mRNA
 sequence.
 ACCESSION CB286391
 VERSION CB286391.1 GI:28577345
 KEYWORDS EST
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus
 1 (bases 1 to 581)
 Dvorak, C.M.T., Hyland, K.A., Machado, J.G., Zhang, Y., Fahrenkrug, S.C.
 and Murrtaugh, M.P.
 TITLE Gene discovery and expression profiling in porcine Peyer's patch
 JOURNAL Vet Immunol. Immunopathol. 105 (3-4), 301-315 (2005)
 PUBMED 15808308
 COMMENT Contact: Murrtaugh, M.P.
 Department of Veterinary Pathobiology
 University of Minnesota
 1971 Commonwealth Ave., St. Paul, MN 55108, USA
 Tel: 612-625-6735
 Fax: 612-625-5203
 Email: murrta001@umn.edu

The PHRED quality scores of this sequence are supplied below: 35 40
 45 42 44 42 51 46 42 37 37 37 35 40 35 22 35 35 29 35 35 35
 35 28 33 33 45 45 45 45 45 45 45 45 45 45 45 45 45 45 45 45
 46 51 46 43 42 42 37 35 45 45 45 45 45 45 45 45 45 45 45 45
 37 50 56 56 50 42 37 35 45 45 45 45 45 45 45 45 45 45 45 45
 37 40 34 34 28 28 28 42 42 50 56 56 46 46 40 38 38 38 56 56
 56 56 50 44 42 33 46 46 46 51 51 51 51 51 39 35 32 26 26
 29 35 33 27 42 50 51 56 56 56 56 56 43 40 38 35 35 41 41
 45 46 51 51 56 56 45 41 41 41 45 46 56 56 50 50 50 51 56 56
 36 36 36 36 40 40 35 35 42 40 41 41 41 41 41 43 46 51 56 56
 56 56 56 56 51 46 46 42 42 42 40 40 37 35 35 35 40 40 43 43 43

FEATURES
 source

42 40 40 35 40 40 40 42 37 35 40 42 51 51 56 56 56 56 56 56
 46 42 43 43 46 46 51 37 37 32 35 35 37 35 32 35 35 35 35 40
 35 35 40 45 45 51 51 45 45 45 45 45 45 43 46 42 42 44 48 56
 40 40 40 40 40 40 56 56 46 42 42 37 40 40 40 40 40 40 42
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 35 35 35 35 51 51 35 35 35 35 37 37 37 35 35 35 31 40 39
 40 40 40 40 37 42 42 32 32 32 32 32 32 32 32 32 32 32 32
 35 35 40 40 42 37 42 46 46 51 45 51 35 35 35 35 35 35 35
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 40 44 44 40 40 26 29 24 18 15 24 29 48 48 40 29 25 19 20 24 23
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 23 21 18 25 48 48 48 48 48 40 40 32 29 22 25 15 16 11 10 20 24 26
 23 29 29 25 27 25 22 32 32 32 27 29 34 34 40 40 29 20 15 11 11
 13 24 33 40 40 46 40 37 37 22 22 21 27 23 22 22 25 29 29 34 40
 40 32 32 26 32 26 24 Sequences were generated on ABI 3100 and 3700
 capillary sequencers. Raw sequence data was batch processed
 analyzed, groomed and submitted by the Animal Biotechnology Center
 (URL: <http://piloter.ansci.umn.edu/software.html>), University of
 Minnesota. Trace files have been submitted to the NCBI trace
 archive (<http://www.ncbi.nlm.nih.gov/Trace/trace.cgi?>).
 Chromosome maps were analyzed with Phred Version: 0.000925.c. Vector
 (PCMBP) and InVivoGen) Sus scrofa mitochondrion
 (g15835862) ref|NC_00845.1|, Escherichia coli K12 (g15835862)
 ref|NC_009413.1|, Escherichia coli K12 (g15835862) and respiratory syndrome
 virus (g111878202) ref|AF03357.1| (AF03357), Alzetomys sp.168 rRNA
 gene (g11184721) ref|Y15322.1| (Y15322), Sus scrofa 28S ribosomal
 RNA (g11388170) ref|AF080393.1| (AF080393), and Sus scrofa 18S ribosomal
 RNA (g11388592) ref|AF02857.1| (AF02857). Sequences were identified
 and masked by Cosmatch -mismatch=20, -mismatch=12, -penalty=-8.
 SWAL aligned scores were set to match score=1, gap initial
 penalty=-3 and gap extension penalty=-2. A continuous stretch of at
 least 3 bases of a PHRED quality 20 were required for
 subassembly, 5 and 3' TERMIN were defined by a continuous stretch
 of 10 nucleotides with a PHRED quality not less than 20. A terminal
 stretch of at most 40 un-masked bases were automatically trimmed
 when flanking masked sequence. Sequences with an INTERNAL continuous
 stretch of at most 20 bases with PHRED quality less than 20 were
 automatically prepared for submission. HIGHQUAL, START and HIGHQUAL STOP
 refer to the coordinates on CLIP_QUALITY and CLIP_VECTOR at the
 NCBI trace archive.
 Plate: 21 row: C column: 09
 Seq primer: Sp6 primer
 High quality sequence start: 67
 High quality sequence stop: 502.
 Location/Qualifiers
 1..581
 /organism="Sus scrofa"
 /mol_type="mRNA:9823"
 /db_xref="taxon:9823"
 /clone="PPSUBLIB_21C09"
 /issue_type="Peyer's patch"
 /note="Organ: small intestine, jejunum; Vector:
 PCMBP; Site: 1: NotI, Site 2: SalI; 6 week old
 patches were isolated from healthy and aged pigs
 or cross-bred pigs. RNA was extracted either immediately or
 after 3 hours stimulation in an airtight chamber with one of
 the following treatments: 1) no treatment; 2) Salmonella
 choleraesuis vaccine strain SC 54, 3) pCic AMP, and 4)
 acetate, concanavalin A, and 8-bromo-cyclic AMP. Each treatment was
 performed in the presence and absence of cycloheximide.
 Purified poly A+ RNA from each of the treated tissues
 and (2-4) was combined together, reverse transcribed, and
 cloned in to PCMBP to make a library of approximately
 530,000 recombinant clones with an average insert size of
 1.0 kbp. Poly A+ RNA from freshly isolated and non-treated
 tissue from an airtight chamber (untreated) was cloned in
 the same manner to produce an (untreated) cDNA library of
 approximately 900,000 clones with an average insert size
 of 1.5 kbp. Equal portions of the two libraries were

ORIGIN

pooled and then subtracted with porcine ST fibroblast RNA to create a subtracted porcine Peyer's patch library of approximately 6,000 clones with an average insert size of 1.0 kbp."

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:
27.6	581	45.00	9
Percent Similarity:		100.0%	Conservative: 0
Best Local Similarity:		100.0%	Mismatches: 0
Query Match:		100.0%	Indels: 0
DB:		6	Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CB286391 (1-581)

Qy 1 Proaspvalli1lePhelengIngluval 9

Db 265 CCAGATGATATTTCTACAGGAGTT 291

RESULT 69

BM507091

LOCUS 582 bp mRNA linear EST 15-FEB-2002

DEFINITION ih24h01.y1 Human insulinoma Homo sapiens cDNA 5' similar to

TR:095551 095551 DJ30M3.3 ; mRNA sequence.

ACCESSION BM507091

VERSION BM507091.1 GI:18678234

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 582)

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, R.,

Lemishka, I., Scease, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blisstein, A.,

Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCam, R., Cole, R., Tsagaris, R.,

Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: ih24h01.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to

PubMed SK- by Dr. H. Inoue DNA sequencing by: Washington

University Genome Sequencing Center For information on obtaining a

clone please contact: Dr. Hiroshi Inoue (hinoue@um.wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence scop: 269.

Location/Qualifiers

1..582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/tissue_type="insulinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="Human insulinoma"

/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:

XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system

(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to

pBluescript SK- by Dr. H. Inoue following the Washington

University protocol

(http://genome.wustl.edu/esc/lambda_protocol.shtml).

Please contact Hiroshi Inoue, MD/PhD for further

information on this library (Metabolism Division, Permut

ORIGIN

Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:
27.6	582	45.00	9
Percent Similarity:		100.0%	Conservative: 0
Best Local Similarity:		100.0%	Mismatches: 0
Query Match:		100.0%	Indels: 0
DB:		3	Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BM507091 (1-582)

Qy 1 Proaspvalli1lePhelengIngluval 9

Db 235 CCAGATGATATTTCTACAGGAGTT 261

RESULT 70

BP219740

LOCUS 582 bp mRNA linear EST 15-SEP-2004

DEFINITION BP219740 Sugano cDNA library, caudate nucleus Homo sapiens cDNA

clone CNR08985, mRNA sequence.

ACCESSION BP219740

VERSION BP219740.1 GI:52092643

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Medical Science, University of Tokyo

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1..582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CNR08985"

/tissue_type="caudate nucleus"

/clone_lib="Sugano cDNA library, caudate nucleus"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Score:	Matches:
27.6	582	45.00	9
Percent Similarity:		100.0%	Conservative: 0
Best Local Similarity:		100.0%	Mismatches: 0
Query Match:		100.0%	Indels: 0
DB:		3	Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP219740 (1-582)

Qy 1 Proaspvalli1lePhelengIngluval 9

Db 448 CCAGATGATATTTCTACAGGAGTT 474

RESULT 71

BP233592

LOCUS 582 bp mRNA linear EST 15-SEP-2004

DEFINITION BP233592 Sugano cDNA library, coronary artery endothelial cell Homo

sapiens cDNA clone HCR00774, mRNA sequence.

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ACCESSION BP233592 GI:52106502
VERSION BP233592.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR00774"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
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endothelial cell"
ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP233592 (1-582)
QY 1 ProAppValIIlePheLeuGInGluVal 9
Db 448 CCAGATGTGATATTCTACAGAGAGTT 474
RESULT 72
LOCUS BP234218 582 bp mRNA linear EST 15-SEP-2004
DEFINITION BP234218 Sugano cDNA library, coronary artery endothelial cell Homo
sapiens cDNA clone HCR02378, mRNA sequence.
ACCESSION BP234218
VERSION BP234218.1 GI:52107128
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR02378"
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/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery
endothelial cell"
ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP261141 (1-582)
QY 1 ProAppValIIlePheLeuGInGluVal 9
Db 460 CCAGATGTGATATTCTACAGAGAGTT 486
RESULT 73
LOCUS BP261141 582 bp mRNA linear EST 16-SEP-2004
DEFINITION BP261141 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS102806, mRNA sequence.
ACCESSION BP261141
VERSION BP261141.1 GI:52176372
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
JOURNAL block structure in the promoter regions
PUBMED Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS102806"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"
ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP261141 (1-582)
QY 1 ProAppValIIlePheLeuGInGluVal 9
Db 339 CCAGATGTGATATTCTACAGAGAGTT 365
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RESULT 74
BP261789
LOCUS BP261789 582 bp mRNA linear EST 16-SEP-2004
DEFINITION BP261789 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS105013, mRNA sequence.
ACCESSION BP261789
VERSION BP261789.1 GI:52177020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS105013"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP261789 (1-582)

QY 1 Proasparviallephelengingluval 9
|||||
Db 61 CCAGATGATATTTCTACAGAGATT 87

RESULT 75
BP263516
LOCUS BP263516 582 bp mRNA linear EST 16-SEP-2004
DEFINITION BP263516 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS111929, mRNA sequence.
ACCESSION BP263516
VERSION BP263516.1 GI:52178747
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

FEATURES
source
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS111929"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP270415 (1-582)

QY 1 Proasparviallephelengingluval 9
|||||
Db 431 CCAGATGATATTTCTACAGAGATT 457

RESULT 76
BP270415
LOCUS BP270415 582 bp mRNA linear EST 17-SEP-2004
DEFINITION BP270415 Sugano cDNA library, small intestine Homo sapiens cDNA
clone KAR02166, mRNA sequence.
ACCESSION BP270415
VERSION BP270415.1 GI:52219764
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.fst

Page 40

```
RESULT 77
BP275810 582 bp mRNA linear EST 16-SEP-2004
LOCUS BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION K0404583, mRNA sequence.
ACCESSION BP275810
VERSION BP275810.1 GI:52189542
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 582)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source 1..582
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="K0404583"
/tissue_type="kidney"
/clone_lib="Sugano cDNA library, kidney"
ORIGIN
Alignment Scores:
Pred. No.: 27.6 Length: 582
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP275810 (1-582)
QY 1 Probpvalli1lephelenglnlva1 9
DB 422 CCAGATGTGATATTTCTACAGAGAGATT 448
FEATURES
source 583 bp mRNA linear EST 14-SEP-2004
LOCUS BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION AB080961, mRNA sequence.
ACCESSION BP195721
VERSION BP195721.1 GI:52039998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source 1..583
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="AB080961"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"
ORIGIN
Alignment Scores:
Pred. No.: 27.7 Length: 583
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP262103 (1-583)
QY 1 Probpvalli1lephelenglnlva1 9
DB 490 CCAGATGTGATATTTCTACAGAGAGATT 516
FEATURES
source 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
ACCESSION BP262103
VERSION BP262103.1 GI:52177334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source 1..583
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS105902"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"
ORIGIN
Alignment Scores:
Pred. No.: 27.7 Length: 583
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP262103 (1-583)
QY 1 Probpvalli1lephelenglnlva1 9
DB 490 CCAGATGTGATATTTCTACAGAGAGATT 516
```

```
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source 1..583
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="AB080961"
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/clone_lib="Sugano cDNA library, brain"
ORIGIN
Alignment Scores:
Pred. No.: 27.7 Length: 583
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP262103 (1-583)
QY 1 Probpvalli1lephelenglnlva1 9
DB 490 CCAGATGTGATATTTCTACAGAGAGATT 516
FEATURES
source 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
ACCESSION BP262103
VERSION BP262103.1 GI:52177334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 583)
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source 1..583
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS105902"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"
ORIGIN
Alignment Scores:
Pred. No.: 27.7 Length: 583
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BP262103 (1-583)
QY 1 Probpvalli1lephelenglnlva1 9
DB 490 CCAGATGTGATATTTCTACAGAGAGATT 516
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DB 367 CCAGATGATATTTCTACAGAGATT 393

RESULT 80
LOCUS BP262741
DEFINITION BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS107919, mRNA sequence.
ACCESSION BP262741
VERSION BP262741.1 GI:52177972
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
source 1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS107919"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 27.7 Length: 583
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP262741 (1-583)

QY 1 Proasparil11ephelunglunlval 9
DB 303 CCAGATGATATTTCTACAGAGATT 329

RESULT 81
LOCUS BP319548
DEFINITION BP319548 Sugano cDNA library, pericardium Homo sapiens cDNA clone
PCD11128, mRNA sequence.
ACCESSION BP319548
VERSION BP319548.1 GI:52248523
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
CONTACT: Yutaka Suzuki
Department of Virology

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
source 1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PCD11128"
/tissue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"

ORIGIN

Alignment Scores:
Pred. No.: 27.7 Length: 583
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP319548 (1-583)

QY 1 Proasparil11ephelunglunlval 9
DB 482 CCAGATGATATTTCTACAGAGATT 508

RESULT 82
LOCUS BU783229
DEFINITION BU783229 583 bp mRNA linear EST 11-OCT-2002
in01a08.y1 Human insu1lnoma Homo sapiens cDNA clone IMAGE:6123158
5' similar to TR:095551 O95551 D3J0M3.3 ;, mRNA sequence.
ACCESSION BU783229
VERSION BU783229.1 GI:23827207
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 583)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Maria, M., Page, D., Wylie, T., Martin, J., Bliscain, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarashvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: in01a08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40bp from Gibco
High quality sequence stop: 430.
Location/Qualifiers

FEATURES
source 1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6123158"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"

/note=Oleam: pancreas; Vector: plbuescript SK-; Site:1: XhoI; Site:2: SccCI; Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to plbuescript SK- by Dr. H. Inoue following the Washington University protocol (<http://www.wustl.edu/~sambo/protocol.shtml>).

Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library. "

ORIGIN

Alignment Score:	27.7	Length:	58.8
pred. No.:		Matches:	9
Score:	45.00	Conservative:	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%	Gaps:	0
DB:	5		

US-10-757-745-2_COPY_145_153 (1-9) X BU783229 (1-583)

Qy

Qy 1 ProAspValIlePheLeuGlnGluVal 9
Db 431 CCAGATGTGATATTCTACAGAGATT 457

RESULT 83			
BP263059			
LOCUS	BP263059	504 bp	linear mRNA
DEFINITION	BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA clone HS110591, mRNA sequence.		
			EST 16-SRP-2004

**JOURNAL
PUBMED
COMMENT**

FEATURES

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Location/Qualifiers

ORIGIN

Alignment Scores:	
Pred. No.:	27.7
Score:	45.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	3
Gaps:	0
Length:	588
Matches:	9
Conservative:	0
Mismatch:	0
Indels:	0
Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BP263059 (1-584)

Qy

1 ProAspValIlePheLeuGlnGluVal 9

Db 356 CCAGATGTGATATTCTACAGGAAGTT 382

RESULT 84
PD348677

LOCUS	BP348623	584 bp	mRNA	linear	EST 17-SEP-2004
DEFINITION	Sucarno cDNA 14hrayv brain Homo sapiens cDNA clone				
ABBREVIATION	BB348623				

FEATURES

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SOURCE
1..384
/organism="Homo sapiens"
/mol_type="mrna"
/db_xref="taxon:9606"
/clone="SR01143"
/tissue_type="brain"
/clone_id="Sugano cDNA library, brain"

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ORIGIN

Alignment Scores:	
pred. No.:	27.7
Length:	584
Score:	45.00
Percent Similarity:	100.0%
Conservative:	0
Best Local Similarity:	100.0%
Mismatches:	0
Query Match:	100.0%
Indels:	0
Gaps:	0
DB:	3

US-10-757-745-2_COPY_145_153 (1-9) x BP348623 (1-584)

Q27

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Qy      1 ProAspValIlePheLeuGlnIuVal 5
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Db      463 CCAGATGTGATATTCTACAGGAAGTT 4

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RESULT 85	BP236074	LOCUS	DEFINITION
BP236074	588 bp	mRNA	linear EST 15-SRP-2004
BP236074	Sugano cDNA library,	coronary artery endothelial cell	Homom
BP236074	sapiens cDNA clone HCR06784,	mRNA sequence.	

SOURCE

ORGANISM	REFERENCE
<i>Homo sapiens</i>	1 (bases 1 to 568)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	

TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)
PUBMED	15342556
COMMENT	Contact: Yutaka Suzuki

Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..588

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR06784"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN
Alignment Scores:
Pred. No.: 28 Length: 588
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP348796 (1-588)

Qy 1 ProaapValillepHeuGIngluVal 9
|||||
469 CCAGATGTGATATTCTACAGAGATT 495

RESULT 86
LOCUS BP348796 588 bp mRNA linear EST 17-SEP-2004
DEFINITION BP348796 Sugano cDNA library, brain Homo sapiens cDNA clone
SZR01880, mRNA sequence.
ACCESSION BP348796
VERSION BP348796.1 GI:52278781
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 588)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..588

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZR01880"
/tissue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN
Alignment Scores:
Pred. No.: 28 Length: 588
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP348796 (1-588)
Qy 1 ProaapValillepHeuGIngluVal 9
|||||
461 CCAGATGTGATATTCTACAGAGATT 487

RESULT 87
LOCUS AL703449 602 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686G0621.r1.686 (synonym: h1cc3) Homo sapiens cDNA clone
DKFZp686G0621.5', mRNA sequence.
ACCESSION AL703449
VERSION AL703449.1 GI:19686804
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 602)
Ansoerge,W., Winkner,U., Mewes,W., Weil,B. and Wiemann,S.
EST (Ansoerge,W., Winkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
CONTACT: MIPS

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories, of the
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp686G0621) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
Location/Qualifiers
1..602

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686G0621"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: h1cc3)"
/note="vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Alignment Scores:
Pred. No.: 28.7 Length: 602
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AL703449 (1-602)

Qy 1 ProaapValillepHeuGIngluVal 9
|||||
434 CCAGATGTGATATTCTACAGAGATT 460

RESULT 88
LOCUS CB069952 621 bp mRNA linear EST 21-JAN-2003
DEFINITION is1j1e10.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5554035 5'
similar to TR:095551 095551.D3J0M3.3', mRNA sequence.
ACCESSION CB069952
VERSION CB069952.1 GI:27814472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

ORIGIN
Alignment Scores:
Pred. No.: 28 Length: 621
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

REFERENCE 1 (bases 1 to 621)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Keestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Page,D., Wylie,T., Martin,J., Bistain,A., Schmitt,A., Reising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagariswill,R., Williams,T., Jackson,Y. and Bowers,Y.
JOURNAL Endocrine Pancreas Consortium
COMMENT Unpublished (2000)
Other ESTs: 1831e10.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohpc.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 476.
Location/Qualifiers
1..621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6554035"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR5 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site:1; NotI; Site 2: XhoI; cDNA made by oligo-dt priming. Size selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN
Alignment Scores:
Pred. No.: 29.7 Length: 621
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CB069952 (1-621)

QY 1 ProkaryoticPhleungGluVal 9
DB 439 CCAGATGTATTTCTACGAGAGTT 465

RESULT 89
BP977971 626 bp mRNA linear EST 22-JAN-2001
LOCUS 602148451f1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4307317 5',
DEFINITION mRNA sequence.
ACCESSION BP977971
KEYWORDS BP977971.1 GI:12345186
SOURCE EST
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 626)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL National ID (1999)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: greg@biml.nih.gov
Tissue Procurement: ATCC/DC/DTP
DNA Library Preparation: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://imgc11nl.gov
Plate: LNCMI177 row: e column: 14
High quality sequence stop: 614.
Location/Qualifiers
1..626
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4307317"
/tissue_type="melanotic melanoma, high MDR"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 62"
/note="Organ: Skin; Vector: pDNR-LIB (Clontech); Site:1; SfiI (ggccgacgagc); Site 2: SfiI (ggccatcagc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCRAGAGCCGAGCCGAGCAGC-AT(30)BN-3' (where B = A, T, C, G, or N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 clones contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN
Alignment Scores:
Pred. No.: 30 Length: 626
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BP977971 (1-626)

QY 1 ProkaryoticPhleungGluVal 9
DB 447 CCAGATGTATTTCTACGAGAGTT 473

RESULT 90
CB157906 634 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0217150 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-5-F06
DEFINITION 5', mRNA sequence.
ACCESSION CB157906
VERSION CB157906.1 GI:28143040
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 634)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.W., Park,H.S., Kim,S. and Kim,Y.S.
JOURNAL 21C Frontier Korean EST Project 2001
COMMENT Unpublished (2002)
Contact: Kim YS
Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52, Boeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: F column: 06
High quality sequence stop: 634.
Location/Qualifiers

FEATURES

source

1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L18POOL1n1-5-P06"
/cell_line="SNU-354-Cho-CK+Choi-CK+HLK-3"
/lab_host="Top10"
/clone_lib="L18POOL1n1"
/note="Organ: Liver; Vector: p7773-Pac; Site 1: EcoRI;
Site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Alignment Scores:

Pred. No.:	30.5	Length:	634
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CB157906 (1-634)

Qy 1 ProaPVal1lePheLeuGInGluVal 9
DB 385 CCAGATGCATATTTCTACAGAGATT 411

RESULT 91
LOCUS CV023369 634 bp mRNA linear EST 20-AUG-2004
DEFINITION 288 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC017553, mRNA sequence.
ACCESSION CV023369
VERSION CV023369.1 GI:51481130
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 634)
Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Seguerre,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
Vandenhaute,J., Casick,M.E., Alcala,V.S., Hill,D.E. and Vidal,M.
Humana Reproductive Version 1.1: a Platform for Reverse Proteomics
Genome Res. (2004) in press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR primers
FORWARD: ATGAGATTGGGAGTTGCCTGGA
BACKWARD: TACAATATTAATCTAAGTTCCACAGAG
Insert length: 634 Std Error: 32.00

Plate: 11008 row: 05 column: F
Seq primer: ACTGGCCGTCTTACACAGCTGCTGACTGGGAAAC
High quality sequence start: 97
High quality sequence stop: 633
POLYA=No.
Location/Qualifiers

FEATURES

source

1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian Gene
Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor vector. Reference: MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

ORIGIN

Alignment Scores:

Pred. No.:	30.5	Length:	634
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CV023369 (1-634)

Qy 1 ProaPVal1lePheLeuGInGluVal 9
DB 433 CCAGATGCATATTTCTACAGAGATT 459

RESULT 92
LOCUS B1333830 644 bp mRNA linear EST 30-JUL-2001
DEFINITION 60299339P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141577 5',
mRNA sequence.
ACCESSION B1333830
VERSION B1333830.1 GI:15018487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 644)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNM at:
http://image.llnl.gov
Plate: L14M11348 row: n column: 10
High quality sequence stop: 531.
Location/Qualifiers

FEATURES

source

1..644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5141577"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_lib="NIH_MGC_12"

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae; Homo.

AUTHORS 1 (bases 1 to 657)

TITLE Brandenberger R., Wei, H., Zhang, S., Lei, S., Muraige, J., Flak, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.

JOURNAL Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation

PUBMED Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT 15146197

CONTACT: Brandenberger R

REGENERATIVE MEDICINE Regenerative Medicine

GERON CORPORATION 230 Constitution Drive, Menlo Park, CA 94025, USA

TEL: 650 473 8658

FAX: 650 473 7760

EMAIL: rbrandenberger@geron.com

INSERT LENGTH: 657

STD ERROR: 0.00.

LOCATION/QUALIFIERS 1..657

FEATURES source

ORIGIN /organism="Homo sapiens"

mol_type="mRNA"

db_xref="taxon:9606"

cisue_type="embryonic stem cell, retinoic acid and

mitogen-created hES cell line H7"

/clone_lib="GRN PRENEU"

/note="oligo dT primed, full-length enriched cDNA library

from hES cell line H7 (p2) maintained in feeder-free

conditions. Embryoid bodies were generated in the presence

of all-trans retinoic acid and mitogens."

ALIGNMENT SCORES:

Pred. No.:	31.7	Length:	657
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN298920 (1-657)

QY 1 Proaspvallephelengingluval 9

DB 389 CCAGATGATATTTCTACAGAGATT 415

RESULT 96

LOCUS CN791432. 674 bp mRNA linear EST 26-MAY-2004

DEFINITION 4126159 BARC 8BOV Bos taurus cDNA clone 8BOV_42B11 5', mRNA

SEQUENCE sequence.

ACCESSION CN791432

VERSION CN791432.1

GI: 47687412

EST. EST.

KEYWORDS Bos taurus (cow).

SOURCE Bos taurus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 674)

AUTHORS Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassel, C.P. and Matkumali, L.K.

TITLE Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle

JOURNAL Unpublished (2004)

COMMENT Contact: Richard G. Baumann

BOVINE FUNCTIONAL GENOMICS LAB ANRI BLDG 162: BARC-EAST, Beltsville, MD 20705, USA

TEL: 3015048604

FEATURES source

ORIGIN /organism="Bos taurus"

mol_type="mRNA"

strain="Holstein"

db_xref="taxon:9913"

/clone="8BOV_42B11"

/sex="Female"

/tissue_type="Epithelial, Muscle"

/dev_stage="Lactating, Neonatal"

/lab_host="DH10B Torus"

/clone_lib="BARC 8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site: 1: NotI; Site 2: EcoRI; Normalized cow cDNA intestinal

library in pCMVSPORT6.1, constructed from equimolar mRNA

pools derived from 5 sources; 4 lactating intestinal, 1

neonatal intestinal 4/5 lactating, proximal duodenum,

jejunum, distal ileum, colon, 1/5 neonatal, proximal

duodenum, jejunum, distal ileum"

ALIGNMENT SCORES:

Pred. No.:	32.7	Length:	674
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN791432 (1-674)

QY 1 Proaspvallephelengingluval 9

DB 340 CCTGATGATATTTCTACAGAGATC 366

RESULT 97

LOCUS BG719113 678 bp mRNA linear EST 08-MAY-2001

DEFINITION 60269045F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831186 5', mRNA sequence.

ACCESSION BG719113

VERSION BG719113.1

GI: 13998300

EST. EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 678)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strusberg, Ph.D.

EMAIL: cgephs-remail.nih.gov

TISSUE PROCUREMENT: Miklos Palkovits, M.D., Ph.D.

CDNA LIBRARY PREPARATION: Michael J. Brownstein (NHGRI), Shitaki Toshitsuki and Piero Carninci (RIKEN)

CDNA LIBRARY ARRAYED BY: The I.M.A.G.E. Consortium (LNL)

DNA SEQUENCING BY: Incyte Genomics, Inc.

CLONE DISTRIBUTION: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

HTTP://image.llnl.gov

PLATE: L1AM10753

ROW: 1

COLUMN: 11

HIGH QUALITY SEQUENCE STOP: 672.

LOCATION/QUALIFIERS

source 1..678

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:481186"
/lab_host="DH10B"
/note="Organ: testis; Site:1: BamHI; Site:2: SalI-XhoI
pBluescript KS+; size-selected for average
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to RQF 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ALIGNMENT SCORES:

Pred. No.: 32.9 Length: 678
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 2

US-10-757-745-2_COPY_145_153 (1-9) x BG719113 (1-678)

QY 1 PROAPVALLIephelengingluva1 9
DB 455 CCGAGTGTGATTTCTACAGAGATT 481

RESULT 98
LOCUS CK952220 680 bp mRNA linear EST 15-MAR-2004
DEFINITION 4091710 BARC 10BOV Bos taurus cDNA clone 10BOV29_F21 5', mRNA
ACCESSION CK952220
VERSION CK952220.1 GI:45466600
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 680)
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rudenfeld, M. and Gasbarre, L.C.,
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
Unpublished (2004)
JOURNAL Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim.fasta. Vector identified
by cross_match using options -mismatch 12 -minscore 18
Plate: 29 row: F column: 21
Seq primer: CCCAGTCACGACGTTGTAACG
High quality sequence stop: 680.
Location/Qualifiers
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/organism="Bos taurus"
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/clone="10BOV29_F21"
/sex="Male"

/class_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pagen-1; Site:1:
EcoRI; Site:2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunums of 18 and 21 wk old steers, and
distal ileums of 14 day old calves, proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"

ORIGIN

Alignment Scores:
Pred. No.: 33 Length: 680
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 7

US-10-757-745-2_COPY_145_153 (1-9) x CK952220 (1-680)

QY 1 PROAPVALLIephelengingluva1 9
DB 76 CCGATGTGTGATTTCTACAGAGAGTC 102

RESULT 99
LOCUS CN789157 683 bp mRNA linear EST 26-MAY-2004
DEFINITION 4123581 BARC 8BOV Bos taurus cDNA clone 8BOV_37N03 5', mRNA
ACCESSION CN789157
VERSION CN789157.1 GI:47685137
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 683)
Matukumalli, L.K., Baldwin, R.L., Sonstegard, T.S., Van Tassel, C.P. and
Baumann, R.G.,
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
JOURNAL Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI 162, BARC-East, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt "-trim.fasta. Vector identified
by cross_match using options -mismatch 12 -minscore 18
Plate: 37 row: N column: 03
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Location/Qualifiers
1..683
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/clone_lib="BARC 8BOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site:1:
NotI; Site:2: EcoRI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA

ORIGIN pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 lactating, proximal duodenum, jejunum, distal ileum, colon, 1/5 neonatal, proximal duodenum, jejunum, distal ileum"

Alignment Scores:

Pred. No.: 33.1 Length: 683
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN789157 (1-683)

Qy 1 Proaspvalillepheleunglinguval 9
DB 334 CCTGATGATATTTCTACAGAAATC 360

RESULT 100

CK981492 685 bp mRNA linear EST 16-MAR-2004
LOCUS 4114013 BARC 9BOV Bos taurus cDNA clone 9BOV43_H04 5', mRNA
DEFINITION sequence.

ACCESSION CK981492
VERSION CK981492.1 GI:45499472
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 685)
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut

~TITLE Unpublished (2004)
JOURNAL Contact: Tad S. Sonstegard
COMMENT Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred 0.000925 using options -trim alt "-trim fasta. Vector identified by cross match using options -mismatch 12 -minscore 12
Plate: 43 row: H column: 04
Seq primer: CCCAGTCACGACCTGTAAACG
High quality sequence stop: 685.
Location/Qualifiers
1..685

FEATURES

source
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="9BOV43_H04"
/sex="Male"
/tissue_type="Pooled"
/dev_stage="Multiple"
/lab_host="DH10B T1 phage resistant"
/clone_1ib="BARC 9BOV"
/note="Organ: Abomasum; Vector: pagen-1; Site 1: EcorV; Site 2: NotI; Equimolar amounts of mRNA extracted from fundic and pyloric abomasum of 18 and 21 week old steers. Exposure to *Ostreia* gastritis was initiated at 15 weeks of age. fundic and pyloric abomasum"

ORIGIN

Alignment Scores:
Pred. No.: 33.3 Length: 685

Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CK981492 (1-685)

Qy 1 Proaspvalillepheleunglinguval 9
DB 127 CCTGATGATATTTCTACAGAAATC 153

RESULT 101

CR767236 701 bp mRNA linear EST 23-SEP-2004
LOCUS DKFZP469E1236_r1_469 (synonym: pk1d1) Pongo pygmaeus cDNA clone
DEFINITION DKFZP469E1236_5', mRNA sequence.
CR767236
VERSION CR767236.1 GI:52609173
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pongo.
1 (bases 1 to 701)
Ansoorge, W., Krieger, S., Regiert, T., Rittmüller, C., Schwager, B., Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
Pongo pygmaeus mRNA (Ansoorge, W., Krieger, S., Regiert, T., et al.)
Unpublished (2004)
Contact: MIPS

~TITLE Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
JOURNAL This is the 5' sequence of the clone insert. Clone from S. Wiemann,
COMMENT Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZP469E1236
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

source
1..701
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP469E1236"
/tissue_type="Kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1ib="469 (synonym: pk1d1)"
/note="Vector: pSPORT1_Sfi; Site 1: SfiIA; Site 2: SfiIB"

ORIGIN

Alignment Scores:
Pred. No.: 34.1 Length: 701
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR767236 (1-701)

Qy 1 Proaspvalillepheleunglinguval 9
DB 361 CCAGATGATATTTCTACAGAAATC 387

RESULT 102

B1334620 704 bp mRNA linear EST 30-JUL-2001
LOCUS 602998939P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE5141193 5',
DEFINITION mRNA sequence.

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 50

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ACCESSION      B1334820
VERSION        B1334820.1
KEYWORDS       GI:15019477
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;
               Homiidae; Homo.

REFERENCE
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
COMMENT       Unpublished (1999)
               Contact: Robert Strauberg, Ph.D.
               Email: cgsab@remail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: Incyte Genomics, Inc.
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/BLNI at:
               http://image.jnl.gov
               Plate: LHAM11347 row: n column: 10
               High quality sequence stop: 704.

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20892, USA
Tel: 301 402 2373
Fax: 301 435 5148
Email: jmf@nih.gov
The 'c' library was constructed by Alexander Gublin, Ph.D. in the Laboratory of Chemical Biology, NIDDK, NIH. DNA sequencing and/or analyses by National Institutes of Health Intramural Sequencing Center (NISC). More information available at:
<http://hembase.nidk.nih.gov>
Plate: 72 Row: d column: 11
Seq primer: 5' lambda-TripLx2 Sequencing Primer.
Location/Qualifiers
1..710
source

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FEATURES
SOURCE
Location/Qualifiers
1..710
/organism="Homo sapiens"
/mol_type="mrna"
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/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
/seq_source="Precursor erythroblasts; GPA++"
/lab_host="MD5alpha"
/clone_idb="Hembase; Erythroid Precursor Cells (LCB:c1 library)"
/notes="Organ: blood; Vector: pRiDex2; Site: 1: Sf11; Site: 2: Sf11. A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/l peptide nucleic acid (PNA) oligos (N-terminal)-biotin-GTC-CAC-CCG-AGA-CTT-G-(C-terminal) and (N-terminal)-biotin-C/T/C/T-GAA-GTT-CTC-AGA-A-(C-terminal). Synthesized cDNA was digested with Sf11 and size-selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC; Http://www.nisc.nih.gov/)."

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ORIGIN
Alignment Scores:
Pred. No.: 34.6 Length: 710
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BU661472 (1-710)
QY 1 ProkspValIIePheLeuGInGluVal 9
|||
349 CCGAGTGTGTATTCTTCTACAGGAGTT 375

RESULT 104
CN298923 711 bp mRNA linear EST 16-MAY-2004
LOCUS 17000600002122 GRN_PPREHP Homo sapiens CDNA 5', mRNA sequence.
ACCESSION CN298923
VERSION CN298923.1 GI:47315337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 711)
Brundenberger R., Wei H., Zhang S., Lei S., Murage J., Flek G.J.,
Li X., Xu C., Fang R., Guegler K., Rao M.S., Mandelam R.,

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TITLE Lebikowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation.
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 711 Std Error: 0.00.
Location/Qualifiers

FEATURES
source 1..711
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_1lb="GRN_PREHEP"
/note="oligo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 34.7 Length: 711
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN298923 (1-711)

QY 1 ProAapValIlePheLeuGlnGluVal 9
Db 398 CCAGATGATATTTCTACAGAGATT 424

RESULT 105
CN298922 729 bp mRNA linear EST 16-MAY-2004
LOCUS 1700060007717 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298922
ACCESSION CN298922
VERSION CN298922.1 GI:47315336
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R., Lebikowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers

FEATURES
source 1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
/clone_1lb="GRN_PREHEP"
/note="oligo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 35.7 Length: 729
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN298924 (1-729)

QY 1 ProAapValIlePheLeuGlnGluVal 9
Db 425 CCAGATGATATTTCTACAGAGATT 451

RESULT 106
CN298924 729 bp mRNA linear EST 16-MAY-2004
LOCUS 17000424496911 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298924
ACCESSION CN298924
VERSION CN298924.1 GI:47315338
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R., Lebikowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 729 Std Error: 0.00.
Location/Qualifiers

FEATURES
source 1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
/clone_1lb="GRN_ES"
/note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 35.7 Length: 729
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN298924 (1-729)

QY 1 Proaspyalllephelungluval 9
Db 367 CCAGATGTGATTTCTACAGAGATT 393

RESULT 107
CX760857 731 bp mRNA linear EST 24-JAN-2005
LOCUS NC005007.40963393 NIH MGC 281 Homo sapiens cDNA clone
DEFINITION CX760857 7785600 3', mRNA sequence.
ACCESSION CX760857.1 GI:58057513
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 731)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gerdas@mail.nih.gov
Issue Description: Meri Ripio
CNA Library Preparation: Express Genomics
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://imgsc.llnl.gov
Plate: Image594 Row: b Column: 14
High quality sequence stop: 574.
Location/Qualifiers
1..731
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cds="IMAGE:7783600"
/feature_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B TONa"
/clone_lib="NIH MGC 281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site 1:
EcoRV, Site 2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSE-6 NIH Registry designation UC06. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tyr-1-81, Tyr-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dT primer:
5'-TGACTGCTGATGATCGAGCGCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
library is normalized (non-normalized primary
library is NIH MGC 280) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN
Alignment Scores:
Pred. No.: 35.8 Length: 731
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CX760857 (1-731)
QY 1 Proaspyalllephelungluval 9

Db 437 CCAGATGTGATTTCTACAGAGATT 463

RESULT 108
CR791801 739 bp mRNA linear EST 01-OCT-2004
LOCUS DKFZp4681522.t1.468 (synonym: phrt1) Pongo pygmaeus cDNA clone
DEFINITION DKFZp4681522.5', mRNA sequence.
ACCESSION CR791801
VERSION CR791801.1 GI:53710641
KEYWORDS
SOURCE EST.
ORGANISM Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo
1 (bases 1 to 739)
Ostenwælder, B.; Ostermaler, B.; Deutschenbaur, S.; Schaidt, A.;
Wiemann, S.;
Newes, H.W.; Weil, B.; Amd, C.; Oester, A.; Fodor, G.; Han, M. and
Deutschenbaur, S., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ),
Email: s.wiemann@dkfz-heidelberg.de, sequenced by Medigenomix
(Martinsried, Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZp4681522) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/c1.cgi?cloneid=DKFZp4681522
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/project/cdna/.
Location/Qualifiers
1..739
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/cds="DKFZp4681522"
/feature_type="heart"
/issue_type="adult"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="468 (synonym: phrt1)"
/note="Vector: pSport1_Sfi; Site_1: Sfi1A; Site_2: Sfi1B"

ORIGIN
Alignment Scores:
Pred. No.: 36.3 Length: 739
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR791801 (1-739)
QY 1 Proaspyalllephelungluval 9
Db 451 CCAGATGTGATTTCTACAGAGATT 477

RESULT 109
CR767800 749 bp mRNA linear EST 23-SEP-2004
LOCUS DKFZp4690058.t1.469 (synonym: pkidl) Pongo pygmaeus cDNA clone
DEFINITION DKFZp4690058.5', mRNA sequence.
ACCESSION CR767800
VERSION CR767800.1 GI:52610302
KEYWORDS
SOURCE EST.
ORGANISM Pongo pygmaeus (orangutan)

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pongo.
1 (bases 1 to 749)
Ostenwaelder, B., Obermaier, B., Deutschenbaur, S., Schajp, A., Mewes, H.W., Weill, B., Amid, C., Osanger, A., Fodor, G., Han, M. and Wiemann, S.

TITLE

Pongo pygmaeus mRNA (Ostenwaelder, B., Obermaier, B., Deutschenbaur, S., et al.)

JOURNAL
COMMENT

Unpublished (2004)
Contact: MIPS

MIPS

Ingolstedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix (Martinried/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp69C058) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp69C058
Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES

source

Location/Qualifiers
1..749
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp69C058"
/issue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_idb="469 (synonym: pkid1)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:

Pred. No.:	36.8	Length:	749
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CR767800 (1-749)

QY 1 ProaPVALIIepheLungluVal 9

DB 46 CCAGATGATATTTCTACAGAGATT 72

RESULT 110

BI181461 750 bp mRNA linear EST 10-JUL-2001

LOCUS UNL-P-FN-ak-a-12-0-UNL.81 UNL-P-FN Sus scrofa cDNA clone

DEFINITION UNL-P-FN-ak-a-12-0-UNL 3', mRNA sequence.

ACCESSION BI181461

VERSION BI181461.1 GI:14655870

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 750)

AUTHORS Caetano, A.R., Johnson, R.K. and Pomp, D.

TITLE Generation and sequence characterization of a normalized cDNA library from swine ovarian follicles

JOURNAL Mamm. Genome 14 (1), 65-70 (2003)

PUBMED
COMMENT

Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA

Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu
Oligo-dT track not found, Not 1 site shown in beginning of sequence
is likely internal to the message.
Seq primer: M13 -29
POLY(A)=No.

FEATURES

source

Location/Qualifiers
1..750
/organism="Sus scrofa"
/mol_type="mRNA"
/strain="University of Nebraska, Lincoln Swine Selection lines"
/db_xref="taxon:9623"
/clone="UNL-P-FN-ak-a-12-0-UNL"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_idb="UNL-P-FN"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UNL-P-FN library is a normalized library representing porcine ovarian follicles, ranging between 2.0 to 10.0 mm in diameter, collected during 7 days of the follicular phase of the pig estrous cycle. This library was derived from the library UNL-P-F2. The tag is a string of 5-6 nucleotides present between the Not I site and the oligo-dT track. The library was constructed as described by Bonaldi, Lennon and Soares, Genome Research 6: 791-806, 1996.
TAG_SEQ=None found"

ORIGIN

Alignment Scores:

Pred. No.:	36.9	Length:	750
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BI181461 (1-750)

QY 1 ProaPVALIIepheLungluVal 9

DB 447 CCAGATGATATTTCTACAGAGATT 473

RESULT 111

BF243927 751 bp mRNA linear EST 14-NOV-2000

LOCUS 601877278F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105866 5',

DEFINITION mRNA sequence.

ACCESSION BF243927

VERSION BF243927.1 GI:11157869

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 751)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>

Plate: L10C984 row: k column: 19

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 54

High quality sequence stop: 533.
Location/Qualifiers
1..751
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4105866"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH-MGC 55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site: 1: SfiI (ggccgctcgcc); Site: 2: SfiI (ggccatcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGACATG-AT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Alignment Scores:
Pred. No.: 36.9 Length: 751
Score: 45.00 Matches: 9
Percent Similarity: 100.04 Conservative: 0
Best Local Similarity: 100.04 Mismatches: 0
Query Match: 100.04 Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF243927 (1-751)

QY 1 ProapvAl11ephelengInguva1 9
|||||

DB 422 CCAGATGTGATATTCTACAGNAGTT 448
|||||

RESULT 112
AUI39147 752 bp mRNA linear EST 02-AUG-2002
LOCUS AUI39147 PLACE1 Homo sapiens cDNA clone PLACE1010031 5', mRNA
DEFINITION
Sequence.
ACCESSION AUI39147
VERSION AUI39147
KEYWORDS EST
SOURCE EST
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo
Homnidae; Homo
1 (bases 1 to 752)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y., Yamoto.O., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and Iwagaki.T.
HRI human cDNA project
Unpublished (2000)
Contract: Takao Iwagaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5' - & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute
Location/Qualifiers
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="PLACE1010031"
/tissue_type="Placenta"
/clone_1lb="PLACE1"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:
Pred. No.: 37 Length: 752
Score: 45.00 Matches: 9
Percent Similarity: 100.04 Conservative: 0
Best Local Similarity: 100.04 Mismatches: 0
Query Match: 100.04 Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AUI39147 (1-752)

QY 1 ProapvAl11ephelengInguva1 9
|||||

DB 433 CCAGATGTGATATTCTACAGNAGTT 459
|||||

RESULT 113
BI760756 757 bp mRNA linear EST 25-SEP-2001
LOCUS BI760756
DEFINITION
mRNA sequence.
ACCESSION BI760756
VERSION BI760756.1 GI:15752334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo
Homnidae; Homo
1 (bases 1 to 757)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11462 row: m column: 15
High quality sequence start: 6
High quality sequence stop: 755.
Location/Qualifiers
1..757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:518534"
/lab_host="DH10B"
/lab_1lb="NIH-MGC 116"
/note="Organ: pooled neon., kidney, stomach; Vector: pCMV-SPORT6; Site: 1: NCI; Site: 2: BcoRI (destroyed); RNA source anonymous pool; Age 26 yo male, 49 yo female, 71 yo male; colon, 46 yo male; kidney, and pool of 2 stomachs, 62 yo male and directionally cloned (Ecovy site is oligo-dT primed and destroyed upon cloning). Library is insert size range 1-3 kb. Library is normalized and enriched for full-length research Genetics tracking code Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH-MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 37.3 Length: 757
Score: 45.00 Matches: 9

Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%
 DB: 3
 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B160756 (1-757)

QY 1 Proaepvalli1ephelenglnc1uval 9
 DB 340 CCAGATGATATTTCTACAGGAAGTT 366

RESULT 114

B1258848

LOCUS 6025663F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109303 5',
 DEFINITION mRNA sequence.

ACCESSION B1258848
 VERSION B1258848
 KEYWORDS GI:14815606
 SOURCE EST.

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 767)
 NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: L1AM11264 row: m column: 16
 High quality sequence stop: 758.

FEATURES Location/Qualifiers

source

1..767

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5109303"

/tissue_type="cervical carcinoma cell line"

/lab_host="DH10B"

/clone_lib="NIH_MGC_12"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1: NotI;

Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.4 Kb. Library prepared by Life

Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 37.8 Length: 767
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1258848 (1-767)

QY 1 Proaepvalli1ephelenglnc1uval 9
 DB 370 CCAGATGATATTTCTACAGGAAGTT 396

RESULT 115

BG391295

LOCUS 602417344F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4536634 5',
 DEFINITION mRNA sequence.

ACCESSION BG391295
 VERSION BG391295.1 GI:13284743
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: L1AM10460 row: h column: 11
 High quality sequence stop: 693.

FEATURES Location/Qualifiers

source

1..770

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4536634"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_92"

/note="Organ: testis; Vector: pCMV-SPORT6; Site: 1: NotI;

Site: 2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 2.5 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 38 Length: 770
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG391295 (1-770)

QY 1 Proaepvalli1ephelenglnc1uval 9
 DB 445 CCAGATGATATTTCTACAGGAAGTT 471

RESULT 116

BG498689

LOCUS 60254301F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:466633 5',
 DEFINITION mRNA sequence.

ACCESSION BG498689
 VERSION BG498689.1 GI:13460206
 KEYWORDS EST.

ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 770)
 NIH-MGC http://mgi.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP.

CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLCM1474 row: a column: 02
 High quality sequence stop: 668.
 Location/Qualifiers

FEATURES
 source
 1..770
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:466653"
 /issue_type="adenocarcinoma"
 /lab_host="DH10B (TI phase-resistant)"
 /clone_lib="NIH_MGC_60"
 /note="Organ: prostate; Vector: pDMR-11B (Clontech);
 Site_1: SfiI (ggcgctcgcc); Site_2: SfiI
 (ggcattatggcc); Double-stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were added in cloning as
 follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and
 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCCGACATG-dT(10)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.5
 kb (range 0.9-4.0 kb). 14/15 clones contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 38 Length: 770
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG498689 (1-770)

CY 1 ProaspValliepheleungingjuva1 9
 DB 17 CCAGATGATATTTCTACAGGAAGTT 43

RESULT 117
 BI754101 774 bp mRNA linear EST 25-SEP-2001
 LOCUS 603027659P1 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5197838 5',
 DEFINITION mRNA sequence.
 ACCESSION BI754101.1 GI:15745679
 VERSION BI754101.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 774)
 NIH_MGC <http://mgs.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLCM1495 row: f column: 15
 High quality sequence stop: 756.

FEATURES

source

Location/Qualifiers
 1..774
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5197838"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_114"
 /note="Organ: brain; Vector: pCMV-SPORT6, Site_1: NotI;
 Site_2: BclRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcorV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 38.2 Length: 774
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BI754101 (1-774)

CY 1 ProaspValliepheleungingjuva1 9
 DB 492 CCAGATGATATTTCTACAGGAAGTT 518

RESULT 118
 BX374579 780 bp mRNA linear EST 27-APR-2004
 LOCUS BX374579 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
 DEFINITION CDNA clone CS0DB007YB11 5-PRIME, mRNA sequence.
 ACCESSION BX374579
 VERSION BX374579.2 GI:46618956
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 780)
 Li, W.-B., Gruber, C., Jesse, J., and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 8, 2003 this sequence version replaced gi:30452317.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and Ecor V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?cs=CS0DB007C060P1sc=3474.r>.
 Location/Qualifiers
 1..780
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DB007YB11"
 /issue_type="NEUROBLASTOMA COT 10-NORMALIZED"
 /clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ALIGNMENT SCORES:

Pred. No.:	38.6	Length:	780
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX374579 (1-780)

QY 1 Proasppvalillepheleunglguval 9
DB 445 CCAGATGATATTTCTACAGAGATT 471

RESULT 119

LOCUS BX365835 783 bp mRNA linear EST 08-APR-2004
DEFINITION BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
ACCESSION BX365835
VERSION BX365835.2 GI:46288859
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo;
1 (bases 1 to 783)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSIDB0022ZF03P1c=3474.r.

FEATURES
source
Location/Qualifiers
1..783
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB007YB11"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_1fb="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	38.7	Length:	783
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX365835 (1-783)

QY 1 Proasppvalillepheleunglguval 9

DB 445 CCAGATGATATTTCTACAGAGATT 471

RESULT 120

LOCUS BG719977 786 bp mRNA linear EST 08-MAY-2001
DEFINITION 602691335F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4823432 5',
mRNA sequence.
ACCESSION BG719977
VERSION BG719977.1 GI:13999164
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo;
1 (bases 1 to 786)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Place: LLM10733 row: f column: 09
High quality sequence stop: 784.
Location/Qualifiers
1..786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4823432"
/lab_host="DH10B"
/clone_1fb="NIH MGC 97"
/note="Organ: testis; Vector: pBluescriptR (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTCTTTTCT-3', size-selected for average
insert size 2.2 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH-MGC Library."

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	38.9	Length:	786
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BG719977 (1-786)

QY 1 Proasppvalillepheleunglguval 9

DB 578 CCAGATGATATTTCTACAGAGATT 604

RESULT 121

LOCUS BG533717 793 bp mRNA linear EST 03-APR-2001
DEFINITION 602562373F1 NIH_MGC_76 Homo sapiens CDNA clone IMAGE:4700059 5',
mRNA sequence.
ACCESSION BG533717
VERSION BG533717.1 GI:13525257

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 58

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homidae; Homo.
REFERENCE NIH-MGC http://mgs.nci.nih.gov/ 1 (bases 1 to 793)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapds-remail@nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: LNCM1533 row: a column: 20
High quality sequence stop: 666.
Location/Qualifiers
1..793
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_library="MGC" (T1 phage-resistant)
/db_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 76"
/note="Organ. liver. Vector: pDNR-LIB (Clontech); Site 1: still (ggcgccatgggc); Site 2: sflr (ggcgccatgggc); 5' adaptor 3' adaptor 5'-CACGCCATTAGGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGACGCCGACGATG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 39.3 Length: 793
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BG53J17 (1-793)
CY 1 ProaPVal11lePhleuGngJlUvAl 9
DB 289 CCAGATGATATTTCTACAGAAATT 315

RESULT 122
LOCUS DNI22208 798 bp mRNA linear EST 15-FEB-2005
DEFINITION DNI22208 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION DNI22208.1 GI:59816487
VERSION DNI22208.1
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Suidae; Sus (bases 1 to 798)
REFERENCE Smith,T.P.L., Ford,J.J., Vallet,J.L., Wise,T.A.,
AUTHORS Nomenan,D.J., Wray,J.E. and Keale,J.W.
TITLE Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
JOURNAL Unpublished (2003)

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alo option. Vector identified with cross_match v0.990329.
Plate: HHY8024 row: L column: 17
Seq primer: GTAAATGACCTCATATGGG.
Location/Qualifiers
1..798
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9923"
/tissue_type="pooled"
/db_host="DH10B"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1, Site 1: EcoRI, Site 2: NotI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."

ORIGIN
Alignment Scores:
Pred. No.: 39.6 Length: 798
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x DNI22208 (1-798)
CY 1 ProaPVal11lePhleuGngJlUvAl 9
DB 453 CCAGATGATATTTCTACAGAAATT 479

RESULT 123
LOCUS CX756424 799 bp mRNA linear EST 24-JAN-2005
DEFINITION AGENCOURT_41337854 NIH_MGC_261 Homo sapiens cDNA clone
IMAGS:7779791 3', mRNA sequence.
ACCESSION CX756424
VERSION CX756424
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 799)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhardt, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapds-remail@nih.gov
Tissue Procurement: Meri Fitzo
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: LNCM15934 row: c column: 21
High quality sequence stop: 579.
Location/Qualifiers
1..799
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:7779791"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B Tona"
/clone_1lb="NIH_MGC_281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
ECORV; Site_2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSP-6, NIH Registry designation UC06. Positive for OCT4
expression by RT-PCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dT primer:
5'-pgactgattctagatcgacgagccgccccc(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
primary library is normalized (non-normalized primary
library is NIH_MGC_280) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN

Alignment Scores:
Pred. No.: 39.6 Length: 799
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CX756424 (1-799)

Qy 1 Proaspva111ephelenglnlva1 9
Db 450 CCAGATGATATTTCTACAGAGATT 476

RESULT 124

LOCUS CX166335 810 bp mRNA linear EST 23-DEC-2004
DEFINITION HESG2_39_B09.g1_A035 NIH_MGC_258 Homo sapiens cDNA clone
IMAGE:7469923 5', mRNA sequence.
ACCESSION CX166335
VERSION CX166335
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 810)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: BreaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
Plate: L14M15771 row: d column: 17
Seg primer: JENREV (CAGGAAACAGCTACACC)
High quality sequence stop: 810.
Location/Qualifiers
1..810
/organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7469923"
/sex="male"
/tissue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_type="human embryonic stem cells"
/clone_1lb="B601"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="Vector: pExpress-1; Site_1: NotI; Site_2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
id and NIH Registry designation is B601. Positive for
GATA4, Mixl1, Msx1, HNF4alpha expression; negative for AFP
expression. Passage number 40. cDNA primed using oligo-dT
primer: 5'-pgactgattctagatcgacgagccgccccc(T)25-3' and
cloned into the EcoRV/NotI sites of pExpress-1. This
primary library is non-normalized (normalized primary
library is NIH_MGC_259). It was constructed by Express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below phred quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."

ORIGIN

Alignment Scores:
Pred. No.: 40.3 Length: 810
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CX166335 (1-810)

Qy 1 Proaspva111ephelenglnlva1 9
Db 390 CCAGATGATATTTCTACAGAGATT 416

RESULT 125

LOCUS BI908925 838 bp mRNA linear EST 16-OCT-2001
DEFINITION 603067028P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215926 5',
mRNA sequence.
ACCESSION BI908925
VERSION BI908925
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 838)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
Plate: L14M1542 row: h column: 07
High quality sequence stop: 773.
Location/Qualifiers
1..838
/organism="Homo sapiens"

FEATURES
source
1..810
/organism="Homo sapiens"

FEATURES
source
1..838
/organism="Homo sapiens"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5215926"
/issue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH MGC 118"
/note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library."

Alignment Scores:

Pred. No.: 41.8 Length: 838
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Caps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1908925 (1-838)

QY 1 Proapevalli1lephelaugingluva1 9
DB 434 CCAGTGTGATATTCTACAGAGATT 460

RESULT 126

CR765451 846 bp mRNA linear EST 23-SEP-2004
LOCUS CR765451
DEFINITION DKFZP469E2434.1 469 (synonym: pk1d1) Pongo pygmaeus CDNA clone
ACCESSION CR765451
VERSION CR765451.1 GI:52605526
KEYWORDS EST
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Pongo.
1 (bases 1 to 846)
Ostenwelder, B.; Ostermaier, B.; Deutschenbaur, S.; Schallp, A.;
Mewes, H.W.; Weil, B.; Amid, C.; Oesinger, A.; Fobo, G.; Han, M. and
Wiemann, S.
Pongo pygmaeus mRNA (Ostenwelder, B.; Ostermaier, B.,
Deutschenbaur, S., et al.)
Unpublished (2004)

COMMENT

MIPS

REFERENCE

1 (bases 1 to 846)
Ostenwelder, B.; Ostermaier, B.; Deutschenbaur, S.; Schallp, A.;
Mewes, H.W.; Weil, B.; Amid, C.; Oesinger, A.; Fobo, G.; Han, M. and
Wiemann, S.
Pongo pygmaeus mRNA (Ostenwelder, B.; Ostermaier, B.,
Deutschenbaur, S., et al.)
Unpublished (2004)

JOURNAL

MIPS

TITLE

MIPS

FEATURES

source

FEATURES

source

1 846
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="DKFZP469E2434"
/issue_type="leukocyte"
/dev_stage="adult"
/lab_host="DH10B"

ORIGIN

/clone_lib="469 (synonym: pk1d1)"
/note="Vector: pSPORT1_SfiI; Site 1: SfiIA; Site 2: SfiIB"

Alignment Scores:

Pred. No.: 42.3 Length: 846
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR765451 (1-846)

QY 1 Proapevalli1lephelaugingluva1 9
DB 336 CCAGTGTGATATTCTACAGAGATT 362

RESULT 127

BE784416 853 bp mRNA linear EST 20-OCT-2000
LOCUS BE784416
DEFINITION 601473891P1 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:3876862.5,
mRNA sequence.
ACCESSION BE784416 GI:10205614
VERSION BE784416.1 GI:10205614
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 853)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strubeberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DP/Genetics, Inc.
CDNA Library Preparation: TIGR/Life Technologies, Inc.
DNA Sequencing by: Incyte Genetics, Inc.
Clone distribution: MGC/CDNA Consortium information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LHM9638 row: e column: 23
High quality sequence stop: 660.
Location/Qualifiers

COMMENT

1. 853

FEATURES

source

FEATURES

source

FEATURES

source

FEATURES

source

FEATURES

source

FEATURES

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FEATURES

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FEATURES

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DB 437 CCAGATGATATTTCTACAGAACTT 463

RESULT 128

BI553412 858 bp mRNA linear EST 05-SEP-2001

LOCUS 603193558F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5264582 5', mRNA sequence.

ACCESSION BI553412

VERSION BI553412.1 GI:15440724

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC http://mhc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLM11667 row: c column: 15
High quality sequence stop: 829.
Location/Qualifiers

FEATURES

source 1..858

location/Qualifiers

1..858

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5264582"

/tissue_type="hippocampus"

/lab_host="DH10B"

/clone_lib="NIH_MGC_95"

/note="Organ: brain; Vector: pBluescriptCR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3', size selected for average insert size 2.5 kb and normalized to R07 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 43

Score: 45.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 3

Length: 858

Matches: 9

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BI553412 (1-858)

QY 1 Proaapvalillepheleugingluval 9

DB 453 CCAGATGATATTTCTACAGAACTT 479

RESULT 129

BI553412 870 bp mRNA linear EST 15-MAY-2001

LOCUS 602634171F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779449 5', mRNA sequence.

ACCESSION BI553412

VERSION BI553412.1 GI:14051049

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC http://mhc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC http://mhc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLM10636 row: m column: 18
High quality sequence stop: 826.
Location/Qualifiers

FEATURES

source 1..870

location/Qualifiers

1..870

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4779449"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI CGAP_Skn3"

/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.: 43.7

Score: 45.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 2

Length: 870

Matches: 9

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BI553412 (1-870)

QY 1 Proaapvalillepheleugingluval 9

DB 344 CCAGATGATATTTCTACAGAACTT 370

RESULT 130

BI553412 870 bp mRNA linear EST 04-SEP-2002

LOCUS 602634171F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:6144208

ACCESSION BI553412

VERSION BI553412.1 GI:22673821

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NIH-MGC http://mhc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 plate: LLAM13468 row: n column: 17
 High quality sequence stop: 677.
 Location/Qualifiers
 1..870
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6144208"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1b="NIH_MGC_67"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.75 kb. Library constructed by Life
 Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	43.7	Length:	870
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BU159911 (1-870)

OY 1 ProaPyValllePhelengIngluVal 9
 DB 368 CCAGATGTGATATTCTACAGAGACTT 394

RESULT 131

LOCUS BU169945 883 bp mRNA linear EST 04-SEP-2002
 DEFINITION AGENCOURT 7913097 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6024760
 5', mRNA sequence.
 ACCESSION BU169945
 VERSION BU169945.1 GI:22683929
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 883)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgaapb-remail.nih.gov
 Tissue Procurement: DCTD/DTF/Gazdar
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13468 row: n column: 17
 High quality sequence stop: 413.
 Location/Qualifiers
 1..883
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6024760"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1b="NIH_MGC_68"
 /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 1.8 kb. Library constructed by Life

FEATURES

source

ORIGIN

Technologies."

Alignment Scores:

Pred. No.:	44.4	Length:	883
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BU169945 (1-883)

OY 1 ProaPyValllePhelengIngluVal 9
 DB 313 CCAGATGTGATATTCTACAGAGACTT 339

RESULT 132

LOCUS BU179107 883 bp mRNA linear EST 04-SEP-2002
 DEFINITION AGENCOURT 7984768 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6174958
 5', mRNA sequence.
 ACCESSION BU179107
 VERSION BU179107.1 GI:22693091
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 883)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strauberg, Ph.D.
 Email: cgaapb-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM13548 row: 0 column: 23
 High quality sequence stop: 672.
 Location/Qualifiers
 1..883
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6174958"
 /tissue_type="leiomyosarcoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1b="NIH_MGC_71"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
 Average insert size 2.1 kb."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	44.4	Length:	883
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BU179107 (1-883)

OY 1 ProaPyValllePhelengIngluVal 9
 DB 291 CCAGATGTGATATTCTACAGAGACTT 317

RESULT 133
 BX422491 904 bp mRNA linear EST 03-MAY-2004
 LOCUS BX422491 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
 DEFINITION CS0DM007YE11 5-PRIME, mRNA sequence.
 ACCESSION BX422491
 VERSION BX422491.2 GI:46955237
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 904)
 Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 15, 2003 this sequence version replaced gi:30766188.
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?c=CS0DM007AC06Plc=3474.r.
 Location/Qualifiers
 1..904
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM007YE11"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_1lb="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

FEATURES
 source
 1..904
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DM007YE11"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_1lb="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 45.6 Length: 904
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BX422491 (1-904)

QY 1 ProaepVallllePheLeuGInGluVal 9
 DB 376 CCAGATGTGATATTCTTACAGGAAGTT 402

RESULT 134
 CD251503 906 bp mRNA linear EST 22-MAY-2003
 LOCUS CD251503
 DEFINITION AGENCOURT_14212105 NIH_MGC_179 Homo sapiens cDNA clone
 IMAGE:30385385 5', mRNA sequence.
 ACCESSION CD251503
 VERSION CD251503.1 GI:310111969
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 906)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Dr. Michael Brownstein
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: NDM452 row: f column: 18
 High quality sequence stop: 588.
 Location/Qualifiers
 1..906
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30385385"
 /tissue_type="Pituitary"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
 /clone_1lb="NIH_MGC_179"
 /note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
 (destroyed); Site 2: NotI; Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.1 kb. Library was
 constructed by (Invitrogen). Note: this is a NIH_MGC
 library."

FEATURES
 source
 1..906
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30385385"
 /tissue_type="Pituitary"
 /lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
 /clone_1lb="NIH_MGC_179"
 /note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV
 (destroyed); Site 2: NotI; Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.1 kb. Library was
 constructed by (Invitrogen). Note: this is a NIH_MGC
 library."

ORIGIN

Alignment Scores:
 Pred. No.: 45.7 Length: 906
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 6 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CD251503 (1-906)

QY 1 ProaepVallllePheLeuGInGluVal 9
 DB 474 CCAGATGTGATATTCTTACAGGAAGTT 500

RESULT 135
 BG391213 908 bp mRNA linear EST 12-MAR-2001
 LOCUS BG391213
 DEFINITION 602417244F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:453635 5',
 mRNA sequence.
 ACCESSION BG391213
 VERSION BG391213.1 GI:13284661
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 908)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

REFERENCE 1 (bases 1 to 908)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

Thu Mar 16 10:39:26 2006

US-10-757-745-2_copy_145_153.rst

Page 64

found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10460 row: h column: 12
High quality sequence stop: 732.
Location/Qualifiers

FEATURES

source

1..908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:453635"
/cdate="1998-01-01"
/tissue="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: SalI; Cloned: unidirectionally, oligo-dT-primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: This is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 45.8 Length: 908
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG391213 (1-908)

OY

1 Proapevalli11epheleuglgluval 9
DB 436 CCAGATGATATTTCTACAGAAAGTT 462

RESULT 136

LOCUS B1915865 915 bp mRNA linear EST 16-OCT-2001
DEFINITION 603184527p1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248495 5',
mRNA sequence.
ACCESSION B1915865
VERSION B1915865.1 GI:16179808
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapdb-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11627 row: e column: 08
High quality sequence stop: 696.
Location/Qualifiers

FEATURES

source

1..915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5248495"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI;
Site: 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb. Insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 46.2 Length: 915
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1915865 (1-915)

OY

1 Proapevalli11epheleuglgluval 9
DB 444 CCAGATGATATTTCTACAGAAAGTT 470

RESULT 137

LOCUS CN801806 922 bp mRNA linear EST 26-MAY-2004
DEFINITION U11UM1GCM MQ0 37066 Katze MMR Macaca mulatta cDNA clone
BT01W:15450 5' similar to Bases 18 to 922 highly similar to human
TTPAP (Hs.210628), mRNA sequence.
ACCESSION CN801806.1 GI:47697782
VERSION CN801806
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta

REFERENCE

AUTHORS Mammalian Genome Project, The Wellcome Trust, and
Cercopithecidae; Cercopithecinae; Macaca.
Mammals; Eutheria; Eumarchontoglires; Primates; Catarrhini;
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Eumarchontoglires; Primates; Catarrhini;
1 (bases 1 to 922)
Magness C.L., Fellin P.C., Thomas M.J., Korth M.J., Agy M.B.,
Pegall S.C., Fitzgibbon M., Scherer C.A., Miner D.G., Katze M.G. and
Radnor S.P. The Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
15998449
CONTACT: C. Magness
Illumina Biociences Inc.
2203 Abbott Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumina.com
sequenced on 2004.05.13. 514 Q20 bases.
PCR primers: CCTCACTAAGCAACAA
BACKWARD: CACTTACCGGCAATTCGTA
Insert length 922 Std Error: 0.00
Plate: C000291.1 row: H column: 09
Seq primer: CCTCACTAAGCAACAA
FOLTA=No.

FEATURES

source

1..922
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="indian"
/cd_xref="taxon:9544"
/clone="BT01W:15450"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze MMR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site: 1: EcoR I;
Site: 2: Xho I; Created from StrataGene ZAP-cDNA synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold

ORIGIN Cloning Kit (Catalog #200450) "

Alignment Scores:

Pred. No.: 46.6 Length: 922
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG119064 (1-922)

QY 1 Proaapvalillepheleugingluval 9
DB 315 CCAGATGATATTTCTACAGGAAGTT 341

RESULT 138

LOCUS BG119064 927 bp mRNA linear EST 30-JUN-2001
DEFINITION 602347389F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:444239 5',
mRNA sequence.

ACCESSION BG119064
VERSION BG119064.1 GI:12612570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS 1 (bases 1 to 927)
TITLE NIH-MGC http://mgs.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0215 row: a column: 24
High quality sequence stop: 676.

FEATURES

source Location/Qualifiers
1..927

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:444239"
/tissue_type="adenoecarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 46.9 Length: 927
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG119064 (1-927)

QY 1 Proaapvalillepheleugingluval 9
DB 315 CCAGATGATATTTCTACAGGAAGTT 341

DB 265 CCAGATGATATTTCTACAGGAAGTT 291

RESULT 139

LOCUS BG740339 932 bp mRNA linear EST 15-MAY-2001
DEFINITION 602635289F1 NCI_CGAP_Skin3 Homo sapiens cDNA clone IMAGE:4780318 5',
mRNA sequence.
ACCESSION BG740339
VERSION BG740339.1 GI:14050992
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/
AUTHORS 1 (bases 1 to 932)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0639 row: a column: 23
High quality sequence stop: 759.

FEATURES

source Location/Qualifiers
1..932

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4780318"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Skin3"
/note="Organ: skin; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP library."

ORIGIN

Alignment Scores:

Pred. No.: 47.2 Length: 932
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG740339 (1-932)

QY 1 Proaapvalillepheleugingluval 9
DB 264 CCAGATGATATTTCTACAGGAAGTT 290

RESULT 140

LOCUS BG541819 937 bp mRNA linear EST 03-APR-2001
DEFINITION 602569712F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694066 5',
mRNA sequence.

ACCESSION BG541819
VERSION BG541819.1 GI:13534052
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
1 (bases 1 to 937)
NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: CLOMTECH Laboratories, Inc.
 CDNA Library Preparation: CLOMTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM1517 row: h column: 03
 High quality sequence stop: 714.

FEATURES

Location/Qualifiers
 1..937
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4694066"
 /lab_host="DH10B (TI phage-resistant)"
 /clone_lib="NIH_MGC_77"
 /note="Organ: Lung; Vector: pDNF-LIB (Clontech); Site 1:
 SfiI (ggcgccctggcc); Site 2: SfiI (ggcgccctggcc); 5' and
 3' adaptor were used in the following: 5' adaptor
 sequence: 5'-CACGCCCATATGCGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCCGACGCGCGACGACG-3' (30 bp) (Where B = A,
 C, or G and N = A, C, G, T) 12/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
 Pred. No.: 47.5 Length: 937
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Inserts: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG54189 (1-937)

QY 1 ProaPVal111epheleungluval 9
 |||||
 |||||
DB 449 CCAGATGATATTTCTACGAGATT 475

RESULT 141
LOCUS BX358707 942 bp mRNA linear EST 08-APR-2004
DEFINITION BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
ACCESSION BX358707
VERSION BX358707.2 GI:46306560
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 Hom (bases 1 to 942)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length CDNA libraries and normalization
 Unpublished (2001)
 On May 5, 2003 this sequence version replaced gi:30378261.
COMMENT Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seq@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a

FEATURES

Location/Qualifiers
 1..942
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1042Y119"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with NotI and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 47.8 Length: 942
 Score: 45.00 Matches: 9
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Inserts: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BX358707 (1-942)

QY 1 ProaPVal111epheleungluval 9
 |||||
 |||||
DB 302 CCAGATGATATTTCTACGAGATT 328

RESULT 142
LOCUS AL555333 948 bp mRNA linear EST 10-MAR-2004
DEFINITION AL555333 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 CDNA clone CSODK007YK05 5-PRIME, mRNA sequence.
ACCESSION AL555333
VERSION AL555333.3 GI:45860070
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo
 Hom (bases 1 to 948)
 L1, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length CDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31277141.
COMMENT Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seq@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime
 end enriched, double-strand cDNA was digested with NotI and cloned
 into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.x
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CSODK007AF03QPl&c=3474.x>.
FEATURES
 Location/Qualifiers
 1..948
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK007YK05"
 /tissue_type="HELA CELLS COT 25-NORMALIZED"
 /clone_lib="HELA"
 /note="1st strand cDNA was primed with a NotI-oligo (dt)
 primer. Five prime end enriched, double-strand cDNA was
 digested with NotI and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ALIGNMENT SCORES:

Pred. No.:	48.1	Length:	948
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AL555333 (1-948)

QY 1 Proaapvalli1lephleugIngluVal 9

DB 452 CCAGATGATATTTCTACAGGAGTT 478

RESULT 143

LOCUS BX433489 952 bp mRNA linear EST 04-MAY-2004

DEFINITION BX433489 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone

ACCESSION BX433489

VERSION BX433489.2 GI:47002503

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE Homidae; Homo.

JOURNAL 1 (bases 1 to 952)

COMMENT Li W.B., Gruber C., Jessee J. and Polayes D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30775195.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?cs=CSDBA10562D12_CS05372_1&c=3474.r

FEATURES

Location/Qualifiers

1..952

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS05372_1"

/issue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/note="Organ: Brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	48.4	Length:	952
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX433489 (1-952)

QY 1 Proaapvalli1lephleugIngluVal 9

DB 711 CCAGATGATATTTCTACAGGAGTT 685

RESULT 144

LOCUS BI161201 959 bp mRNA linear EST 05-JUL-2001

DEFINITION 602865659P1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019639 5',

mRNA sequence.

ACCESSION BI161201

VERSION BI161201.1 GI:14621202

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE Homidae; Homo.

JOURNAL 1 (bases 1 to 959)

COMMENT NIH-MGC http://mhc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LMC1835 row: e column: 16

High quality sequence stop: 551.

Location/Qualifiers

1..959

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5019639"

/tissue_type="epitheloid carcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_42"

/note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;

Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Site-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

ORIGIN

ALIGNMENT SCORES:

Pred. No.:	48.8	Length:	959
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BI161201 (1-959)

QY 1 Proaapvalli1lephleugIngluVal 9

DB 451 CCAGATGATATTTCTACAGGAGTT 477

RESULT 145

LOCUS CN803230

DEFINITION CN803230

ILUMIGEN MCQ_32551 Katze_MBR Macaca mulatta cDNA clone

IBIUM:12605 5' similar to Bases 1 to 965 highly similar to human

Thu Mar 16 10:39:26 2006

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TRAP (Hs.210628), mRNA sequence.
ACCESSION CN803230.1 GI:47699206
VERSION
KEYWORDS
SOURCE
ORGANISM
Macaca mulatta (rhesus monkey)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
REFERENCE
AUTHORS
Magnes, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Proff, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
TITLE
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
JOURNAL
Genome Biol. 6 (7), R60 (2005)
COMMENT
Contact: C. Magnes
1598449
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnes@illumigen.com
Sequenced on 2004.04.02. 780 Q20 bases.
PCR Primers
FORWARD: CCTCTACTTAAGGACAAACAAA
BACKWARD: CACTATAGGGGAGATGGGTA
Insert Length: 965 Std Error: 0.00
Plate: CL000288 row: D column: 11
Seq primer: CCTCTACTTAAGGACAAACAAA
POLYA=NO.
FEATURES
source
1..965
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIDW:12605"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze_MMR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Strategene ZAP-CDNA Synthesis
Kit (catalog #200400) and ZAP-CDNA GigaPack III Gold
Cloning Kit (catalog #200450)"
ORIGIN
Alignment Scores:
Pred. No.: 49.1 Length: 965
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CN803230 (1-965)
QY 1 PROASPVALIIIEPHELEUNGINGUVAL 9
DB 200 CCAGATGTGATATTCTTACAGGAAGTT 226
RESULT 146
LOCUS BM468826 972 bp mRNA linear EST 05-FEB-2002
DEFINITION ACENCOUPT_6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154
5', mRNA sequence.
ACCESSION BM468826
VERSION BM468826.1 GI:18517868
KEYWORDS
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 972)
NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LHAM12356 row: d column: 03
High quality sequence stop: 707.
FEATURES
source
1..972
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5587154"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 49.5 Length: 972
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x BM468826 (1-972)
QY 1 PROASPVALIIIEPHELEUNGINGUVAL 9
DB 328 CCAGATGTGATATTCTTACAGGAAGTT 354
RESULT 147
LOCUS BX338160 981 bp mRNA linear EST 08-APR-2004
DEFINITION BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS00D1056YC3 5-PRIME, mRNA sequence.
ACCESSION BX338160
VERSION BX338160.2 GI:46283046
KEYWORDS
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 981)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:30345671.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer 1 and cloned
end enriched, double-strand cDNA was digested with NotI and cloned
into the Not I and EcoR V sites of the pCMVSPORT6 vector. Library
was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?c=CSODI056AB120P1c=3474.r>.

FEATURES

Location/Qualifiers

1..981

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI056YC23"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	50.1	Length:	981
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX338160 (1-981)

Qy 1 ProaepVal11ephelengIngluVal 9

Db 446 CCAGATGATATTTCTACAGAACTT 472

RESULT 148

BE892886 995 bp mRNA linear EST 20-OCT-2000

LOCUS 601435730F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920790 5',

DEFINITION mRNA sequence.

ACCESSION BE892886

VERSION BE892886.1 GI:10353510

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 995)

NIH-MGC <http://mhc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LHM9752 row: 1 column: 07

High quality sequence stop: 573.

Location/Qualifiers

1..995

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3920790"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH MGC 72"

/note="Organ: Skin; Vector: pCMV-SPORT6; Site: 1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life

Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	50.9	Length:	995
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BE892886 (1-995)

Qy 1 ProaepVal11ephelengIngluVal 9

Db 462 CCAGATGATATTTCTACAGAACTT 488

RESULT 149

BX337141 1018 bp mRNA linear EST 07-APR-2004

DEFINITION BX337141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA

clone CSODI036YJ02 5-PRIME, mRNA sequence.

ACCESSION BX337141

VERSION BX337141.2 GI:46271144

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 1018)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30337585.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

3474.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna?c=CSODI036BO1QP1c=3474.r>.

FEATURES

Location/Qualifiers

1..1018

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI036YJ02"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	52.2	Length:	1018
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX337141 (1-1018)

Qy 1 ProaepVal11ephelengIngluVal 9

Db 423 CCAGATGATATTTCTACAGAACTT 449

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 70

```
RESULT 150
BM554324 1035 bp mRNA linear EST 20-FEB-2002
LOCUS BM554324
DEFINITION AGENCOURT 6546794 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742466
5' mRNA sequence.
ACCESSION BM554324.1 GI:18793827
VERSION BM554324.1
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1035)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM12760 row: k column: 11
High quality sequence stop: 738.
Location/Qualifiers
1..1035
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742466"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_119"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."
```

```
REFERENCE
BM554324 1035 bp mRNA linear EST 20-FEB-2002
LOCUS BM554324
DEFINITION AGENCOURT 6546794 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742466
5' mRNA sequence.
ACCESSION BM554324.1 GI:18793827
VERSION BM554324.1
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1035)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM12817 row: o column: 01
High quality sequence start: 4
High quality sequence stop: 632.
Location/Qualifiers
1..1046
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5764440"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_114"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
```

Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 ends enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by life technologies, a
 division of invitrogen. This sequence belongs to sequence cluster
 3474.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0D1052CG070P1ec=3474.r.
 Location/Qualifiers

FEATURES
 source
 1..1067
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1052YN13"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime ends enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ALIGNMENT SCORES:

Pred. No.:	55.1	Length:	1067
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX337905 (1-1067)

QY 1 Proaspvalli11epheleungl1uval 9
 |||||
 DB 457 CCAGATGTCATATTCTACAGGAGTT 483

RESULT 153

BX444691

LOCUS BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DN005YN02 5-PRIME, mRNA sequence.

ACCESSION BX444691
 VERSION BX444691
 KEYWORDS BX444691.2 GI:47009162

SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 15, 2003 this sequence version replaced gi:30780264.
 Contact: Genoscope

Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 ends enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by life technologies, a
 division of invitrogen.
 This sequence belongs to sequence cluster 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0DN005DG01Q1P1ec=3474.r.
 Location/Qualifiers

FEATURES
 source
 1..1081
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DN005YN02"

/issue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_1ib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime ends
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.:	55.9	Length:	1081
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BX444691 (1-1081)

QY 1 Proaspvalli11epheleungl1uval 9
 |||||
 DB 459 CCAGATGTCATATTCTACAGGAGTT 485

RESULT 154

CN642527

LOCUS CN642527 1087 bp mRNA linear EST 12-MAY-2004
 DEFINITION ILLUMIGEN MCQ 6530 Katze MPMPL2 Macaca mulatta cDNA clone IB1W:4699
 5' similar to Bases 1 to 1084 highly similar to human TTRAP
 (Hs.210628), mRNA sequence.

ACCESSION CN642527.1 GI:47153537
 VERSION CN642527.1
 KEYWORDS EST.

SOURCE
 ORGANISM Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE
 AUTHORS Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
 Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
 Iadonato, S.P.
 TITLE Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 JOURNAL Genome Biol. 6 (7), R60 (2005)
 PUBMED 15998449

COMMENT
 CONTACT: C. Magness
 Illumigen BioSciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2003.12.24, 840 Q20 bases.
 PCR Primers
 FORWARD: CCTCCTCAAGGGAACAA
 BACKWARD: CACTATGCGCGAATTCGCTA
 Insert Length: 1087 Sd Error: 0.00
 Plate: C1000066 row: D column: 10
 Seq primer: CCTCCTCAAGGGAACAA
 POLYA=No.

FEATURES
 source
 1..1087
 Location/Qualifiers

1..1087
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IB1W:4699"
 /sex="male"
 /dev_stage="newborn infant"
 /lab_host="E. coli SOLR"
 /clone_1ib="Katze_MPMPL2"
 /note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR
 I; Site 2: Xho I; Created from StrataGene ZAP-cDNA

ORIGIN
Synthesis kit (catalog #200400) and ZAP-CDNA GigaPack III
Gold Cloning Kit (catalog #200450)"

Alignment Scores:

Pred. No.:	56.3	Length:	1087
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN642527 (1-1087)

OY 1 Proappv111epheleunglgluval 9

DB 152 CCAGATGATATTTCTACGAGAGTT 178

RESULT 155

LOCUS DQ049205 1089 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens TTRAP gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049205.1 GI:66902404
VERSION DQ049205.1 GI:66902404
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE

1 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.

TITLE

A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees

JOURNAL

PLoS Biol. 3 (6), E170 (2005)

PUBMED

1569325

AUTHORS

2 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.

JOURNAL

Submitted (05 MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES

Location/Qualifiers
1..1089
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
<1..>1089
/gene="TTRAP"
/locus_tag="HCL17203"

ORIGIN

Alignment Scores:
Pred. No.: 56.4 Length: 1089
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x DQ049205 (1-1089)

OY 1 Proappv111epheleunglgluval 9

DB 433 CCAGATGATATTTCTACGAGAGTT 459

RESULT 156

LOCUS DQ049206 1089 bp DNA linear GSS 02-JUN-2005
DEFINITION Pan troglodytes TTRAP gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049206
VERSION DQ049206.1 GI:66902405
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes (chimpanzee)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.

REFERENCE

1 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.

TITLE

A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees

JOURNAL

PLoS Biol. 3 (6), E170 (2005)

PUBMED

1569325

AUTHORS

2 (bases 1 to 1089)
Nielsen, R., Bustamante, C., Clark, A.G., Gianowski, S., Sackton, T.B.,
Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.

JOURNAL

Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT

This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES

Location/Qualifiers
1..1089
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1089
/gene="TTRAP"
/locus_tag="HCL17203"

ORIGIN

Alignment Scores:
Pred. No.: 56.4 Length: 1089
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x DQ049206 (1-1089)

OY 1 Proappv111epheleunglgluval 9

DB 433 CCAGATGATATTTCTACGAGAGTT 459

RESULT 157

LOCUS CN641671 1090 bp RNA linear EST 12-MAY-2004
DEFINITION HUMAN MCO 5159 Katze WMR Macaca mulatta CDNA clone IBITW:5970
5' sequence to bases 11 to 990 highly similar to human TTRAP
(HE210628), mRNA sequence.
ACCESSION CN641671
VERSION CN641671.1 GI:47152681
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecoidea; Macaca.

REFERENCE

1 (bases 1 to 1090)
Magnien, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agay, M.B.,
Proll, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and

TITLE Iadonato, S.P.
 ANALYSIS of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 JOURNAL Genome Biol. 6 (7), R60 (2005)
 PUBMED 15998449
 COMMENT Contact: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2003.12.04. 732 Q20 bases.
 PCR Primers
 FORWARD: CCTCCTAAGGGAACAAAA
 BACKWARD: CACTATAGGCGCAATGGGTA
 Insert length: 1090 Std Error: 0.00
 Plate: CL000043 row: E column: 07
 Seq primer: CCTCCTAAGGGAACAAAA
 POLYA=No.

FEATURES
 source location/Qualifiers
 1. 1090
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBI0W:5970"
 /sex="female"
 /dev_stage="adult"
 /lab_host="E. coli SOLR"
 /clone_lib="Katz MMBR"
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
 Site 2: Xho I; Created from Stratagene ZAP-cDNA synthesis
 kit (catlog #200400) and ZAP-cDNA Gigapack III Gold
 Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.:	56.4	Length:	1090
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x CN641671 (1-1090)

Qy 1 Proaspvallephleuglncgluval 9
 |||
 DB 305 CCAGATGATATTTCTACAGAGATT 331

RESULT 158

BM555041 1103 bp mRNA linear EST 20-FEB-2002
 LOCUS AGENCOURT 6545705 NIH_MGC_88 Homo sapiens cDNA IMAGE:5737150
 DEFINITION 5', mRNA sequence.
 ACCESSION BM555041
 VERSION BM555041.1 GI:18795166
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1103)
 NIH-MGC http://mhc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)
 DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILML at:
 http://image.llnl.gov
 Plate: LILMI2746 row: m column: 23
 High quality sequence atop: 678.

FEATURES

source location/Qualifiers
 1. 1103
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5737150"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_88"
 /note="Organ: small intestine; Vector: pCMV-SPORT6;
 Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	57.2	Length:	1103
Score:	45.00	Matches:	9
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x BM555041 (1-1103)

Qy 1 Proaspvallephleuglncgluval 9
 |||
 DB 462 CCAGATGATATTTCTACAGAGATT 488

RESULT 159

CR601303 1168 bp mRNA linear HTC 21-UTL-2004
 LOCUS Full-length cDNA CSDDN005YN02 of Adult Brain of Homo sapiens
 DEFINITION (human).
 ACCESSION CR601303
 VERSION CR601303.1 GI:50482110
 KEYWORDS HTC; CNSLT_cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 1168)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Feng Liang Email: fliang@lifeatech.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Paraday Avenue
 2 (bases 1 to 1168)
 Genoscope.
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 COMMENT location/Qualifiers
 1. 1168
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSDDN005YN02"
 /tissue_type="Adult brain"

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 74

ORIGIN /plasmid="pCMVSPORT_6"

Alignment Scores:

Pred. No.: 61.1 Length: 1168
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR601303 (1-1168)

OY 1 PROAPPVall1ephelengingluval 9

DB 458 CCAGATGTGATATTCTACAGGAAGTT 484

RESULT 160

LOCUS

BM553049 1192 bp mRNA linear EST 20-FEB-2002

AGENCOURT 6542413 NIH_MGC_119 Homo sapiens CDNA clone IMAGE:5742798

5', mRNA sequence.

ACCESSION BM553049

VERSION BM553049.1 GI:18791437

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1192)

NIH-MGC http://mgs.nci.nih.gov/.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: LHAM12761 row: 1 column: 07

High quality sequence stop: 747.

Location/Qualifiers

1..1192

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_image="5742798"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_id="NIH_MGC_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dt primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb. Insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 62.5 Length: 1192
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BM553049 (1-1192)

OY 1 PROAPPVall1ephelengingluval 9

DB 490 CCAGATGTGATATTCTACAGGAAGTT 516

RESULT 161

LOCUS

CR592636 1620 bp mRNA linear HTC 21-JUL-2004

full-length cDNA clone CS0DM007YELL of fetal liver of Homo sapiens (human).

ACCESSION CR592636

VERSION CR592636.1 GI:50473443

KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1620)

Li, W.B., Gruber, C., Jessee, J. and Polyes, D.

Full-length cDNA libraries and normalization

Unpublished

Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue

2 (bases 1 to 1620)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seq@genoscope.cns.fr

- Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

Location/Qualifiers

1..1620

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_image="CS0DM007YELL"

/tissue_type="fetal liver"

/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 88.6 Length: 1620
Score: 45.00 Matches: 3
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CR592636 (1-1620)

OY 1 PROAPPVall1ephelengingluval 9

DB 376 CCAGATGTGATATTCTACAGGAAGTT 402

RESULT 162

LOCUS

CR602029 1743 bp mRNA linear HTC 21-JUL-2004

full-length cDNA clone CS0D1042YLL9 of Placenta Cot 25-normalized

of Homo sapiens (human).

ACCESSION CR602029

VERSION CR602029.1 GI:50482836

KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 Homidae; Homo.
AUTHORS 1 (bases 1 to 1743)
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1743)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1. 1743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001042Y1.9"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 96.3 Length: 1743
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CR602029 (1-1743)

QY 1 Proapval11ephelengingluval 9
Db 302 CCAGATGATATTTCTACAGAGATT 328

RESULT 163
CR597293 1894 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DK007YK05 of Hela cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1894)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1894)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

FEATURES division of Invitrogen.
source
1. 1894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK05"
/tissue_type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 106 Length: 1894
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_145_153 (1-9) x CR597293 (1-1894)

QY 1 Proapval11ephelengingluval 9
Db 451 CCAGATGATATTTCTACAGAGATT 477

RESULT 164
CR595644 1909 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0D1052Y1N3 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR595644
VERSION CR595644.1 GI:50476451
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1909)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
REMARK Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1909)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source
1. 1909
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1052Y1N3"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
Alignment Scores:
Pred. No.: 107 Length: 1909
Score: 45.00 Matches: 9
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CG895644 (1-1909)

OY 1 Proaspvalli11ephelengInguval 9
DB 457 CCAGATGTGATTTCTCCAGAGTT 483

RESULT 165

CG887267 154 bp mRNA linear GSS 16-JUN-2004
LOCUS CG887267
DEFINITION R88512 BayGenomics Gene Trap Library pGT0Lxf Mus musculus cDNA,
mRNA sequence.
ACCESSION CG887267 GI:38641677
VERSION CG887267.1
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 154)
BayGenomics.ucsf.edu/
http://baygenomics.ucsf.edu/
Unpublished (2001)
Contract: BayGenomics
Contact: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RAGE of total RNA from gene trap BS
sequence. ES cell lines harboring insertion mutation of target
gene are available upon request from BayGenomics. Annotation
information available from
http://baygenomics.ucsf.edu/cgi-bin/BaySearch.py?OPTION=EXACTTYPE=
URL_LINKEY=R88512
Class: Gene Trap

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source
1..154
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/seq="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0Lxf"
/note="Vector: pGT0Lxf"

ORIGIN

Alignment Scores:
Pred. No.: 10 Length: 154
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 10 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CG887267 (1-154)

OY 1 Proaspvalli11ephelengInguval 9

DB 54 CCAGATGTGATTTCTCCAGAGTT 80

RESULT 166

AZ146818 303 bp DNA linear GSS 28-AUG-2000
LOCUS AZ146818/c
DEFINITION SF_0030_B1.A04_SPM6 Strongylocentrotus purpuratus, purple sea
urchin, sperm plate30 Col=7 Row=B, genomic survey sequence.
ACCESSION AZ146818
VERSION AZ146818.1 GI:8298719
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoida;

Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 303)

AUTHORS Cameron, R.A., Mahira, G., Raat, J.P., Martinez, P., Blondi, T.R.,
Swartzell, S., Wallace, J.C., Pouetka, A.O., Livingston, B.T.,
Wray, G.A., Ettensohn, C.A., Lénach, H., Britten, R.J., Davidson, E.H.
and Hood, L.
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)

JOURNAL PUBLISHED
10920195
Contract: Cameron, R.A., Davidson, E.H., Hood, L.
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 30 row: B column: 7
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 303.

FEATURES

source
1..303
/organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone_plate="30 Col=7 Row=B"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library
/note="Organ: Sperm, Vector: BAC3.6; BAC Clones in F-Col1
DH10B"

ORIGIN

Alignment Scores:
Pred. No.: 21.7 Length: 303
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AZ146818 (1-303)

OY 1 Proaspvalli11ephelengInguval 9

DB 125 CCAGACGTGTCTCTCCAGAGTG 99

RESULT 167

BCG091909 410 bp mRNA linear EST 26-JAN-2001
LOCUS BCG091909
DEFINITION mac18c11.y1 Soares mouse 3Nbms Mus musculus cDNA clone
IMAGE:4000125 5', similar to TR:095551 095551 D03045.3 ;, mRNA
sequence.
ACCESSION BCG091909 GI:12574472
VERSION BCG091909
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 410)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1497853
Seq primer: -40RP from Gibco
High quality sequence stop: 408.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 303)
A sea urchin genome project: Sequence scan, virtual map, and
additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
Contract: Cameron, R.A., Davidson, E.H., Hood, L.
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 30 row: B column: 7
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 303.

Query Match: 97.8% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x AA163045 (1-493)

Qy 1 ProapvalillepHeuengIngluval 9
DB 140 CCAGATGTGTATTCTACAGGAAGTT 166

RESULT 172

CC248786 517 bp mRNA linear GSS 13-MAY-2003
LOCUS CC248786
DEFINITION XK529 BayGenomics Gene Trap Library pGT0LxTf Mus musculus cDNA, mRNA sequence.

ACCESSION CC248786
VERSION CC248786.1 GI:30585518
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 517)
BayGenomics.
http://baygenomics.ucsf.edu/
Unpublished (2001)

REFERENCE AUTHORS
TITLE
JOURNAL
COMMENT

CONTACT: BayGenomics
Bay Area Functional Genomics Consortium (BayGenomics)
Email: info@baygenomics.ucsf.edu
Sequence tag generated by 5' RACE of total RNA from gene trap ES cell line. ES cell lines harboring insertion mutation of target gene are available upon request from BayGenomics. Annotation information available from http://baygenomics.ucsf.edu/cgi-bin/Baysearch.py?OPTION=EXACT&TYPE=CELL_LINE&KEY=XK529
Class: Gene Trap.
Location/Qualifiers
1. 517
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 Ola"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic stem cell"
/clone_lib="BayGenomics Gene Trap Library pGT0LxTf"
/note="Vector: pGT0LxTf"

ORIGIN
Alignment Scores:
Pred. No.: 39.8 Length: 517
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CC248786 (1-517)

Qy 1 ProapvalillepHeuengIngluval 9
DB 143 CCAGATGTGTATTCTACAGGAAGTT 169

RESULT 173

BE290901 525 bp mRNA linear EST 13-JUL-2000
LOCUS BE290901
DEFINITION 601084205F1 NCI_CGAP_Mame Mus musculus cDNA clone IMAGE:3498336 5', mRNA sequence.

ACCESSION BE290901
VERSION BE290901.1 GI:9172261
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE 1 (bases 1 to 525)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM8553 row: j column: 01
High quality sequence stop: 500.

FEATURES
source

1. 525
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3498336"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mame"
/note="Organ: mammary; Vector: PCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

ORIGIN

Alignment Scores:
Pred. No.: 40.5 Length: 525
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BE290901 (1-525)

Qy 1 ProapvalillepHeuengIngluval 9
DB 171 CCAGATGTGTATTCTACAGGAAGTT 197

RESULT 174

CN233559 531 bp mRNA linear EST 09-APR-2004
LOCUS RJA113F02.ab1 Rubrain Gallus gallus cDNA 5', mRNA sequence.
DEFINITION CN233559
ACCESSION CN233559
VERSION CN233559.1 GI:4637303
KEYWORDS EST.

SOURCE Gallus gallus (chicken)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 531)
Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and Lundberg, J.
EST analysis of brain and testis cDNA libraries from white leghorn and Red Jungle Fowl
Unpublished (2004)
CONTACT: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0) 8 5537 8481
Fax: +46 (0) 8 5537 8335
Email: Peter.Savolainen@biotech.kth.se

FEATURES
Seq primer: M13 reverse primer.
Location/Qualifiers

1..531
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Red junglefowl"
/db_xref="taxon:9031"
/sex="female"
/lab_host="ElectronMAX DH10B (Invitrogen)"
/clone_lib="RDBrain"
/note="Organ: brain; Vector: pSPORT-1; Site_1: Hind III;
Site_2: EcoRI; The cDNA libraries were created with the
Superscript plasmid system (Invitrogen)."

ORIGIN

Alignment Scores:
Pred. No.: 41 Length: 531
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
Gaps: 0
DB: 7

US-10-757-745-2_COPY_145_153 (1-9) x CN233559 (1-531)

QY 1 Proaspvalillepheleunglunval 9

DB 393 CCAGATGCTGCTTTTACAGAGGCTT 419

RESULT 175

CD321260

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CD321260 541 bp mRNA linear EST 17-SEP-2003
Strp538.002622 Sea urchin embryo 7hr cleavage stage cDNA library
MEMG538 Strongylocentrotus purpuratus cDNA clone
CALTP538D0924.MPI_538_24D9 5', mRNA sequence.
CD321260.1 GI:34793321

Strongylocentrotus purpuratus
EST.
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoda;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 541)
Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A.,
Reinhardt, R., Herwig, R., Panopoulou, G., and Lehnach, H.
Generation, annotation, evolutionary analysis, and database
integration of 20,000 unique sea urchin EST clusters
Genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka, A.J.
Laboratory 145, dept. Lehnach
Max-Planck-Institut fuer Molekulare Genetik
Insestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: poustka@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/sg_seaurchin/. cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (<http://www.rzpd.de>)
PCR Primers
FORWARD: 5' CCCAGGCTTACATTATGCTTCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTGACGAGCTCGGAAAGGAGGATGG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGCTCGGAAATCCCGGTG-3' pSPORT3/86
High quality sequence stop: 541.

FEATURES
Source

Location/Qualifiers
1..541
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="CALTP538D0924.MPI_538_24D9"
/tissue_type="whole embryo"
/dev_stage="embryonic 7hr"
/lab_host="E.coli, Xui blue"
/clone_lib="Sea urchin embryo 7hr cleavage stage cDNA
library MPKG538"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; Random
primed and directionally cloned in pSPORT1 using a
NotI (5'-pACTGATCTTACGACGAGCGAGCGCCGCTT)153 and a
SalI 5'-TCGACCCAGCGCTCG-3 adapters (Gibco BRL)."

ORIGIN

Alignment Scores:
Pred. No.: 41.9 Length: 541
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
Gaps: 0
DB: 6

US-10-757-745-2_COPY_145_153 (1-9) x CD321260 (1-541)

QY 1 Proaspvalillepheleunglunval 9

DB 288 CCAGACGTGCTTCTCCAGAGGCTG 314

RESULT 176

AA208842

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA208842 544 bp mRNA linear EST 18-SEP-1997
mw73d02.t1 Soares mouse NML Mus musculus cDNA clone IMAGE:676323
5', mRNA sequence.
AA208842.1 GI:1806779

Mus musculus (house mouse)
EST.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Mus.
1 (bases 1 to 544)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Gschel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellander, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B.,
Waters, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The Mashu-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra, M./Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.lln.gov) for further information.
MGI:416027

Seq primer: -28m13 rev2 ET from Amerham
High quality sequence stop: 491.
Location/Qualifiers
1..544
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:676323"
/tissue_type="Liver"
/lab_host="DH10B"
/clone_lib="Soares mouse NML"

FEATURES
Source

Location/Qualifiers
1..544
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:676323"
/tissue_type="Liver"
/lab_host="DH10B"
/clone_lib="Soares mouse NML"

ORIGIN

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'; TGTTACCAATCTGAAGTGGAGCGCCGCGAATGTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed and normalized by Bento Soares and M.Fátima Bonaldo."

Alignment Scores:

Pred. No.:	42.2	Length:	544
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AA208842 (1-544)

Qy 1 Proaspvalillepheleunglunval 9

Db 269 CCAGATGTGTATTTCTACAGAGATT 295

RESULT 177

LOCUS

AA476073 547 bp mRNA linear EST 18-JUN-1997

DEFINITION vnt26306.r1 Soares mammary_gland_NBMNG Mus musculus cDNA clone

IMAGE:876634 5', mRNA sequence.

AA476073

VERSION AA476073.1 GI:2203924

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 547)

AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gettel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Maria M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:516114

Seq primer: -28m3 rev2 ET from Amerham

High quality sequence stop: 493.

Location/Qualifiers

1..547

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:876634"

/sex="male"

/tissue_type="mammary gland"

/dev_stage="4 weeks"

/lab_host="DH10B"

/clone_11b="Soares_mammary_gland_NBMNG"

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

ORIGIN

oligo(dT) primer [5'; TGTTACCAATCTGAAGTGGAGCGCCGCGAATGTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fátima Bonaldo."

Alignment Scores:

Pred. No.:	42.4	Length:	547
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AA476073 (1-547)

Qy 1 Proaspvalillepheleunglunval 9

Db 501 CCAGATGTGTATTTCTACAGAGATT 527

RESULT 178

LOCUS

BG148976 552 bp mRNA linear EST 01-FEB-2001

DEFINITION u87b07.y1 Soares mouse NMGB bcell Mus musculus cDNA clone

IMAGE:338338 5', similar to TR:095551 095551 D3J0M3.3 ;, mRNA sequence.

BG148976

VERSION BG148976.1 GI:12652398

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 552)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Other ESTs: u87b07.xl

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1088384

Seq primer: -40RP from Gibco

High quality sequence stop: 455.

Location/Qualifiers

1..552

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:338338"

/lab_host="DH10B (phage-resistant)"

/clone_11b="Soares mouse NMGB bcell"

/note="Organ: germinal B-cell; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5'; TGTTACCAATCTGAAGTGGAGCGCCGCGAATGTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, constructed by Bento Soares and M.Fátima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.:	42.9	Length:	552
Score:	44.00	Matches:	8
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	88.9%	Mismatches:	0
Query Match:	97.8%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_145_153 (1-9) x AA476073 (1-547)

Qy 1 Proaspvalillepheleunglunval 9

Db 501 CCAGATGTGTATTTCTACAGAGATT 527

RESULT 178

LOCUS

BG148976 552 bp mRNA linear EST 01-FEB-2001

DEFINITION u87b07.y1 Soares mouse NMGB bcell Mus musculus cDNA clone

IMAGE:338338 5', similar to TR:095551 095551 D3J0M3.3 ;, mRNA sequence.

BG148976

VERSION BG148976.1 GI:12652398

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 552)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Other ESTs: u87b07.xl

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:1088384

Seq primer: -40RP from Gibco

High quality sequence stop: 455.

Location/Qualifiers

1..552

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:338338"

/lab_host="DH10B (phage-resistant)"

/clone_11b="Soares mouse NMGB bcell"

/note="Organ: germinal B-cell; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I -

oligo(dT) primer [5'; TGTTACCAATCTGAAGTGGAGCGCCGCGAATGTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, constructed by Bento Soares and M.Fátima Bonaldo."

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_145_153.rst

Page 82

Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BX148976 (1-552)

QY 1 ProaPValIIlePheLeuGInGluVal 9
DB 352 CCAGATGCTGTTTCTACAGAGATT 378

RESULT 179

BX258258 558 bp mRNA linear EST 18-FEB-2005
LOCUS BX258258 AGENAE Gallus gallus multi-tissues normalized library
DEFINITION (gcag) Gallus gallus cdna clone gcag0006c.e.22 5prim, mRNA
sequence.

ACCESSION BX258258 GI:59947831
VERSION BX258258
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 558)
AUTHORS Herault, F., Le Meuth-Metzinger, V., Desert, C., Retout, E., Piuml, F.,
Klopp, C. and Douaire, M.
TITLE Construction and primary characterization of chicken normalized
multi-tissue cDNA libraries
JOURNAL Unpublished (2003)
COMMENT On Feb 27, 2003 this sequence version replaced gi:47582959.
Contact: Douaire M
INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.63
Fax: +33 (0) 2.23.48.54.70
Email: Madeleine.Douaire@rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
plate: 0006 row: e column: 22
Seq primer: M13R.

FEATURES

Location/Qualifiers
1..558
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="gcag0006c.e.22"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="AGENAE Gallus gallus multi-tissues normalized
library (gcag)"
/note="Vector: pTR73D-Pac; tissue: adipose tissue, brain,
intestine, kidney, liver, multi-tissues, muscle, ovary,
testis, adrenal gland, bone marrow, caecum, duodenum,
embryos, fabricius gland, genital tract, granulosa,
hypothalamus, ileon, jejunum, lymphoid tissue, oviduct,
pancreas, skin, spleen, thymus, utero-vaginal gland,
pituitary gland, small intestine, hematopoietic progenitor
cells. Clone distribution: AGENAE Resource centre.
Francois Piuml, Francois.Piuml@jouy.inra.fr, INRA, CEA
Radiobiologie et Etude du genome (IREG), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0)
1.34.65.28.02, +33 (0) 1.34.65.22.73"

ORIGIN

Alignment Scores:
Pred. No.: 43.4 Length: 558
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1

Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BX258258 (1-558)

QY 1 ProaPValIIlePheLeuGInGluVal 9
DB 73 CCAGATGCTGTTTCTACAGAGATT 99

RESULT 180

BX397611 570 bp mRNA linear EST 27-NOV-2002
LOCUS BX397611 CSEBCHN58 Gallus gallus cdna clone CSEB749314 5', mRNA
DEFINITION 603534333F1 CSEBCHN58 Gallus gallus cdna clone CSEB749314 5', mRNA
sequence.

ACCESSION BX397611 GI:25766654
VERSION BX397611
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 570)
AUTHORS Boardman, P. E., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
TITLE A Comprehensive Collection of Chicken CDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1OD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES

Location/Qualifiers
1..570
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CSEB749314"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEBCHN58"
/note="Organ: small intestine; Vector: pBluescript II
KS(+); Site: 1: EcoRI; Site: 2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 44.5 Length: 570
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BX397611 (1-570)

QY 1 ProaspVal1lePheLeuGlnGluVal 9
 DB 170 CCAGATGTGCTGTTTACAGAGAGTT 196

RESULT 181
 LOCUS B1444674
 DEFINITION de27d10.y3 Wellcome CRC PRN3 oocyte Xenopus laevis cDNA clone
 IMAGE:3472962.5, similar to TR:095551 095551 DJ30M3.3, mRNA
 sequence.

ACCESSION B1444674
 VERSION B1444674.1 GI:15269381
 KEYWORDS EST
 SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 581)
 Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L.,
 Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,
 Person, B., Gibbons, M., Harvey, N., Rittner, E., Jackson, Y., McCann, R.,
 Waterston, R. and Wilson, R.
 Washu Xenopus EST project, 1999
 Unpublished (1999)
 Contact: Sandy Clifton, Ph.D.
 Washu Xenopus EST project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Fax: 314 286 1800
 Email: est@wustl.edu
 Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.
 Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
 University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available
 through the I.M.A.G.E. Consortium/HLN at: info@image.llnl.gov
 High quality sequence stop: 403.

FEATURES
 source
 1..581
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="IMAGE:3472962"
 /issue_type="oocyte"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Wellcome CRC PRN3 oocyte"
 /note="Vector: pBSRN3; Site 1: NotI; Site 2: EcoRI; cDNAs
 were oligo-dT primed and directionally cloned. Sequencing
 according to Newkirk and Faber. Library was constructed
 by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon
 (Wellcome/CRC Institute)."

ORIGIN

Alignment Scores:
 Pred. No.: 45.4 Length: 581
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1444674 (1-581)

QY 1 ProaspVal1lePheLeuGlnGluVal 9
 DB 333 CCAGATGTGCTGTTTACAGAGAGTT 359

RESULT 182
 LOCUS B1064472
 DEFINITION pgfin.pk001.h17.normalized chicken fat cDNA library Gallus gallus

CDNA clone pgfin.pk001.h17.5, similar to gi|7705262
 ref|NP_057698.1| TRAF and TNF receptor-associated protein [Homo
 sapiens] gb|AA64144.1|AF223469_1 (AF223469) AD022 protein [Homo
 sapiens]g, mRNA sequence.

ACCESSION B1064472
 VERSION B1064472.1 GI:14471994
 KEYWORDS EST
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 600)
 Cogburn, L.A., Morgan, R.W. and Burnside, J.
 Chicken ESTs from fat
 Unpublished (2001)
 Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
 source
 1..600
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="pgfin.pk001.h17"
 /sex="Male and Female"
 /tissue_type="fat"
 /lab_host="E.coli BMD10B"
 /clone_lib="normalized chicken fat cDNA library"
 /note="Vector: pSPORT1"

ORIGIN

Alignment Scores:
 Pred. No.: 47.1 Length: 600
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1064472 (1-600)

QY 1 ProaspVal1lePheLeuGlnGluVal 9
 DB 329 CCAGATGTGCTGTTTACAGAGAGTT 355

RESULT 183
 LOCUS B1990829
 DEFINITION 4081-88 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
 mRNA sequence.

ACCESSION B1990829
 VERSION B1990829.1 GI:17961846
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 600)
 Mu, X., Zhao, S., Perahad, R., Heieh, T.-F., Scarpa, A., Wang, S.W.,
 White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.
 Gene expression in the developing mouse retina by EST sequencing
 and microarray analysis
 Nucleic Acids Res. 29 (24), 4983-4993 (2001)

JOURNAL
 PUBMED
 COMMENT
 Contact: Klein WH
 Department of Biochemistry and Molecular Biology
 University of Texas M.D. Anderson Cancer Center
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA

Thu Mar 16 10:39:26 2006

US-10-757-745-2_copy_145_153.rst

Page 84

Tel: 713 792 3646
Fax: 713 790 0329
Location/Qualifiers
1..600
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/clone_idb="Mouse E14.5 retina lambda ZAP II library"

ORIGIN

Alignment Scores:

Pred. No.: 47.1 Length: 600
Score: 44.00 Matches: 9
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x B1990829 (1-600)

OY 1 PROSPYALLPheLeuGlnGluVal 9

DB 496 CCAGATGTGTATTTCTACAGAGATT 522

RESULT 184
CB579756 615 bp mRNA linear EST 03-APR-2003
LOCUS AMGNOC:NRD1-00175-B9-A nrdg1 (10855) Rattus norvegicus cDNA clone
DEFINITION nrdg1-00175-e9 5', mRNA sequence.
ACCESSION CB579756
VERSION CB579756.1 GI:29523797
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 615)
REFERENCE
AUTHORS Amgen Rat EST Program
TITLE Unpublished (2003)
JOURNAL Contact: Dan Fitzpatrick
COMMENT Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00175 row: e column: 9.

FEATURES

source

1..615
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone_idb="nrdg1-00175-e9"
/tissue_type="dorsal root ganglia"
/clone_idb="nrdg1a855"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat
dorsal root ganglia"

ORIGIN

Alignment Scores:

Pred. No.: 48.5 Length: 615
Score: 44.00 Matches: 8
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 88.9% Mismatches: 0
Query Match: 97.8% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CB579756 (1-615)

OY 1 PROSPYALLPheLeuGlnGluVal 9

DB 507 CCAGACGTGTATTTCTACAGAGATT 533

RESULT 185
CB594288 617 bp mRNA linear EST 18-MAY-2004
LOCUS E0348B09-5 NIA Mouse E10.5 whole embryo cDNA library (Long) Mus
DEFINITION musculus cDNA clone NIA:E0348B09 IMAGE:30863576 5', mRNA sequence.
ACCESSION CB594288
VERSION CB594288.1 GI:47463037
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 617)
REFERENCE
AUTHORS Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,
VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Baese, U.C.,
Wang, Y., Carter, M.G., Hamatani, T., Alpa, K., Akutsu, H., Sharov, L.,
Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,
Nagaraja, R., Boheler, K.R., Taub, D., Hodges, R.J., Longo, D.L.,
Schlesinger, D., Keller, J., Klotz, E., Klesse, G., Umezawa, A.,
Vescovi, A.L., Rosenthal, J., Kunath, T., Hogan, B.L., Curci, A.,
D'Urso, M., Klesse, J., Hide, W., and Ko, M.S.
TITLE Transcriptional analysis of mouse stem cells and early embryos
JOURNAL Plos Biol. 1 (3), 410-419 (2003)
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: E0348 row: E column: 09
Seq primer: M13 Reverse
High quality sequence stop: 617
POLYA=No.

FEATURES

source

1..617
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_idb="NIA:E0348B09-5"
/tissue_type="whole embryo including extraembryonic
tissues at 10.5-days postcoitum"
/dev_stage="E10.5"
/lab_host="DH10B"
/clone_idb="NIA Mouse E10.5 whole embryo cDNA library
(Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
Site_2: NotI; Mouse cDNA project by the Laboratory of
Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://igsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library. Total
Genome Res. 11: 1553-1558 (2001). [PMID: 11544197]
RNAs were extracted from a pool of 8 embryos at 10.5 days
postcoitum. Double-stranded cDNAs were synthesized with an
Oligo(dT) primer [Invitrogen:
5'-pGACTGTTCTAGATCGGAGCGCCGCTTTTCTTTT-3'] from
2ug of total RNA, treated with 74 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker L1-SalI, purified by phenol/chloroform and
separated from free linkers by centrifugation. The PCR using
Ex Taq polymerase (Takara) with a primer SalI-S
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pCMV-SPORT6 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by the standard chemical method. The
average insert size is about 3.4kb. The library was
constructed by Yulan Piao."

ORIGIN

Alignment Scores:

Pred. No.: 48.7 Length: 617
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x CN694288 (1-617)

Qy 1 Proaspvalillepheleugingluval 9
 DB 92 CCAGATGCTGTATTTCTACAGAGATT 118

RESULT 186

BF182465 621 bp mRNA linear EST 31-OCT-2000
 LOCUS 601804232F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4035319 5',
 DEFINITION mRNA sequence.
 ACCESSION BF182465.1 GI:11060608
 VERSION BF182465.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgabbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM9308 row: P column: 08
 High quality sequence stop: 615.
 Location/Qualifiers

FEATURES

1..621:
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="mix FVB/N, C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:4035319"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /clone_11b="NCI CGAP Mam5"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

ORIGIN

Alignment Scores:

Pred. No.: 49 Length: 621
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BF182465 (1-621)

Qy 1 Proaspvalillepheleugingluval 9
 DB 495 CCAGATGCTGTATTTCTACAGAGATT 521

RESULT 187

BU471395 625 bp mRNA linear EST 30-NOV-2002
 LOCUS 603163114F1 CSEQRBN21 Gallus gallus cDNA clone CHEST258k3 5', mRNA
 DEFINITION sequence.
 ACCESSION BU471395.1 GI:25964972
 VERSION BU471395.1
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE Boardman, P.E., Sanz-Ezquerro, O., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)

PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES

1..625
 Location/Qualifiers
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer"
 /db_xref="taxon:9031"
 /clone="CHEST258k3"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_11b="CSEQRBN21"
 /note="Organ: ovary; Vector: pBluescript II KS(+); Site 1:
 EcoRI; Site 2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.: 49.4 Length: 625
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BU471395 (1-625)

Qy 1 Proaspvalillepheleugingluval 9
 DB 376 CCAGATGCTGTATTTCTACAGAGATT 402

RESULT 188

CD807796 625 bp mRNA linear EST 15-JUL-2003
 LOCUS CD807796
 DEFINITION UI-M-GWO-clq-g-15-0-UI.r1 NIH_BMAP_GWO Mus musculus cDNA clone

IMAGE:30539966 5', mRNA sequence.

ACCESSION
CD807796
VERSION
CD807796.1 GI:32466622
KEYWORDS
EST
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

REFERENCE
Bukacynski, M.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
NIH-MGC http://mgc.ncl.nih.gov/
1 (bases 1 to 625)
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1998)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: rstra@remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouse1.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
source
The following repetitive elements were found in this CDNA
sequence: 215-278, >IDS#SINE/ID (matched complement)
Seq primer: PIX-5.
Location/Qualifiers
1..625
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="TM68:30539966"
/tissue_type="whole eye"
/dev_stage="embryo.15.5,16.5,17.5,18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH-BMAP-GMO"
/note="Organ: Eye; Vector: pYX-Asc; Site:1: Ecor I;
Site:2: Not I; The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CCGCGTCTCC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
49.4	625	8	1	0	0	0
Score:	44.00					
Percent Similarity:	100.0%					
Best Local Similarity:	88.9%					
Query Match:	97.8%					

US-10-757-745-2_COPY_145_153 (1-9) x CD807796 (1-625)

Qy 1 PROSPYALILEPHELENGINGUVA1 9

Db 459 CCAAGATGTGTATTCTACAGGAAGTT 485

RESULT 189
C5577890
LOCUS
DEFINITION
C5577890 627 bp mRNA linear EST 03-APR-2003
AMGNNUC:NRDQ1-00195-C6-A nrdg1 (10855) Rattus norvegicus CDNA clone
nrdg1-00195-c6 5', mRNA sequence.

ACCESSION
C5577890
VERSION
C5577890.1 GI:29521931
KEYWORDS
EST
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus

REFERENCE
Bukacynski, M.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 627)
Angen Rat EST Program
JOURNAL
Unpublished (2003)

COMMENT
Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805.447.4881
Plate: 00195 row: C Column: 6.
Location/Qualifiers
1..627
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrdg1-00195-c6"
/tissue_type="dorsal Root Ganglia"
/clone_lib="nrdg1 (10855)"
/note="Vector: pSPOR1; Site:1: SalI; Site:2: NotI; rat
dorsal root ganglia"

FEATURES
source
The following repetitive elements were found in this CDNA
sequence: 215-278, >IDS#SINE/ID (matched complement)
Seq primer: PIX-5.
Location/Qualifiers
1..625
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="TM68:30539966"
/tissue_type="whole eye"
/dev_stage="embryo.15.5,16.5,17.5,18.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH-BMAP-GMO"
/note="Organ: Eye; Vector: pYX-Asc; Site:1: Ecor I;
Site:2: Not I; The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CCGCGTCTCC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
49.6	627	8	1	0	0	0
Score:	44.00					
Percent Similarity:	100.0%					
Best Local Similarity:	88.9%					
Query Match:	97.8%					

US-10-757-745-2_COPY_145_153 (1-9) x C5577890 (1-627)

Qy 1 PROSPYALILEPHELENGINGUVA1 9

Db 537 CCAAGATGTGTATTCTACAGGAAGTT 563

RESULT 190

AL858410
LOCUS
DEFINITION
AL858410 634 bp mRNA linear EST 02-DEC-2003
AMGNNUC:XR001-00195-C6-A nrdg1 (10855) Rattus norvegicus CDNA clone XR001-00195-c6 5', mRNA
sequence.

ACCESSION
AL858410
VERSION
AL858410.2 GI:38633375
KEYWORDS
EST
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis

REFERENCE
Bukacynski, M.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 634)
Angen Rat EST Program
JOURNAL
Unpublished (2003)

COMMENT
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPCALIS_SEQUENCE_ID: TR95059p03.p1x5p6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
CDNA was oligo dT primed from 5' end of poly A+ RNA from egg
ECORI-NotI cut CDNA was then ligated into pCIS107 with EcorI at the
5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers

FEATURES

1..634
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TB9059p03"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA was oligo dt primed from 5ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:
Score: 44.00	634	8	100.0%
Percent Similarity: 100.0%			
Best Local Similarity: 88.9%		Mismatches: 0	
Query Match: 97.8%		Indels: 0	
DB: 1	Gaps: 0		

US-10-757-745-2_COPY_145_153 (1-9) x AB58410 (1-634)

Qy 1 ProaSpVal11lePheLeuGlnGluVal 9

Db 436 CCAGATGTAGTATTCTTACAGAGGTT 462

RESULT 191

DN091361 634 bp mRNA linear EST 14-FEB-2005
LOCUS JGI CABE4216.fwd NIH XCC tropOval Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7822728 5', mRNA sequence.
ACCESSION DN091361
VERSION DN091361.1 GI:59758465
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae; Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 634)
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI CABE4216.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Robert M. Grainger
CDNA Library Preparation: Bruce Blumberg Laboratory, University of California, Irvine
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.jnl.gov
Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
Place: CABE 0041 row: p column: 22
High quality sequence stop: 575.
Location/Qualifiers

FEATURES

1..634
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/strain="N6 (Nigerian 6th generation inbred)"

ORIGIN

Pred. No.:	Length:	Matches:	Conservative:
Score: 44.00	634	8	100.0%
Percent Similarity: 100.0%			
Best Local Similarity: 88.9%		Mismatches: 0	
Query Match: 97.8%		Indels: 0	
DB: 8	Gaps: 0		

US-10-757-745-2_COPY_145_153 (1-9) x DN091361 (1-634)

Qy 1 ProaSpVal11lePheLeuGlnGluVal 9

Db 280 CCAGATGTAGTATTCTTACAGAGGTT 306

RESULT 192

BM539358 635 bp mRNA linear EST 20-FEB-2002
LOCUS hb08d09.g1 Canis cDNAs from testes cells Canis familiaris cDNA
DEFINITION clone hb08d09 5', mRNA sequence.
ACCESSION BM539358
VERSION BM539358.1 GI:18821216
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 635)
O'Shaughnessy, A.L., McCombie, W.R., Baker, J.P., Balija, V., Cummins, D., Dedhia, N.N., de la Baetide, M., Katzenberger, P., King, L., Kirchoff, K.A., Miller, B., Miller, S., Nascimento, L.U., Palmer, L., Santos, L., Shah, R.S., Spiegel, L.A., Zucavern, T., Preston, R. and Hammon, G.J.
Expressed sequence tags from Canis familiaris (dog) (2002)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Place: hb08 row: d column: 09
Seq primer: -21M3UnivRev
High quality sequence stop: 635.
Location/Qualifiers

FEATURES

1..635
/organism="Canis familiaris"
/mol_type="mRNA"
/db_xref="taxon:9615"

REFERENCE 1 (bases 1 to 640)
 AUTHORS Crouling, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M., and Rogers, J.
 TITLE Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Sep 15, 2002 this sequence version replaced gi:22874895.
 Contact: Taylor R

Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS SEQUENCE ID: TEG9019p19.plkSP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NotI at the 3' end.
 Vector: pCS107, Site 1: EcoRI; Site 2: NotI
 Host: Escherichia coli XL1-blue.
 Location/Qualifiers
 1..640
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TEG9019p19"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_1b="XGC-egg"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end"

Alignment Scores:
 Pred. No.: 50.7 Length: 640
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 1 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x ALB54676 (1-640)

QY 1 Proaapvalillephelaungluval 9
 DB 456 CCAGATGTAGTATTCTTACAGAGGTT 482

RESULT 196

LOCUS BG083167 644 bp mRNA linear EST 18-DEC-2003
 DEFINITION H3085C02-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
 H3085C02 5' mRNA sequence.
 ACCESSION BG083167
 VERSION BG083167.2 GI:40069892
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 644)
 AUTHORS Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.U., Wang, X.,
 Gralovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H.,
 Wood, W.H. III, Becker, K.G., and Ko, M.S.H.
 TITLE Genome-wide expression profiling of mid-gestation placenta and
 embryo using a 15,000 mouse developmental cDNA microarray
 Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

JOURNAL PUMED
 COMMENT On Jan 26, 2001 this sequence version replaced gi:12565735.
 Other ESTs: H3085C02-3
 Contact: George J. Kargul

FEATURES
 source Laboratory of Genetics
 National Institute on Aging/National Institutes of Health
 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
 Email: cdna@gsun.grc.nia.nih.gov
 This clone set has been freely distributed to the community. Please
 visit <http://lgsun.grc.nia.nih.gov/cDNA/15k.html> for details.
 Plate: H3085 row: C column: 02
 Seq primer: -21M13 Reverse
 High quality sequence stop: 644
 POLY(A)=No.

FEATURES
 source Location/Qualifiers
 1..644
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6J"
 /db_xref="labEST:H3085C02-5"
 /db_xref="taxon:10090"
 /clone="H3085C02"
 /sex="Clones arrayed from a variety of cDNA libraries"
 /dev_stage="Clones arrayed from a variety of cDNA
 libraries"
 /lab_host="DH10B"
 /clone_1b="NIA Mouse 15K cDNA Clone Set"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This
 clone is among a rearranged set of 15,247 clones from 11
 embryo cDNA libraries (including preimplantation stage
 embryos from unfertilized egg to blastocyst, embryonic
 part of E7.5 embryos, extraembryonic part of E7.5
 embryos, and E12.5 female mesonephros/gonad) and one
 newborn ovary cDNA library. Average insert size 1.5 kb.
 All source libraries are cloned unidirectionally with
 Oligo(dT)-Not primers. References include: (1)
 genome-wide expression profiling of mid-gestation
 placenta and embryo using a 15,000 mouse developmental
 cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97:
 9127-9132; (2) large-scale cDNA analysis reveals phased
 gene expression patterns during preimplantation mouse
 development, 2000, Development, 127: 1737-1749; (3)
 genome-wide mapping of unselected transcripts from
 extraembryonic tissue of 7.5-day mouse embryos reveals
 enrichment in the t-complex and under-representation on
 the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

Alignment Scores:
 Pred. No.: 51.1 Length: 644
 Score: 44.00 Matches: 8
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 88.9% Mismatches: 0
 Query Match: 97.8% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_145_153 (1-9) x BG083167 (1-644)

QY 1 Proaapvalillephelaungluval 9
 DB 229 CCAGATGTAGTATTCTTACAGAGGTT 255

RESULT 197

LOCUS BM426270 645 bp mRNA linear EST 30-JAN-2002
 DEFINITION p9f2n.pk002.c6 Normalized Chicken Abdominal Fat Library (p9f2n)
 Gallus gallus cDNA clone p9f2n.pk002.c6 5' similar to gi|11418470
 ref|XP_004263.1| TRAF and TNF receptor-associated protein [Homo
 sapiens] gi|14747264 ref|XP_041298.1| TRAF and TNF
 receptor-associated protein [Homo sapiens] emb|CA21141.1|
 (A033175) d3j0m3.3 (novel protein similar to C. elegans, mRNA
 sequence.
 ACCESSION BM426270
 VERSION BM426270.1 GI:18430455
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 16, 2006, 00:29:49 ; Search time 6832.46 Seconds

(without alignments)
595.756 Million cell updates/sec

Title: US-10-757-745-2_COPY_54_140

Sequence: 1 MERALNSYFPPPEVSALER.....IDGLDINNLSERAGVCYL 87

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1000 summaries

Command line parameters:
-MODEL=frame2_p2n.model -DEV=xlh
-O=/abs/ABSSMBE/spool/US10757745/runat_15032006_165652_3610/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=ext -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsun62 -TRANS=humana0.cdt -LIST=1000
-DOCALLIGN=200 -THR.SCOR=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=200 -MODE=LOCAL
-OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs02h
-USER=US10757745@CGN_1_1.8148@runat_15032006_165652_3610 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_hic: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_esc7: *
9: gb_ges1: *
10: gb_ges2: *
11: gb_ges3: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	100.0	429	5	BOS62059 1112C11.Y
2	448	100.0	471	5	CR543841 DKFZ04590
3	448	100.0	473	6	CB120234 K-EST0167
4	448	100.0	480	1	A1750554 CN04601.Y
5	448	100.0	485	1	AA486032 ab40D10.Y
6	448	100.0	530	3	BM646221 K-EST0125
7	448	100.0	554	3	BP220985 BP220985

8	448	100.0	565	3	BP226620
9	448	100.0	566	3	BP220508
10	448	100.0	568	3	BP257211 BP257211
11	448	100.0	570	3	BP221518
12	448	100.0	573	1	AU279894
13	448	100.0	573	3	BP221260
14	448	100.0	573	3	BP261500
15	448	100.0	576	3	BP262642
16	448	100.0	577	7	CN298919
17	448	100.0	580	3	BP274368
18	448	100.0	581	3	BP207751
19	448	100.0	581	3	BP225088
20	448	100.0	581	3	BP262638
21	448	100.0	581	3	BP270744
22	448	100.0	581	3	BP379659
23	448	100.0	582	3	BP219740
24	448	100.0	582	3	BP261141
25	448	100.0	582	3	BP270415
26	448	100.0	582	3	BP275810
27	448	100.0	583	3	BP195721
28	448	100.0	583	3	BP262103
29	448	100.0	583	3	BP262741
30	448	100.0	583	3	BP319548
31	448	100.0	583	5	BP783329
32	448	100.0	584	3	BP263059
33	448	100.0	584	3	BP348623
34	448	100.0	588	3	BP236074
35	448	100.0	602	1	AL703449
36	448	100.0	621	6	CB069952
37	448	100.0	634	6	CB157906
38	448	100.0	634	7	CN023369
39	448	100.0	644	7	BI333830
40	448	100.0	652	7	CR753214
41	448	100.0	657	7	CN298920
42	448	100.0	678	2	CG119113
43	448	100.0	701	5	CG167236
44	448	100.0	710	7	BP661472
45	448	100.0	711	7	CN298923
46	448	100.0	729	7	CN298922
47	448	100.0	729	7	CN298924
48	448	100.0	731	8	CK760857
49	448	100.0	767	2	BI258848
50	448	100.0	774	3	BI754101
51	448	100.0	786	2	BG119977
52	448	100.0	799	8	CK756424
53	448	100.0	810	8	CK166335
54	448	100.0	838	3	BI908925
55	448	100.0	846	7	CR765451
56	448	100.0	853	2	BE784416
57	448	100.0	858	3	BI553412
58	448	100.0	870	2	BG740396
59	448	100.0	870	5	BU159911
60	448	100.0	883	5	BU169945
61	448	100.0	883	5	BU179107
62	448	100.0	906	6	CD251503
63	448	100.0	937	2	BS418139
64	448	100.0	948	1	AL555333
65	448	100.0	952	3	BI161201
66	448	100.0	979	3	BM468826
67	448	100.0	981	5	CK338160
68	448	100.0	995	2	BE892886
69	448	100.0	1018	5	BM337141
70	448	100.0	1035	4	BM554324
71	448	100.0	1067	5	BM337905
72	448	100.0	1081	5	BM444691
73	448	100.0	1089	11	DQ049205
74	448	100.0	1103	4	BM555041
75	448	100.0	1168	4	CR601303
76	448	100.0	1192	3	BM553049
77	448	100.0	1620	4	CR592636
78	448	100.0	1894	4	CR597293
79	448	100.0	1909	4	CR595644
80	445	99.3	581	1	AV717253

81	444	99.1	582	3	BP234218	BP234218	154	211.5	47.2	600	3	BT990829	4081-88	M
80	444	98.9	582	3	BP233592	BP233592	155	211.5	47.2	645	5	BT737520	BY737520	
83	440	98.2	572	3	BP262485	BP262485	156	211.5	47.2	645	5	AM321603	U03606	Y
84	440	98.2	582	3	BP263516	BP263516	157	211.5	47.2	691	3	BT648868	603275826	
85	440	98.2	582	3	BF977971	602148451	158	211.5	47.2	761	3	CC2326137	MEMO1355	
86	440	98.2	582	3	BX358707	BX358707	159	211.5	47.2	961	9	BT784732	602111139	
87	440	98.2	582	3	BM926092	AGENCOURT	160	211.5	47.2	943	3	BM298330	603297112	
88	440	98.2	1046	5	BM926092	AGENCOURT	161	211.5	47.2	961	3	BT656151	603283518	
89	439	98.0	1743	4	CR602029	Full-1eng	162	211.5	47.2	1046	6	CA976386	AGENCOURT	
90	439	98.0	752	1	AU139147	AU139147	163	211.5	47.2	615	6	CB579756	AGENCOURT	
91	439	98.0	783	5	BX365835	BX365835	164	210.5	47.0	724	7	CB577890	AGENCOURT	
92	437	97.8	739	7	CR791801	DKF2P468J	165	210.5	47.0	639	4	CB545297	AGENCOURT	
93	437	97.5	310	8	T26956	1d155Pc01	166	206.5	46.1	640	1	BM546676	AGENCOURT	
94	436	97.3	780	5	BX374579	BX374579	167	201	44.3	842	8	CA959565	AGENCOURT	
95	435	97.1	580	3	BP261787	BP261787	168	201	44.3	866	8	CA959565	AGENCOURT	
96	435	96.7	927	2	BG119064	602347589	169	201	44.3	879	8	CA959565	AGENCOURT	
97	432	96.4	704	3	B134820	602998939	170	195.5	44.3	712	2	BM609356	AGENCOURT	
98	431	96.2	581	3	BP199948	BP199948	171	195.5	44.3	475	6	CB699206	AGENCOURT	
99	430	96.0	582	3	BP348796	BP348796	172	195.5	44.3	475	6	CB728877	AGENCOURT	
100	429	95.8	932	2	BG740339	602635289	173	198.5	43.6	703	5	BY719852	BT19852	
101	428	95.5	1089	11	DQ049206	Pan-1c0g1	174	195.5	43.6	600	2	BM600090	AGENCOURT	
102	427	95.3	904	5	BX422491	BX422491	175	195.5	43.6	600	2	BM600090	AGENCOURT	
103	427	95.3	556	3	BP243301	BP243301	176	195.5	43.6	631	1	BT682465	AGENCOURT	
104	427	95.3	570	3	BM172060	imageqc_3	177	192	42.9	634	1	AL901140	AL901140	
105	421	94.0	584	3	BP274942	BP274942	178	192	42.9	638	1	AL901140	AL901140	
106	421	94.0	584	3	BT670756	603044763	179	182	42.2	654	1	AL901140	AL901140	
107	421	94.0	584	3	BP537046	602565130	180	189	42.2	671	3	BM622875	AGENCOURT	
108	415	92.6	581	3	BP264149	BP264149	181	189	42.2	816	7	CA960677	AGENCOURT	
109	408	91.6	1090	7	CN641671	ILLUMIGEN	182	189	42.2	876	7	CA972607	AGENCOURT	
110	405	90.5	915	3	CV805216	ILLUMIGEN	183	189	42.2	927	6	CA972607	AGENCOURT	
111	405	90.4	915	3	B1915865	603184527	184	189	42.2	927	6	CA972607	AGENCOURT	
112	401	89.5	922	7	BQ787387	IM09C09.Y	185	184.5	41.2	519	2	BB667803	AGENCOURT	
113	400	89.3	922	7	CN801806	ILLUMIGEN	186	184.5	41.2	425	6	BB667803	AGENCOURT	
114	389	86.8	793	5	BU070378	IM09C09.X	187	182.5	40.5	1289	4	AK009089	AGENCOURT	
115	384	85.7	908	2	BG533717	BG533717	188	181	40.4	782	8	CN937111	JGI CANOS	
116	383	85.5	770	2	BG391213	602417244	189	179.5	40.1	444	10	AK204589	BT444674	
117	365	81.5	582	3	BM507091	IM09C09.Y	190	179.5	40.1	581	10	BT444674	de27d10.Y	
118	363	80.6	548	1	AL516230	AL516230	191	179	40.0	688	2	BT189858	BT189858	
119	361	81.0	548	1	AL516230	AL516230	192	179	40.0	744	9	CE158280	L1gr-g8s	
120	357	79.7	394	1	AV661333	AV661333	193	179	40.0	744	9	CE158280	L1gr-g8s	
121	357	79.7	394	1	AV661333	AV661333	194	179	40.0	744	9	CE158280	L1gr-g8s	
122	338	75.4	325	8	T31666	EST376732.Hu	195	179	40.0	750	8	CA981008	AGENCOURT	
123	331	73.9	674	7	CN791432	4126159.B	196	179	40.0	821	6	CA981008	AGENCOURT	
124	329	73.4	388	1	AV659558	AV659558	197	179	40.0	876	5	CA9797649	AGENCOURT	
125	327	73.0	467	6	CF764797	4123581.B	198	179	40.0	896	6	CA9797649	AGENCOURT	
126	327	73.0	467	6	CF764797	4123581.B	199	179	40.0	900	6	CA9797649	AGENCOURT	
127	325	72.5	653	7	CN789157	PNM-BT075	200	178.5	41.2	919	6	CA9797649	AGENCOURT	
128	325	72.5	653	7	CN789157	PNM-BT075	201	178.5	41.2	919	6	CA9797649	AGENCOURT	
129	325	72.5	653	7	CN789157	PNM-BT075	202	178.5	41.2	919	6	CA9797649	AGENCOURT	
130	321	71.7	378	1	AV655175	AV655175	203	178.5	41.2	919	6	CA9797649	AGENCOURT	
131	312	69.6	581	6	CB286391	CM036.C09	204	174	38.8	942	6	CA980929	AGENCOURT	
132	312	69.6	581	6	CB286391	CM036.C09	205	174	38.8	942	6	CA980929	AGENCOURT	
133	310	69.2	952	5	BM433489	BM433489	206	173	38.6	555	3	BM060342	AGENCOURT	
134	310	69.2	952	5	BM433489	BM433489	207	173	38.6	555	3	BM060342	AGENCOURT	
135	305	66.5	355	7	CR767008	DKF2P469G	208	173	38.6	644	3	BM060342	AGENCOURT	
136	298	66.5	416	8	CR767008	DKF2P469G	209	173	38.6	644	3	BM060342	AGENCOURT	
137	295	66.5	355	7	CR767008	DKF2P469G	210	173	38.6	644	3	BM060342	AGENCOURT	
138	289.5	64.6	751	2	BF243927	601877778	211	172	38.6	814	7	CO795556	AGENCOURT	
139	288	64.3	898	2	BG623866	602649018	212	172	38.6	814	7	CO795556	AGENCOURT	
140	269	60.0	635	3	BM593938	h08d49018	213	173	38.6	834	7	CO795556	AGENCOURT	
141	229	51.1	409	2	BM590023	HOA48-1-G	214	173	38.6	846	7	CA972470	AGENCOURT	
142	224	50.0	645	3	BM426247	PG1fn.pko	215	173	38.6	857	7	CN017421	AGENCOURT	
143	221	49.3	1087	7	CN642527	ILLUMIGEN	216	168.5	37.3	827	8	DN097147	JGI CABE77	
144	220	49.1	625	5	BU471395	603363114	217	167	37.3	451	1	AA761912	AA761912	
145	220	49.1	625	5	BU471395	603363114	218	167	37.3	451	1	AA761912	AA761912	
146	219.5	49.0	646	5	BU046774	PG1fn.pko	219	165	36.8	523	1	AA761912	AA761912	
147	217.5	48.5	906	5	BU046774	PG1fn.pko	220	165	36.8	523	1	AA761912	AA761912	
148	213	48.4	577	9	BZ585137	CH240.232	221	164	36.2	644	1	CO050975	CO050975	
149	213	48.4	577	9	BZ585137	CH240.232	222	164	36.2	644	1	CO050975	CO050975	
150	212.5	47.4	531	7	CN233559	RJTA113F02	223	160.5	35.6	644	1	CO050975	CO050975	
151	212.5	47.4	782	5	BU206549	603483616	224	159.5	35.6	634	8	DN091361	DN091361	
152	212.5	47.4	817	5	BU11103	603127011	225	156	34.8	547	1	AA476073	AA476073	
153	212.5	47.4	1077	5	BU11072	603127011	226	156	34.8	547	1	AA476073	AA476073	

227	155	34.6	570	5	BU937611	60354313	300	96	21.4	568	1	AL727624	AL727624
228	153.5	34.3	847	8	DR867246	JGI_CABG9	301	96	21.4	729	8	DR704222	DR704222
229	153	34.2	304	2	BES19103	G0172729	302	94.5	21.1	441	7	CN807482	CN807482
230	153	34.2	312	3	BMI53209	TCBAP1Q14	303	94	21.0	149	3	BQ336306	BQ336306
231	153	34.2	480	6	CA777110	IP03F10.Y	304	94	21.0	746	2	BF140146	BF140146
232	153	34.2	582	3	BP194502	BP194502	305	92.5	20.6	493	3	AA163045	AA163045
233	153	34.2	685	7	CK981492	4114013 B	306	92.5	20.6	1174	6	CD509260	CD509260
234	153	34.2	722	7	BF679649	602154095	307	92	20.5	433	1	AJ398593	AJ398593
235	153	34.2	802	7	CO918949	AGENCOURT	308	91	20.3	379	5	BY036773	BY036773
236	150.5	33.6	802	8	DN100293	JGI_CABE8	309	90	20.1	260	11	TSP458761	TSP458761
237	150.5	33.6	835	8	CX937110	JGI_CAO5	310	89	19.9	961	2	BI150788	BI150788
238	149.5	33.4	456	1	AA839622	vw97606.r	311	87.5	19.5	918	8	DR946006	DR946006
239	148.5	33.1	757	10	BK198893	BK198893	312	87	19.4	313	2	BF992133	BF992133
240	147.5	32.9	525	2	BE290901	601084205	313	86.5	19.3	723	7	CV740501	CV740501
241	145.5	32.5	675	1	AL722584	AL722584	314	86.5	19.3	730	7	CV756544	CV756544
242	145.5	32.5	827	5	BQ443284	UI-M-EVO-	315	86.5	19.3	809	8	CK863267	CK863267
243	145	32.4	537	7	CR774766	DKF2P469A	316	86.5	19.3	1453	4	AY814979	AY814979
244	144	32.1	891	1	AL879624	AL879624	317	86	19.2	361	5	BY028675	BY028675
245	144	32.1	909	5	BX780455	BX780455	318	85.5	19.1	541	6	CD321260	CD321260
246	143.5	32.0	799	1	AM199574	da05f07.Y	319	85	19.0	654	8	CK682762	CK682762
247	140.5	31.4	672	11	DE094838	DE094838	320	84.5	18.9	880	9	BH207435	BH207435
248	140.5	31.4	894	5	BX776016	BX776016	321	83.5	18.6	586	3	BI789841	BI789841
249	137	30.6	563	8	DR003404	TC114160	322	83	18.5	581	3	BP262101	BP262101
250	136.5	30.5	352	6	CB780491	AMGNNUC.N	323	83	18.5	983	2	BR337260	BR337260
251	136	30.4	1030	5	BU235217	603791177	324	82	18.3	369	5	BF337260	BF337260
252	134	29.9	297	8	BF170990	PCL1883 M	325	82	18.3	448	1	AI208756	AI208756
253	134	29.2	860	8	CX588090	JGI_CAO9	326	82	18.3	463	2	BF89319	BF89319
254	127.5	28.5	808	8	DN932266	AGENCOURT	327	82	18.3	484	3	BI424242	BI424242
255	125	27.9	454	2	BX911124	BX911124	328	82	18.3	552	5	BU080681	BU080681
256	124.5	27.8	839	5	BK911124	AL725543	329	82	18.3	558	3	BM885374	BM885374
257	124	27.7	623	1	AL725543	Mus muscu	330	82	18.3	903	6	CF712017	CF712017
258	123.5	27.6	424	4	AK180792	604152621	331	82	18.2	364	1	AA982672	AA982672
259	123	27.5	760	5	BU204728	BF852284	332	81.5	18.2	416	2	BE624685	BE624685
260	122	27.2	463	2	BF852284	MR3-EN008	333	81.5	18.2	567	3	BP049364	BP049364
261	120	26.8	156	3	BQ311200	MR4-ET014	334	81.5	18.2	624	1	AA536675	AA536675
262	120	26.8	296	2	BF992136	OV3-GN020	335	81.5	18.2	676	6	CF743564	CF743564
263	120	26.8	422	2	BG982044	MR3-CN014	336	81.5	18.2	682	10	C2905189	C2905189
264	120	26.8	435	3	BQ332331	MR4-ET001	337	81.5	18.2	882	5	BU505745	BU505745
265	120	26.8	437	2	BF768820	PM0-IT001	338	81.5	18.2	1012	6	CB209613	CB209613
266	120	26.8	440	2	BG982029	MR3-CN014	339	81	18.1	468	3	BI317492	BI317492
267	120	26.8	440	2	BG982036	MR3-CN014	340	80.5	18.0	665	7	CV249386	CV249386
268	120	26.8	453	2	BF773259	PM0-IT001	341	80	17.9	695	7	CV246027	CV246027
269	120	26.8	453	2	BQ315535	OV3-GN020	342	80	17.9	706	7	CV250470	CV250470
270	120	26.8	456	2	BF969680	MR3-CN014	343	80	17.9	810	9	CC477031	CC477031
271	120	26.8	459	2	BG982034	MR3-CN014	344	80	17.9	810	9	CC477031	CC477031
272	120	26.8	461	2	BG982012	MR3-CN014	345	79.5	17.7	487	3	BI441344	BI441344
273	120	26.8	479	2	BF997052	BF768814	346	79.5	17.7	651	5	BQ852542	BQ852542
274	119	26.6	247	2	BF768814	PM0-IT001	347	79.5	17.7	711	5	BQ995001	BQ995001
275	119	26.6	460	2	BF893150	PM1-MT014	348	79.5	17.7	744	8	DR509044	DR509044
276	117	26.1	134	3	BI061261	PM1-MT014	349	79.5	17.7	797	8	CK863376	CK863376
277	117	26.1	441	2	BF893925	PM1-MT014	350	79.5	17.7	826	8	DR339601	DR339601
278	116.5	26.0	410	2	BG091909	mac18C11	351	79.5	17.7	904	8	DR929708	DR929708
279	116.5	26.0	517	9	CC248786	KK529 Bay	352	79	17.6	470	7	CR746747	CR746747
280	116	25.9	574	3	BI445352	374149 MA	353	79	17.6	476	8	DT071039	DT071039
281	116	25.9	640	6	CB505136	esal1p1b5	354	78.5	17.5	420	4	CN50G674	CN50G674
282	115	25.7	463	2	BF852788	MR3-EN008	355	78.5	17.5	420	4	CK100764	CK100764
283	115	25.7	467	3	BQ329405	MR3-EN008	356	78.5	17.5	447	2	BF891509	BF891509
284	115	25.7	471	2	BF893924	PM1-MT014	357	78.5	17.5	533	5	BQ834029	BQ834029
285	115	25.7	491	2	BI016235	MR4-ET014	358	78.5	17.5	581	5	BQ825655	BQ825655
286	112	25.0	458	1	BQ366782	OV3-GN020	359	78.5	17.5	585	6	CB025685	CB025685
287	109	24.3	431	7	CK695369	ZE101-P00	360	78	17.4	404	8	T08387	T08387
288	109	24.3	570	3	BP258309	BP258309	361	78	17.4	443	3	BM691630	BM691630
289	107	23.9	835	8	DR867245	JGI_CABG9	362	78	17.4	509	6	CA394336	CA394336
290	106	23.7	441	2	BF892415	PM1-MT014	363	78	17.4	512	3	BM707845	BM707845
291	104	23.2	153	2	BF992130	OV3-GN020	364	78	17.4	521	3	BQ340289	BQ340289
292	103.5	23.1	444	2	BF893187	PM1-MT014	365	78	17.4	529	2	BF993341	BF993341
293	103	23.0	617	7	BY067359	BY067359	366	78	17.4	529	7	CN112718	CN112718
294	102	22.8	367	5	CN694288	E0348E09-	367	78	17.4	553	6	CF131579	CF131579
295	101	22.5	680	7	CK952220	4091710 B	368	78	17.4	565	5	BO639714	BO639714
296	100	22.3	935	11	CNS0320E	AL225511 Tetradon	369	78	17.4	566	1	AL047251	AL047251
297	99.5	22.2	625	6	CB190354	PI25610.Y	370	78	17.4	570	6	CB188959	CB188959
298	98	21.9	382	5	BY070423	BY070423	371	78	17.4	577	1	AW247266	AW247266
299	97	21.7	718	6	CB512714	esal1p1b54	372	78	17.4	607	7	CN312708	CN312708
													AL727624
													DR704222
													CN807482
													BQ336306
													BF140146
													AA163045
													CD509260
													AJ398593
													BY036773
													TSP458761
													BI150788
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													CV756544
													CK863267
													AY814979
													BY028675
													CD321260
													CK682762
													BH207435
													BI789841
													BP262101
													BR337260
													BF337260
													BY101168
													AI208756
													BF89319
													BI424242
													BU080681
													BM885374
													CF712017
													BE526774
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													BP049364
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C 373	78	17.4	619	6	CA389704	CS101407	CA389704	CS101407	446	74.5	16.6	541	8	DB612494	ES1100262	DB612494	ES1100262
C 374	78	17.4	620	1	AL046594	DW255861	AL046594	DW255861	447	74.5	16.6	541	8	DB615724	ES1100262	DB615724	ES1100262
C 375	78	17.4	620	1	CA314684	110H4252	CA314684	110H4252	448	74.5	16.6	544	8	DB651027	ES1104114	DB651027	ES1104114
C 376	78	17.4	631	6	CF131546	CF131546	CF131546	CF131546	449	74.5	16.6	552	8	DB626333	ES1101646	DB626333	ES1101646
C 377	78	17.4	663	6	CF131659	110H4250	CF131659	110H4250	450	74.5	16.6	558	5	BU546165	CM880010A	BU546165	CM880010A
C 378	78	17.4	689	6	CF132581	110H4250	CF132581	110H4250	451	74.5	16.6	575	5	BO967059	DB629158	BO967059	DB629158
C 379	78	17.4	711	7	CO403459	CO403459	CO403459	CO403459	452	74.5	16.6	609	8	DB629158	ES1101948	DB629158	ES1101948
C 380	78	17.4	718	7	CO403459	CO403459	CO403459	CO403459	453	74.5	16.6	623	3	BU007386	BU007386	BU007386	BU007386
C 381	78	17.4	726	6	CF131740	CF131740	CF131740	CF131740	454	74.5	16.6	644	8	DB614583	DB614583	DB614583	DB614583
C 382	78	17.4	766	6	CF131869	110004245	CF131869	110004245	455	74.5	16.6	768	8	DB612637	ES1100216	DB612637	ES1100216
C 383	78	17.4	766	6	CF131869	110004245	CF131869	110004245	456	74.5	16.6	768	8	DB614583	ES1100216	DB614583	ES1100216
C 384	78	17.4	793	6	CF132448	CF132448	CF132448	CF132448	457	74.5	16.6	841	8	BO914471	BO914471	BO914471	BO914471
C 385	78	17.4	793	6	CF132448	CF132448	CF132448	CF132448	458	74.5	16.6	854	8	BU906564	ES1100967	BU906564	ES1100967
C 386	78	17.4	823	4	CA361801	CA361801	CA361801	CA361801	459	74.5	16.6	854	8	BU906564	ES1100967	BU906564	ES1100967
C 387	78	17.4	834	1	AU313133	AU313133	AU313133	AU313133	460	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 388	78	17.4	904	1	AU313133	AU313133	AU313133	AU313133	461	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 389	78	17.4	907	2	BF418329	BF418329	BF418329	BF418329	462	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 390	78	17.4	918	2	BF418329	BF418329	BF418329	BF418329	463	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 391	78	17.4	924	2	BF338572	602034247	BF338572	602034247	464	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 392	78	17.4	937	2	BF338572	602034247	BF338572	602034247	465	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 393	78	17.4	957	3	BO673679	AGENCOURT	BO673679	AGENCOURT	466	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 394	78	17.4	1036	5	BO881580	BO881580	BO881580	BO881580	467	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 395	78	17.4	1036	5	BO881580	BO881580	BO881580	BO881580	468	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 396	78	17.4	1116	8	CA362811	CA362811	CA362811	CA362811	469	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 397	77.5	17.3	740	8	CA362811	CA362811	CA362811	CA362811	470	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 398	77.5	17.3	740	8	CA362811	CA362811	CA362811	CA362811	471	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 399	77.5	17.3	740	8	CA362811	CA362811	CA362811	CA362811	472	74.5	16.6	925	5	BO890939	BO890939	BO890939	BO890939
C 400	77	17.2	484	5	BU338911	BU338911	BU338911	BU338911	473	74.5	16.5	874	6	CF592581	CF592581	CF592581	CF592581
C 401	77	17.2	517	5	BM262830	BM262830	BM262830	BM262830	474	74.5	16.5	874	6	CF592581	CF592581	CF592581	CF592581
C 402	77	17.2	564	5	BM271835	BM271835	BM271835	BM271835	475	74.5	16.5	874	6	CF592581	CF592581	CF592581	CF592581
C 403	77	17.2	627	1	AV632851	AV632851	AV632851	AV632851	476	73.5	16.4	54	7	CO065919	CO065919	CO065919	CO065919
C 404	77	17.2	652	10	BM053434	BM053434	BM053434	BM053434	477	73.5	16.4	54	7	CO065919	CO065919	CO065919	CO065919
C 405	77	17.2	652	10	CA216184	CA216184	CA216184	CA216184	478	73.5	16.4	559	8	CV984185	CV984185	CV984185	CV984185
C 406	77	17.2	662	1	AV968700	AV968700	AV968700	AV968700	479	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 407	77	17.2	674	1	AV974206	AV974206	AV974206	AV974206	480	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 408	77	17.2	674	5	BM264653	BM264653	BM264653	BM264653	481	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 409	77	17.2	691	5	BM262563	BM262563	BM262563	BM262563	482	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 410	77	17.2	712	5	BU228796	603399341	BU228796	603399341	483	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 411	77	17.2	720	5	BM314421	BM314421	BM314421	BM314421	484	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 412	77	17.2	753	5	BM044510	BM044510	BM044510	BM044510	485	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 413	77	17.2	800	9	CS050620	CH240_347	CS050620	CH240_347	486	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 414	77	17.2	812	9	BF266988	HV_CHE001	BF266988	HV_CHE001	487	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 415	76.5	17.1	861	2	AA917069	AA917069	AA917069	AA917069	488	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 416	76.5	17.1	417	9	BZ868838	CH240_272	BZ868838	CH240_272	489	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 417	76.5	17.1	445	6	CB744881	AMNENDC:M	CB744881	AMNENDC:M	490	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 418	76.5	17.1	466	8	W47469	W47469	W47469	W47469	491	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 419	76.5	17.1	652	5	BQ523235	NISC_n121	BQ523235	NISC_n121	492	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 420	76.5	17.1	828	9	BP964474	odj0905	BP964474	odj0905	493	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 421	76.5	17.1	864	3	BP698078	BP698078	BP698078	BP698078	494	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 422	76.5	17.1	863	8	BN064081	PMI_CABD1	BN064081	PMI_CABD1	495	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 423	76.5	17.1	195	2	BF893164	PMI_MTD14	BF893164	PMI_MTD14	496	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 424	76.5	17.0	752	8	DR9424250	EST111578	DR9424250	EST111578	497	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 425	76.5	17.0	856	6	CF548156	AGENCOURT	CF548156	AGENCOURT	498	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 426	76.5	17.0	874	6	CF698297	CF698297	CF698297	CF698297	499	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 427	76.5	17.0	894	6	CD254226	AGENCOURT	CD254226	AGENCOURT	500	73.5	16.4	608	10	CA213495	CA213495	CA213495	CA213495
C 428	75.5	16.9	397	1	AM788607	CO0574-F	AM788607	CO0574-F	501	73.5	16.3	775	11	CA368591	CA368591	CA368591	CA368591
C 429	75.5	16.9	439	5	BY654424	BY654424	BY654424	BY654424	502	73.5	16.3	834	9	BU135921	BU135921	BU135921	BU135921
C 430	75.5	16.9	555	5	BJ074024	BJ074024	BJ074024	BJ074024	503	73.5	16.3	834	9	BU135921	BU135921	BU135921	BU135921
C 431	75.5	16.9	656	8	DN593555	CCM1N6E07	DN593555	CCM1N6E07	504	73.5	16.3	834	9	BU135921	BU135921	BU135921	BU135921
C 432	75.5	16.9	698	8	DR629264	EST101939	DR629264	EST101939	505	73.5	16.3	834	9	BU135921	BU135921	BU135921	BU135921
C 433	75.5	16.9	725	8	DN892929	nag3ae03	DN892929	nag3ae03	506	73.5	16.3	834	9	BU135921	BU135921	BU135921	BU135921
C 434	75.5	16.9	740	7	AM097171	fr40FF10.Y	AM097171	fr40FF10.Y	507	72.5	16.2	487	5	BM513765	BM513765	BM513765	BM513765
C 435	75.5	16.9	753	7	CO245583	AGENCOURT	CO245583	AGENCOURT	508	72.5	16.2	487	5	BM513765	BM513765	BM513765	BM513765
C 436	75.5	16.9	814	10	CM900369	RPIC42_13	CM900369	RPIC42_13	509	72.5	16.2	487	5	BM513765	BM513765	BM513765	BM513765
C 437	75.5	16.9	825	5	BU145913	AGENCOURT	BU145913	AGENCOURT	510	72.5	16.2	487	5	BM513765	BM513765	BM513765	BM513765
C 438	75.5	16.7	436	11	DR19G77	Dario_rer	DR19G77	Dario_rer	511	72.5	16.2	487	5	BM513765	BM513765	BM513765	BM513765
C 439	75.5	16.7	531	1	BU805602	haa31f04	BU805602	haa31f04	512	72.5	16.2	487	5	BM513765	BM513765	BM513765	BM513765
C 440	75.5	16.7	582	3	BE261789	BE261789	BE261789	BE261789	513	72.5	16.2	487	5	BM513765	BM513765	BM513765	BM513765
C 441	75.5	16.7	633	10	CZ412775	CZ412775	CZ412775	CZ412775	514	72.5	16.2	487	5	BM5			

519	72.5	16.2	679	8	CX677499	CX677499	Ydci5a01	C 592	71.5	16.0	638	8	DR706559	Asn_07047
520	72.5	16.2	682	8	CX436575	CX436575	JG1_XZG59	593	71.5	16.0	642	4	CNS0EPBC	CR635490 Telradon
521	72.5	16.2	705	5	BX847504	BX847504	BX847504	C 594	71.5	16.0	648	11	CR826929	CR826929 GROAA58C
522	72.5	16.2	721	5	BX853464	BX853464	BX853464	595	71.5	16.0	652	1	AJ773719	AJ773719
523	72.5	16.2	726	7	CR807766	CR807766	CR807766	596	71.5	16.0	657	4	CNS0P1ZT	CR651923 Telradon
524	72.5	16.2	735	8	DR723237	DR723237	DR723237	597	71.5	16.0	653	6	CD318474	CD318474
525	72.5	16.2	763	8	CX923638	CX923638	JG1_CANA9	C 598	71.5	16.0	692	8	DR703249	DR703249 Asn_02943
526	72.5	16.2	766	7	CJ413079	CJ413079	CJ413079	599	71.5	16.0	694	10	CW936835	CW936835 RPCT42_11
527	72.5	16.2	766	8	DR721047	DR721047	DR721047	600	71.5	16.0	715	3	BP765760	BP765760
528	72.5	16.2	768	6	DR727337	DR727337	DR727337	601	71.5	16.0	720	1	AJ773720	AJ773720
529	72.5	16.2	788	6	CF218484	CF218484	CF218484	602	71.5	16.0	726	2	BG595970	BG595970 EST494636
530	72.5	16.2	788	7	CV075303	CV075303	CV075303	603	71.5	16.0	731	5	BU052319	BU052319 UI-M-FCO-
531	72.5	16.2	789	7	CO092265	CO092265	CO092265	604	71.5	16.0	736	7	CNS27669	CNS27669 UI-M-HQO-
532	72.5	16.2	790	8	CX911741	CX911741	JG1_CANA3	C 605	71.5	16.0	804	8	DR180963	DR180963
533	72.5	16.2	804	7	CK032377	CK032377	CK032377	C 606	71.5	16.0	804	11	CR793442	CR793442 GROAA10B
534	72.5	16.2	824	9	CS524394	CS524394	CH240_373	C 607	71.5	16.0	841	8	DR181042	DR181042 RTMNT1_3
535	72.5	16.2	830	6	CD361473	CD361473	CD361473	C 608	71.5	16.0	854	11	CR793752	CR793752 GROAA10D
536	72.5	16.2	830	7	CR563875	CR563875	CR563875	C 609	71.5	16.0	894	9	CS518564	CS518564 CH240_365
537	72.5	16.2	840	7	CO092266	CO092266	CR_Ra13D	610	71.5	16.0	1034	11	CNS0CUMG	CS518564 CH240_365
538	72.5	16.2	867	6	CA988005	CA988005	AGENCOURT	611	71.5	16.0	1045	4	CNS0G1U6	AL401774 T3_end_of
539	72.5	16.2	868	6	CA985313	CA985313	AGENCOURT	612	71.5	16.0	1676	4	BC023102	CR720044 Telradon
540	72.5	16.2	872	9	CJ429442	CJ429442	CJ429442	613	71.5	16.0	3084	4	BC003268	BC023102 Mus muscu
541	72.5	16.2	895	7	CR570901	CR570901	CR570901	614	71.5	16.0	3084	4	BC003268	BC003268 Mus muscu
542	72.5	16.2	895	7	CR570901	CR570901	CR570901	615	71.5	16.0	360	1	AV190324	AZ457714 IM0261X12
543	72.5	16.2	897	8	CX389560	CX389560	JG1_XZT37	616	71.5	16.0	360	8	D76286	AV190324 AV190324
544	72.5	16.2	904	6	CA788883	CA788883	AGENCOURT	C 617	71.5	16.0	404	2	BG264617	D76286 CBKX15E2P
545	72.5	16.2	914	5	BU915292	BU915292	AGENCOURT	618	71.5	16.0	477	7	CF841105	BG264617 daa33c07
546	72.5	16.2	932	5	BU915307	BU915307	AGENCOURT	619	71.5	16.0	481	5	BM201557	CF841105 PSHB012X0
547	72.5	16.2	960	7	CK803693	CK803693	AGENCOURT	620	71.5	16.0	530	1	AM635291	BM201557 BM201557
548	72.5	16.2	974	5	BU901096	BU901096	AGENCOURT	621	71.5	16.0	571	11	CR488239	AM635291 b131909_w
549	72.5	16.2	1061	10	CW932270	CW932270	EDCC45TF	622	71.5	16.0	624	7	CN854346	CA788239 mch2-1571
550	72.5	16.1	385	1	AM429858	AM429858	68351_MAR	623	71.5	16.0	633	2	BB392335	CN854346 Ha_mno_24
551	72.5	16.1	428	9	AQ184550	AQ184550	HS_2205_A	624	71.5	16.0	637	5	BO544985	BB392335
552	72.5	16.1	456	3	BQ323231	BQ323231	MR4_ET014	625	71.5	16.0	675	2	BA429423	BO544985 EST628612
553	72.5	16.1	465	9	BH634807	BH634807	EP(3)3131	626	71.5	16.0	680	1	AM102800	BA429423
554	72.5	16.1	472	2	BE288703	BE288703	601093556	627	71.5	16.0	702	3	BU043297	AM102800 xd38c10_x
555	72.5	16.1	520	7	CO639920	CO639920	USDA-FP_1	628	71.5	16.0	711	6	CA231526	BU043297
556	72.5	16.1	572	3	BI406417	BI406417	163H09_M4	629	71.5	16.0	738	10	CL632581	CA231526 UI-M-FW-
557	72.5	16.1	576	7	CO643601	CO643601	USDA-FP_1	630	71.5	16.0	746	8	DR951154	CL632581 CH243-201
558	72.5	16.1	602	8	DN743815	DN743815	94856_1_F	631	71.5	16.0	786	8	DR951154	DR951154 EST114269
559	72.5	16.1	604	7	CO638143	CO638143	USDA-FP_1	632	71.5	16.0	830	8	DR947737	DR951154 EST114269
560	72.5	16.1	628	1	AU128928	AU128928	1A128928	633	71.5	16.0	833	8	DR924251	DR947737 EST113927
561	72.5	16.1	639	7	CO642694	CO642694	USDA-FP_1	634	71.5	16.0	858	5	BO734611	DR924251 EST11579
562	72.5	16.1	641	2	BE627868	BE627868	RU24603_X	635	71.5	16.0	884	6	CA788235	BO734611
563	72.5	16.1	644	2	BI238249	BI238249	RE34656_S	636	71.5	16.0	1114	4	BF970157	CA788235
564	72.5	16.1	656	6	CF418701	CF418701	USDA-FP_1	637	71.5	16.0	1279	4	AK083210	BF970157
565	72.5	16.1	673	10	CW312491	CW312491	104_802_1	638	71.5	16.0	221	9	BZ834881	AK083210 Mus muscu
566	72.5	16.1	691	7	CK852789	CK852789	1341d_Sto	639	71.5	16.0	349	5	BZ834881	BZ834881
567	72.5	16.1	694	11	CR020362	CR020362	Forward_S	640	71.5	16.0	379	3	BI883542	BY048944
568	72.5	16.1	695	5	BU888553	BU888553	P009C02_P	641	71.5	16.0	471	2	BG622222	BI883542
569	72.5	16.1	698	10	CW417488	CW417488	F8dB001f1	642	71.5	16.0	490	1	AU022672	BG622222
570	72.5	16.1	702	3	BI919891	BI919891	EST539838	643	71.5	16.0	522	3	BU035507	AU022672
571	72.5	16.1	715	7	CO641859	CO641859	USDA-FP_1	644	71.5	16.0	548	9	CS512994	BU035507
572	72.5	16.1	734	10	CW354833	CW354833	F8dB001f0	645	71.5	16.0	554	10	CZ426190	CS512994
573	72.5	16.1	809	7	CV431739	CV431739	56267_1_A	646	71.5	16.0	592	1	AM220866	CZ426190
574	72.5	16.1	810	7	CJ021928	CJ021928	1A128928	647	71.5	16.0	601	1	AM409498	AM220866
575	72.5	16.1	837	7	CJ023977	CJ023977	601851896	648	71.5	16.0	673	10	CZ422203	AM409498
576	72.5	16.1	844	2	BF695497	BF695497	601851896	649	71.5	16.0	677	10	CW896988	CZ422203
577	72.5	16.1	850	8	DN941734	DN941734	2550_2_Tu	650	71.5	16.0	710	10	CW914828	CW896988
578	72.5	16.1	879	7	CJ015578	CJ015578	6015578	651	71.5	16.0	731	9	CC913813	CW914828
579	72.5	16.1	884	3	BP157494	BP157494	60157494	652	71.5	16.0	770	9	BZ238678	CC913813
580	72.5	16.1	892	2	BF031321	BF031321	601559078	653	71.5	16.0	776	3	BE698153	BZ238678
581	72.5	16.1	1292	2	DN714160	DN714160	CMB101-A0	654	71.5	16.0	776	9	CL542474	BE698153
582	72.5	16.1	2292	10	CL959284	CL959284	OBIFC002	655	71.5	16.0	784	10	CL542474	CL542474
583	71.5	16.0	360	1	AV187838	AV187838	AV187838	656	71.5	16.0	785	7	CV522305	AV187838
584	71.5	16.0	375	5	C50183	C50183	C50183	657	71.5	16.0	792	3	BI422031	CV522305
585	71.5	16.0	440	5	BM645653	BM645653	BM645653	658	71.5	16.0	793	3	BM409846	BI422031
586	71.5	16.0	513	7	CK644411	CK644411	61_02_C10	659	71.5	16.0	809	3	BM410631	CK644411
587	71.5	16.0	534	3	BZ937002	BZ937002	BU070740	660	71.5	16.0	815	9	CC916096	BZ937002
588	71.5	16.0	536	3	BM932228	BM932228	CH240_61G	661	71.5	16.0	832	8	DN981091	CC916096
589	71.5	16.0	607	3	BM192228	BM192228	da121C08	662	71.5	16.0	844	8	DN982112	BM192228
590	71.5	16.0	608	3	BU109135	BU109135	BU109135	663	71.5	16.0	847	8	DN981552	BU109135
591	71.5	16.0	632	6	CA662239	CA662239	wimk1.pk0	664	71.5	16.0	856	9	CC364504	CA662239

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665	70.5	15.7	866	8	DN981303	SV6_36A02	738	70	15.6	3057	4	AK034206	AK034206 Mus muscu
666	70.5	15.7	903	6	CA787725	AGENCOURT	739	70	15.6	3447	4	AK046825	AK046825 Mus muscu
667	70.5	15.7	928	6	CF585404	AGENCOURT	740	70	15.6	3783	4	AK046825	AK046825 Mus muscu
668	70.5	15.7	1292	2	BQ419638	602451853	741	70	15.6	5048	4	HSB80203	HSB80203 Mus muscu
669	70	15.6	360	1	AV190541	AV190541	742	69.5	15.5	1122	7	CN325256	CN325256 WLB07407
670	70	15.6	360	1	AV190541	AV190541	743	69.5	15.5	128	5	CB938749	CB938749 OSTR21281
671	70	15.6	429	5	BY288562	BY288562	744	69.5	15.5	260	5	CB938749	CB938749 OSTR21281
672	70	15.6	432	5	BY251134	BY251134	745	69.5	15.5	376	1	BY251134	BY251134 OSTR21281
673	70	15.6	433	5	BY251174	BY251174	746	69.5	15.5	376	1	BY251174	BY251174 OSTR21281
674	70	15.6	435	7	CJ393535	CJ393535	747	69.5	15.5	376	1	BY251174	BY251174 OSTR21281
675	70	15.6	453	5	BY260356	BY260356	748	69.5	15.5	376	1	BY251174	BY251174 OSTR21281
676	70	15.6	467	6	CB831657	CB831657	749	69.5	15.5	468	8	AK420023	AK420023 Mus muscu
677	70	15.6	474	5	BM525720	BM525720	750	69.5	15.5	476	3	AK420023	AK420023 Mus muscu
678	70	15.6	488	1	AM121656	AM121656	751	69.5	15.5	524	10	CB261057	CB261057 Mus muscu
679	70	15.6	531	3	BM525720	BM525720	752	69.5	15.5	532	10	CB261057	CB261057 Mus muscu
680	70	15.6	550	5	AV747667	AV747667	753	69.5	15.5	534	1	BM538021	BM538021 Mus muscu
681	70	15.6	555	5	BM538021	BM538021	754	69.5	15.5	541	3	BM538021	BM538021 Mus muscu
682	70	15.6	575	3	BP244143	BP244143	755	69.5	15.5	543	5	BM538021	BM538021 Mus muscu
683	70	15.6	580	8	DR087707	DR087707	756	69.5	15.5	552	3	BM538021	BM538021 Mus muscu
684	70	15.6	581	3	BP315543	BP315543	757	69.5	15.5	552	3	BM538021	BM538021 Mus muscu
685	70	15.6	587	6	CD285020	CD285020	758	69.5	15.5	554	1	AV934986	AV934986 Mus muscu
686	70	15.6	600	8	CK678686	CK678686	759	69.5	15.5	554	1	AV934986	AV934986 Mus muscu
687	70	15.6	605	9	AO827495	AO827495	760	69.5	15.5	561	1	AV934986	AV934986 Mus muscu
688	70	15.6	607	7	CK319258	CK319258	761	69.5	15.5	565	1	BM538021	BM538021 Mus muscu
689	70	15.6	613	6	CD878524	CD878524	762	69.5	15.5	565	1	BM538021	BM538021 Mus muscu
690	70	15.6	625	2	BM45914	BM45914	763	69.5	15.5	567	2	BM538021	BM538021 Mus muscu
691	70	15.6	626	2	BM45914	BM45914	764	69.5	15.5	590	10	AK02374	AK02374 Mus muscu
692	70	15.6	634	5	BU837191	BU837191	765	69.5	15.5	599	10	AK02374	AK02374 Mus muscu
693	70	15.6	635	7	CK621570	CK621570	766	69.5	15.5	620	9	AK02374	AK02374 Mus muscu
694	70	15.6	647	2	BM646013	BM646013	767	69.5	15.5	626	9	AK02374	AK02374 Mus muscu
695	70	15.6	647	2	BM646013	BM646013	768	69.5	15.5	634	10	AK02374	AK02374 Mus muscu
696	70	15.6	653	2	BM646013	BM646013	769	69.5	15.5	634	10	AK02374	AK02374 Mus muscu
697	70	15.6	656	6	CF512473	CF512473	770	69.5	15.5	660	6	AK02374	AK02374 Mus muscu
698	70	15.6	657	7	BY726955	BY726955	771	69.5	15.5	660	6	AK02374	AK02374 Mus muscu
699	70	15.6	668	7	BM655781	BM655781	772	69.5	15.5	702	10	AK02374	AK02374 Mus muscu
700	70	15.6	677	2	BM655781	BM655781	773	69.5	15.5	715	6	AK02374	AK02374 Mus muscu
701	70	15.6	682	7	CN312686	CN312686	774	69.5	15.5	716	6	AK02374	AK02374 Mus muscu
702	70	15.6	690	2	BM146228	BM146228	775	69.5	15.5	720	6	AK02374	AK02374 Mus muscu
703	70	15.6	692	2	BM146228	BM146228	776	69.5	15.5	758	8	AK02374	AK02374 Mus muscu
704	70	15.6	695	2	BM146228	BM146228	777	69.5	15.5	758	8	AK02374	AK02374 Mus muscu
705	70	15.6	700	7	BM735788	BM735788	778	69.5	15.5	780	8	AK02374	AK02374 Mus muscu
706	70	15.6	701	5	BM735788	BM735788	779	69.5	15.5	780	8	AK02374	AK02374 Mus muscu
707	70	15.6	711	9	BM666646	BM666646	780	69.5	15.5	780	8	AK02374	AK02374 Mus muscu
708	70	15.6	740	7	CJ360059	CJ360059	781	69.5	15.5	803	8	AK02374	AK02374 Mus muscu
709	70	15.6	758	9	BM531930	BM531930	782	69.5	15.5	809	10	AK02374	AK02374 Mus muscu
710	70	15.6	768	7	CJ359176	CJ359176	783	69.5	15.5	821	8	AK02374	AK02374 Mus muscu
711	70	15.6	772	7	CV115759	CV115759	784	69.5	15.5	823	9	AK02374	AK02374 Mus muscu
712	70	15.6	782	7	BM511634	BM511634	785	69.5	15.5	823	9	AK02374	AK02374 Mus muscu
713	70	15.6	802	8	BM511634	BM511634	786	69.5	15.5	840	7	AK02374	AK02374 Mus muscu
714	70	15.6	830	8	BM511634	BM511634	787	69.5	15.5	842	11	AK02374	AK02374 Mus muscu
715	70	15.6	831	5	BM665580	BM665580	788	69.5	15.5	847	7	AK02374	AK02374 Mus muscu
716	70	15.6	845	5	BM665580	BM665580	789	69.5	15.5	847	7	AK02374	AK02374 Mus muscu
717	70	15.6	850	7	CJ385568	CJ385568	790	69.5	15.5	847	7	AK02374	AK02374 Mus muscu
718	70	15.6	852	8	BM666646	BM666646	791	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
719	70	15.6	862	8	BM666646	BM666646	792	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
720	70	15.6	884	2	BM666646	BM666646	793	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
721	70	15.6	902	2	BM666646	BM666646	794	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
722	70	15.6	908	2	BM666646	BM666646	795	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
723	70	15.6	928	2	BM666646	BM666646	796	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
724	70	15.6	944	3	BM666646	BM666646	797	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
725	70	15.6	945	5	BM666646	BM666646	798	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
726	70	15.6	945	5	BM666646	BM666646	799	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
727	70	15.6	981	2	BM666646	BM666646	800	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
728	70	15.6	981	2	BM666646	BM666646	801	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
729	70	15.6	1008	1	BM666646	BM666646	802	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
730	70	15.6	1073	3	BM666646	BM666646	803	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
731	70	15.6	1128	3	BM666646	BM666646	804	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
732	70	15.6	1667	2	BM666646	BM666646	805	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
733	70	15.6	1667	2	BM666646	BM666646	806	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
734	70	15.6	2707	4	AK032763	AK032763	807	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
735	70	15.6	2831	4	AK032763	AK032763	808	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
736	70	15.6	2831	4	AK032763	AK032763	809	69.5	15.5	865	8	AK02374	AK02374 Mus muscu
737	70	15.6	2979	4	AK038480	AK038480	810	69.5	15.5	865	8	AK02374	AK02374 Mus muscu


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957 68 15.2 327 1 AV750144
958 68 15.2 360 5 CS1100
959 68 15.2 376 5 BY684698
960 68 15.2 399 2 DR34113
961 68 15.2 399 2 DR34113
962 68 15.2 408 1 AB881256
963 68 15.2 410 2 AB881256
964 68 15.2 411 9 A2223944
965 68 15.2 413 1 A2223944
966 68 15.2 417 5 A2223944
967 68 15.2 419 2 A2223944
968 68 15.2 421 3 A2223944
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988 68 15.2 421 3 A2223944
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995 68 15.2 421 3 A2223944
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999 68 15.2 421 3 A2223944
1000 68 15.2 421 3 A2223944
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ALIGNMENTS

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RESULT 1
LOCUS BQ582059 429 bp mRNA linear EST 20-JUN-2002
DEFINITION Human insulinoma Homo sapiens cDNA clone IMAGE:6029589
ACCESSION BQ582059
VERSION BQ582059.1 GI:21494955
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Carcharia;
Hominidae; Homo
1 (bases 1 to 429)
Melton D., Brown J., Kenty G., Permutt A., Lee C., Kaestner K.,
Hillier A., Wray M., Pape D., Wylie T., Martin J., Blaisdell A.,
Schiller A., Theisinger B., Rutter E., Ronko I., Bennett J.,
Cargnani M., Gibbons M., McCann R., Cole R., Teagarden W., R.,
Williams M., Jackson Y., and Bowers Y.
Unpublished (2000)
Other ESTs: 112c11.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
```

Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmclondbio@hms.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.

FEATURES

source

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1..429
Location/Qualifiers
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/mol_type="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6029589"
/issue_type="Insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/clone_id="Human Insulinoma"
/clone="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
XhoI; Site 2: EcoRI; Constructed with lambda Zapri system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine Box
8127, 660 S Euclid Ave, St. Louis, MO 63110. Note: this
is a Washington University Pancreas EST project library."
```

ORIGIN

Alignment Scores:

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Pred. No.: 5,928-47 Length: 429
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
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US-10-757-745-2_COPY_54_140 (1-87) x BQ582059 (1-429)

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OY 1 MetGUAARGAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGUAAG 20
DB 103 ATGGAAGAGGCTCTCAACTCTGAGCTCCGCTGAGAGAGAGAGAGAGAGAGAGAG 162
OY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 163 CGACCTGAAGACCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
OY 41 AspSerThrThrSerIleIleSerProSerGluAspThrGlnGlnGlnGlnGlnGln 60
DB 223 GATTCACCAACATCTCAAAATCAAGCCATCTGAGAGAGAGAGAGAGAGAGAGAGAG 282
OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 80
DB 283 TTCTCTCTCATTAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 342
OY 81 ArgGlyValCysSerTyrIleu 87
DB 343 CGAGGGGTGTGTCTCACTTA 363
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RESULT 2
LOCUS CR543841 471 bp mRNA linear EST 07-JUL-2004
DEFINITION DKFZp45900742.p1 459 (synonym: pcor1) Pongo pygmaeus cDNA clone
ACCESSION CR543841
VERSION CR543841.1 GI:49895253
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Pongo.
1 (bases 1 to 471)
Bloeker, H., Boecker, M., Brandt, P., Mewes, H.W., Well, B., Amid, C., Oanger, A., Pobo, G., Han, M. and Wiemann, S. and Brandt, P., et al.)
Pongo pygmaeus mRNA (Bloeker, H., Boecker, M., Brandt, P., et al.)
Unpublished (2004)
Contact: MIPS
MIPS
Ingolstaedter landstr.1, D-85764 Neuberg, Germany

FEATURES
source

This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by GSF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the CDNA sequencing consortium of the German Genome Project. This clone (DKFZp45900742) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.
Location/Qualifiers
1..471
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp45900742"
/issue_type="cortex"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1ib="459 (synonym: pcor1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:

Pred. No.:	6,69e-47	Length:	471
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CR543841 (1-471)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 161 ATGGAAGGGCTCTGAACCTCTACTTCCGAGCTCCGGTGAAGAGAGCCCTTGAACGC 220
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 221 CGCCCTGAACCATCTCTGAGCCCAAGACCTAAGTTCCTTAACCAATGAAGAAACACT 280
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 281 GATTCACACATCTTAAATCAACCCATCTGAAGATCTCAAGCAAGAAATGCGACATG 340
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 341 TTCTCTCATTAACCTGAATATGATGATTGATTAACCAATCTGTCAAGAGAGGCT 400
QY 81 ArgGlyValCysSerTyrLeu 87
DB 401 CGAGGGGTGTGTCTACTTA 421

RESULT 3
LOCUS CB120234 473 bp mRNA linear EST 28-JAN-2003
DEFINITION K-EST0167337 L8SCKO Homo sapiens cDNA clone L8SCKO-29-F06 5', mRNA
sequence.
ACCESSION CB120234
VERSION CB120234.1 GI:27946036
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 473)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.U., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-353, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 row: F column: 06
High quality sequence stop: 473.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L8SCKO-29-F06"
/sex="M"
/cell_line="SCK"
/lab_host="Top10P"
/clone_1ib="L8SCKO"
/note="Organ: Liver; Vector: pRT73-Pac; Site_1: EcoRI; Site_2: NotI; The library was contributed by the Soares Laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	6,73e-47	Length:	473
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CB120234 (1-473)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 109 ATGGAAGGGCTCTGAACCTCTACTTCCGAGCTCCGGTGAAGAGAGCCCTTGAACGC 168
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 169 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTCACCTTACCAATGAAGAAACACT 228
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 229 GATTCACACATCTTAAATCAACCCATCTGAAGATCTCAAGCAAGAAATGCGACATG 288
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 289 TTCTCTCATTAACCTGAATATGATGATTGATTAACCAATCTGTCAAGAGAGGCT 348
QY 81 ArgGlyValCysSerTyrLeu 87
DB 349 CGAGGGGTGTGTCTACTTA 369

RESULT 4
LOCUS A1750554 480 bp mRNA linear EST 20-JUN-2002
DEFINITION cn04a01.y1 Normal Human Triaecular Bone Cells Homo sapiens cDNA
clone NHTBC_cn04a01 random, mRNA sequence.
ACCESSION A1750554

VERSION AT750554.1 GI:5128918
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 480)
Jia, L.B., Young, M.F., Touchman, J.W., Bouffard, G.G.,
Beckstrom-Sternberg, S.M., Green, E.D., Powell, J.L., Yang, L.M.,
Rodey, P.G., Hotchkiss, R.N., and Francomano, C.A.
SGAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
JOURNAL Contact: Libin Jia
COMMENT Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 04 row: A column: 01
Seq primer: M13RP1 reverse primer (ABI).
FEATURES
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1..480
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NHTRC_c04a01"
/sex="Female"
/tissue_type="Bone"
/cell_type="Tribecular Bone Cells"
/lab_host="SURE"
/clone_idb="Normal Human Tribecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site: 1; EcorI;
Library constructed by Dr. Marian Young and Dr. Pamela
Gehron Rodey (NIDCR)"
ORIGIN
Alignment Scores:
Pred. No.: 6.86e-47 Length: 480
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x AT750554 (1-480)
QY 1 MetGUArgAlaLeuAuaenSerTYrPheGluProProValGluGluSerAlaLeuGluAarg 20
Db 154 ATGGAAGGGCTCTGAACCTCTACTTCTGAGCTCCGGTGGAGAGAGACCGCTTGGAAACGC 213
QY 21 ArgProGluThrIleSerGluProGlyThrTYrValAspLeuThrAsnGluGluThrThr 40
Db 214 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAAACAACCT 273
QY 41 AAsPserThrTrsIleSerIleSerProSerGluAAsPThrGlnGlnGlnGlnGlnGlnGln 60
Db 274 GATTCACCACTCTCAAAATCAAGCCCTCTGAAGATATCTCAAGCAAGAAATGGCAGCATG 333
QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAAsPLeuAAsnAAsnLeuSerGluATGAla 80
Db 334 TTCTCTCATTAACCTGGAATATGATGATTGATTAATCTTAACAATCTGTCTCAAGAGGGCT 393
QY 81 ArgGlyValCysSerTYrLeu 87
Db 394 CGAGGGGTGTGTCTTACTTA 414
RESULT 5
AA486032
LOCUS AA486032 485 bp mRNA linear EST 06-MAR-1998

DEFINITION ab40b10.r1 Stratagene Hela cell s3 937216 Homo sapiens cDNA clone
IMAGE:843259 5', mRNA sequence.
AA486032
VERSION AA486032.1 GI:2216248
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 485)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gettel, G., Joet, S.,
Katzman, D., Kucada, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, V., Moore, B., Scheinberg, R., Steptoe, M., Tan, F.,
Theisberg, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI Human EST Project
Unpublished (1997)
JOURNAL Contact: Wilson R.
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1913 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 444.
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/db_xref="taxon:9606"
/clone="IMAGE:843259"
/sex="female"
/dev_stage="Hela S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_idb="Stratagene Hela cell s3 937216"
/note="Vector: pBluescript SK-; Site: 1; EcorI; Site: 2;
XhoI; Cloned unidirectionally. Primer: 0190 dt. Hela S3
epithelioid carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni-ZAP XR
vector. -5' adaptor sequence: 5' GATTCGCGCAGCG 3' -3'
adaptor sequence: 5' CTCGATTTTTTTTTTTTTTTT 3'."
ORIGIN
Alignment Scores:
Pred. No.: 6.95e-47 Length: 485
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x AA486032 (1-485)
QY 1 MetGUArgAlaLeuAuaenSerTYrPheGluProProValGluGluSerAlaLeuGluAarg 20
Db 150 ATGGAAGGGCTCTGAACCTCTACTTCTGAGCTCCGGTGGAGAGAGACCGCTTGGAAACGC 209
QY 21 ArgProGluThrIleSerGluProGlyThrTYrValAspLeuThrAsnGluGluThrThr 40
Db 210 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAAGAAACAACCT 269
QY 41 AAsPserThrTrsIleSerIleSerProSerGluAAsPThrGlnGlnGlnGlnGlnGlnGln 60
Db 270 GATTCACCACTCTCAAAATCAAGCCCTCTGAAGATATCTCAAGCAAGAAATGGCAGCATG 329
QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAAsPLeuAAsnAAsnLeuSerGluATGAla 80
Db 330 TTCTCTCATTAACCTGGAATATGATGATTGATTAATCTTAACAATCTGTCTCAAGAGGGCT 389
QY 81 ArgGlyValCysSerTYrLeu 87

QY 61 Pheserleu1leThTriPAn1leAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
BP220508
LOCUS BP220508 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
DEFINITION
ACCESSION BP220508
VERSION BP220508.1 GI:52093413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 566)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DMC03190"
/clone_lib="Sugano cDNA library, dermoid cancer"

ORIGIN
Alignment Scores:
Pred. No.: 8,49e-47 Length: 565
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3

US-10-757-745-2_COPY_54_140 (1-87) x BP226620 (1-565)
QY 1 MetGluArgAlaLeuAsnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
BP226620
LOCUS BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
DEFINITION
ACCESSION BP226620
VERSION BP226620.1 GI:5209525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 565)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DMC03190"
/clone_lib="Sugano cDNA library, dermoid cancer"

QY 1 MetGluArgAlaLeuAsnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
BP226620
LOCUS BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
DEFINITION
ACCESSION BP226620
VERSION BP226620.1 GI:5209525
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 565)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DMC03190"
/clone_lib="Sugano cDNA library, dermoid cancer"

RESULT 9
BP220508
LOCUS BP220508 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION
ACCESSION BP220508
VERSION BP220508.1 GI:52093413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 566)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL03160"
/clone_lib="Sugano cDNA library, colon"

ORIGIN
Alignment Scores:
Pred. No.: 8,51e-47 Length: 566
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3

US-10-757-745-2_COPY_54_140 (1-87) x BP220508 (1-566)
QY 1 MetGluArgAlaLeuAsnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
BP220508
LOCUS BP220508 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION
ACCESSION BP220508
VERSION BP220508.1 GI:52093413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 566)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL03160"
/clone_lib="Sugano cDNA library, colon"

QY 1 MetGluArgAlaLeuAsnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
BP220508
LOCUS BP220508 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION
ACCESSION BP220508
VERSION BP220508.1 GI:52093413
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 566)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1..566
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL03160"
/clone_lib="Sugano cDNA library, colon"

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 568)
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HRT00430"
 /issue_type="heart"
 /clone_lib="Sugano cDNA library, heart"
ORIGIN
 Alignment Scores:
 Pred. No.: 8,556-47 Length: 568
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x BP257211 (1-568)
 QY 1 MetGUAAGAlaleuanserTYrphgIuPProProValGluGluSerAlaleuGluAarg 20
 Db 130 ATGGAAGAGGCTCTGAACCTCTAATCGAGCCCTCGAGAGAGAGCCCTTGGAACGC 189
 QY 21 ATGProGluThrIleSerGluProLySThrTYrValAspLeuThraSngluGluThr 40
 Db 190 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACA 249
 QY 41 AapSerThrThSerIysIleSerProSerGluAapThrGlnGlnGluSngIysSerMet 60
 Db 250 GATTCACCACTTCTAAATCAAGCCATCTGAAGATACACAGCAAGAAATGCGACAGC 309
 QY 61 PheSerLeuIleThrTrrAsnIleAapGlyLeuAapLeuAsnAsnLeuSerGluAargAla 80
 Db 310 TTCTCTCTCATTAACCTGAATATGTATGATTAAGATCAATCAATCTGTCAAGAGAGGCT 369
 QY 81 ArgGlyValCyseSerTyrlu 87
 Db 370 CGAGGGGTGTGTCTTCTACTTA 390
RESULT 11
 BP221518 570 bp mRNA linear EST 15-SEP-2004
 LOCUS BP221518 Sugano cDNA library, colon Homo sapiens cDNA clone
 DEFINITION COL09203, mRNA sequence.
 ACCESSION BP221518
 VERSION BP221518.1 GI:52094423
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 570)
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
 source
 1..570
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="COL09203"
 /issue_type="colon"
 /clone_lib="Sugano cDNA library, colon"
ORIGIN
 Alignment Scores:
 Pred. No.: 8,556-47 Length: 570
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x BP221518 (1-570)
 QY 1 MetGUAAGAlaleuanserTYrphgIuPProProValGluGluSerAlaleuGluAarg 20
 Db 68 ATGGAAGAGGCTCTGAACCTCTAATCGAGCCCTCGAGAGAGAGCCCTTGGAACGC 127
 QY 21 ATGProGluThrIleSerGluProLySThrTYrValAspLeuThraSngluGluThr 40
 Db 128 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACA 187
 QY 41 AapSerThrThSerIysIleSerProSerGluAapThrGlnGlnGluSngIysSerMet 60
 Db 188 GATTCACCACTTCTAAATCAAGCCATCTGAAGATACACAGCAAGAAATGCGACAGC 247
 QY 61 PheSerLeuIleThrTrrAsnIleAapGlyLeuAapLeuAsnAsnLeuSerGluAargAla 80
 Db 248 TTCTCTCTCATTAACCTGAATATGTATGATTAAGATCAATCAATCTGTCAAGAGGCT 307
 QY 81 ArgGlyValCyseSerTyrlu 87
 Db 308 CGAGGGGTGTGTCTTCTACTTA 328
RESULT 12
 AU279894 573 bp mRNA linear EST 31-JUL-2003
 LOCUS AU279894 CHON2 Homo sapiens cDNA clone CHON2002038 5', mRNA
 DEFINITION AU279894 sequence.
 ACCESSION AU279894
 VERSION AU279894.1 GI:28299121
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 573)
 Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R., Isogai, T., Hata, J., Tomoya, Y. and Umezawa, A.
TITLE Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis
JOURNAL Exp. Cell Res. 288 (1), 35-50 (2003)
PUBMED 12878157
COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute

1532-3 Yana, Kizarszu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986

Email: genomics@nri.co.jp
HRI human cDNA Project, Sugiyama T., Wakamatsu A., Irie R.,
Umezawa A., Fukuma M., Kuwahara S., Hata J., Ishii S., Yamamoto J.,
Isono Y., Saito K., Nakamura M., Masuko Y., Nagai K., Isogai T.,
HRI human cDNA Project, DNA library construction & 5'-end one
pass sequencing: Helix Research Institute.
Location/Qualifiers

FEATURES

source
1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CHONS20038"
/cell_type="choriocytes"
/issue_type="colony"
/clone_lib="CHONS2"
/note="Vector: pMT18SF13"

ORIGIN

Alignment Scores:

Pred. No.: 8,656-47 Length: 573
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AU279894 (1-573)

QY 1 MetGUAArgAlaLeuAenSerTYrPheGluProProValAGluGluSerAlaLeuGluArg 20
DB 197 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCTCCGCTGGAGAGAGCGCTGGAGCGC 256
QY 21 ArgProGluThrIleSerGluProIleThrTYrValAspLeuThrAsnGluGluThr 40
DB 257 CGACCTGAACCACTCTGAGCCCAAGCCATCTTACCTTAACAATGAACAACT 316
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 317 GATTCACACCTCTTAACATCAGCCCATCTGAATCTCAGAAAGAAAATGGCAGCTG 376
QY 61 PheSerLeuIleThrTPaenIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 377 TTCTCTCATTAACCGAAATTTGCAATTGATTAACAATCTGTCAAGAGGGCT 436
QY 81 ArgGlyValCysSerTYrLeu 87
DB 437 CGAGGGGTGTGTCTACTTA 457

RESULT 13

BP221260 573 bp mRNA linear EST 15-SEP-2004
LOCUS BP221260 Sugano cDNA library, colon Homo sapiens cDNA clone
DEFINITION BP221260, mRNA sequence.
ACCESSION BP221260
VERSION BP221260.1 GI:52094165
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteleostomi; Euteleostomi; Euteleostomi; Euteleostomi;

REFERENCE

1 (bases 1 to 573)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

AUTHORS

Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous

TITLE

Block structure in the promoter regions

JOURNAL

Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo

FEATURES

source

1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL08083"
/issue_type="colony"
/clone_lib="Sugano cDNA library, colon"

ORIGIN

Alignment Scores:

Pred. No.: 8,656-47 Length: 573
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP221260 (1-573)

QY 1 MetGUAArgAlaLeuAenSerTYrPheGluProProValAGluGluSerAlaLeuGluArg 20
DB 82 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCTCCGCTGGAGAGAGCGCTGGAGCGC 141
QY 21 ArgProGluThrIleSerGluProIleThrTYrValAspLeuThrAsnGluGluThr 40
DB 142 CGACCTGAACCACTCTGAGCCCAAGCCATCTTACCTTAACAATGAACAACT 201
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 202 GATTCACACCTCTTAACATCAGCCCATCTGAATCTCAGAAAGAAAATGGCAGCTG 261
QY 61 PheSerLeuIleThrTPaenIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 262 TTCTCTCATTAACCGAAATTTGCAATTGATTAACAATCTGTCAAGAGGGCT 321
QY 81 ArgGlyValCysSerTYrLeu 87
DB 322 CGAGGGGTGTGTCTACTTA 342

RESULT 14

BP261500 573 bp mRNA linear EST 16-SEP-2004
LOCUS BP261500 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP261500, mRNA sequence.
ACCESSION BP261500
VERSION BP261500.1 GI:52176731
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Euteleostomi; Euteleostomi; Euteleostomi; Euteleostomi;

REFERENCE

1 (bases 1 to 573)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,

AUTHORS

Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous

TITLE

Block structure in the promoter regions

JOURNAL

Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo

PUBMED

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yuzukit@ims.u-tokyo.ac.jp.

FEATURES

source

1..573
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS103816"

ORIGIN /cissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

Alignment Scores:

Pred. No.: 8,65e-47 Length: 573
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP261500 (1-573)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 66 ATGGAAGGGCTGTGAACCTCACTTCGAGCCCTCCGTGAGAGAGAGCCCTTGGAAACCC 125
QY 21 ATGProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 126 CACCTGAAACCATCTCTGAGCCCAAGACCATGTTGACCTAACCAATGAAAGAACACT 185
QY 41 AASPserThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 186 GATTCCACCATCTCTTAATCAAGCCCATCTGAAGATACACAGAAAGAAATGGCAGCATG 245
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 246 TTCTCTCATTAACCTGAATATGATGATTAGATCAATCAATCTGTGAGAGAGGCT 305
QY 81 ArgGlyValCysSerTyrLeu 87
DB 306 CGAGGGGTGTGTCTTACTTA 326

RESULT 15

BP262642 576 bp mRNA linear EST 16-SEP-2004
LOCUS BP262642 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION clone HS107584, mRNA sequence.

ACCESSION BP262642.1 GI:52177873

VERSION BP262642.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

AUTHORS 1 (bases 1 to 576)

TITLE Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

JOURNAL Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..576
Location/Qualifiers

ORIGIN /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="HS107584"
/cissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

Alignment Scores:

Pred. No.: 8,71e-47 Length: 576
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP262642 (1-576)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 84 ATGGAAGGGCTGTGAACCTCACTTCGAGCCCTCCGTGAGAGAGAGCCCTTGGAAACCC 143
QY 21 ATGProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 144 CACCTGAAACCATCTCTGAGCCCAAGACCATGTTGACCTAACCAATGAAAGAACACT 203
QY 41 AASPserThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 204 GATTCCACCATCTCTTAATCAAGCCCATCTGAAGATACACAGAAAGAAATGGCAGCATG 263
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 264 TTCTCTCATTAACCTGAATATGATGATTAGATCAATCAATCTGTGAGAGAGGCT 323
QY 81 ArgGlyValCysSerTyrLeu 87
DB 324 CGAGGGGTGTGTCTTACTTA 344

RESULT 16

CN298919 577 bp mRNA linear EST 16-MAY-2004
LOCUS CN298919 1700600175228 GRN_PPREHP Homo sapiens cDNA 5', mRNA sequence.

DEFINITION CN298919

ACCESSION CN298919.1 GI:47315333

VERSION CN298919.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

AUTHORS 1 (bases 1 to 577)

TITLE Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.

JOURNAL Transcriptionome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 577 Std Error: 0.00.

FEATURES
source
1..577
Location/Qualifiers

ORIGIN /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PPREHP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated h9s cell line H9 (p22) maintained in
feeder-free conditions"

Alignment Scores:

Pred. No.: 8,73e-47 Length: 577
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0

DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN298919 (1-577)

QY 1 MetGUARGAAlaAuaAuaSerTYRPhGluPProPValGluGluSerAlaLeuGluArg 20

DB 160 ATGGAAGGGCTCTGAAGCTCTTACTTGAGCCCTCCGGTGGAGAGAGCGCTTGGAACCC 219

QY 21 ArgProGluThrIleSerGluPProLYThrTYValAspLeuThrAenGluGluThrThr 40

DB 220 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACACT 279

QY 41 AspSerThrThrSerTYIleSerProSerGluAapThrGluGluGluAenGlySerMet 60

DB 280 GATTCACCACTTAAATCAGCCCATCTGAAGATACCTACAGCAAGAAATGCGAGCATG 339

QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAenAenLeuSerGluArgAla 80

DB 340 TTCTCTCATTAAGTGAATATTGATGATTAATCAATCTGTCAAGAGGCGCT 399

QY 81 ArgGlyValCysSerTYLeu 87

DB 400 CGAGGGGTGTCTTCTACTTA 420

RESULT 17

BP274368 580 bp mRNA linear EST 16-SEP-2004

LOCUS BP274368 Sugano cDNA library, kidney Homo sapiens cDNA clone

DEFINITION K0000894. mRNA sequence.

ACCESSION BP274368

VERSION BP274368.1 GI:52188100

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

1..580

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="K0000894"

/issue_type="kidney"

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ORIGIN

Alignment Scores:

Pred. No.: 8,796-47 Length: 580

Score: 448.00 Matches: 87

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP274368 (1-580)

QY 1 MetGUARGAAlaAuaAuaSerTYRPhGluPProPValGluGluSerAlaLeuGluArg 20

DB 180 ATGGAAGGGCTCTGAAGCTCTTACTTGAGCCCTCCGGTGGAGAGAGCGCTTGGAACCC 239

QY 21 ArgProGluThrIleSerGluPProLYThrTYValAspLeuThrAenGluGluThrThr 40

DB 240 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACACT 299

QY 41 AspSerThrThrSerTYIleSerProSerGluAapThrGluGluGluAenGlySerMet 60

DB 300 GATTCACCACTTAAATCAGCCCATCTGAAGATACCTACAGCAAGAAATGCGAGCATG 359

QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAenAenLeuSerGluArgAla 80

DB 360 TTCTCTCATTAAGTGAATATTGATGATTAATCAATCTGTCAAGAGGCGCT 419

QY 81 ArgGlyValCysSerTYLeu 87

DB 420 CGAGGGGTGTCTTCTACTTA 440

RESULT 18

BP207751 581 bp mRNA linear EST 14-SEP-2004

LOCUS BP207751 Sugano cDNA library, coronary artery smooth muscle cell

DEFINITION Homo sapiens cDNA clone CASH1735, mRNA sequence.

ACCESSION BP207751

VERSION BP207751.1 GI:52064157

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

source

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CASH1735"

/issue_type="coronary artery"

/cell_type="smooth muscle cell"

/clone_lib="Sugano cDNA library, coronary artery smooth muscle cell"

ORIGIN

Alignment Scores:

Pred. No.: 8,816-47 Length: 581

Score: 448.00 Matches: 87

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP207751 (1-581)

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QY 21 ArgProGluThrIleSerGluPProLYThrTYValAspLeuThrAenGluGluThrThr 40

DB 128 CGACCTGAAACCATCTCGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACACT 167

QY 41 AspSerThrThrSerTYIleSerProSerGluAapThrGluGluGluAenGlySerMet 60

Db 188 GATTCACCACTTTAAATACAGCCATCTGAAGATCTAGAGAAATGAGCAGC 247
Qy 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 248 TTCTCTCATTAACCTGGAATATGATGATTAGATTAACAATCTGTCAAGAGGGCT 307
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 308 CGAGGGGTGTCTTCTACTTA 328

RESULT 19
BP225088 581 bp mRNA linear EST 15-SEP-2004
LOCUS BP225088 Sugano cDNA library, lymphocyte Daudi Homo sapiens cDNA
DEFINITION clone DAT05184, mRNA sequence.
ACCESSION BP225088
VERSION BP225088.1 GI:52097993
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
source 1..581
/organism="Homo sapiens"
/mol_type="mRNA"
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/cell_type="lymphocyte"
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/note="Burkitt's lymphoma"

ORIGIN
Alignment Scores:
Pred. No.: 8,81e-47 Length: 581
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP225088 (1-581)

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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 241 GAACCTGAAGACATCTCTGAGCCCAAGACCTTAGTGTGACCTAACCAATGAAAGAAACAAC 300

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 301 GATTCACCACTTCTTAATATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCAG 360

Qy 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 361 TTCTCTCATTAACCTGGAATATGATGATTAGATTAACAATCTGTCAAGAGGGCT 420

Qy 81 ArgGlyValCysSerTyrLeu 87
Db 421 CGAGGGGTGTCTTCTACTTA 441

RESULT 20
BP262638 581 bp mRNA linear EST 16-SEP-2004
LOCUS BP262638 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS107576, mRNA sequence.
ACCESSION BP262638
VERSION BP262638.1 GI:52177869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokane-dai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
source 1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS107576"
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ORIGIN
Alignment Scores:
Pred. No.: 8,81e-47 Length: 581
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP262638 (1-581)

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Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 137 GAACCTGAAGACATCTCTGAGCCCAAGACCTTAGTGTGACCTTACCAATGAAAGAAACAAC 196

Qy 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 197 GATTCACCACTTCTTAATATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCAG 256

Qy 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 257 TTCTCTCATTAACCTGGAATATGATGATTAGATTAACAATCTGTCAAGAGGGCT 316

Qy 81 ArgGlyValCysSerTyrLeu 87
Db 317 CGAGGGGTGTCTTCTACTTA 337

RESULT 21
BP270744 581 bp mRNA linear EST 17-SEP-2004
LOCUS BP270744 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION

clone KAR05146, mRNA sequence.
ACCESSION BP270744
VERSION BP270744.1 GI:52220093
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
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/issue_type="small intestine"
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ORIGIN
Alignment Scores:
Pred. No.: 8,81e-47 Length: 581
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP270744 (1-581)
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DB 68 ATGGAAGGCTCTGAAGCTCTGAGCTCGGCTGAGAGAGAGCGCTTGAGAGCC 127
QY 21 ATGPGGCTCTGAAGCTCTGAGCTCGGCTGAGAGAGAGCGCTTGAGAGCC 40
DB 128 CGACCTGAAACCATCTGAGAGAGAGAGCGCTTGAGAGAGAGAGAGAGAGAG 187
QY 41 AAGGCTCTGAG 60
DB 188 GATTCACCATCTGAG 247
QY 61 PheSerLeuIleThrTPanIleApgJYleuApgJleuApgJleuApgJleuApgJleu 80
DB 248 TTCTCTCATTTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
QY 81 ATGJYleuApgJleuApgJleuApgJleuApgJleuApgJleuApgJleuApgJleu 87
DB 308 CGAGGCTCTGAG 328
RESULT 22
BP379659 581 bp mRNA linear EST 21-SEP-2004
BP379659 Sugano cDNA library, uterus Homo sapiens cDNA clone
LOCUS WMD06642, mRNA sequence.
ACCESSION BP379659
VERSION BP379659.1 GI:52412762
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="WMD06642"
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ORIGIN
Alignment Scores:
Pred. No.: 8,81e-47 Length: 581
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP379659 (1-581)
QY 1 MetGUAAGGCTCTGAAGCTCTGAGCTCGGCTGAGAGAGAGCGCTTGAGAGCC 20
DB 69 ATGGAAGGCTCTGAAGCTCTGAGCTCGGCTGAGAGAGAGCGCTTGAGAGCC 128
QY 21 ATGPGGCTCTGAAGCTCTGAGCTCGGCTGAGAGAGAGCGCTTGAGAGCC 40
DB 129 CGACCTGAAACCATCTGAGAGAGAGAGCGCTTGAGAGAGAGAGAGAGAGAG 188
QY 41 AAGGCTCTGAG 60
DB 189 GATTCACCATCTGAG 248
QY 61 PheSerLeuIleThrTPanIleApgJYleuApgJleuApgJleuApgJleuApgJleu 80
DB 249 TTCTCTCATTTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
QY 81 ATGJYleuApgJleuApgJleuApgJleuApgJleuApgJleuApgJleuApgJleu 87
DB 309 CGAGGCTCTGAG 329
RESULT 23
BP219740 582 bp mRNA linear EST 15-SEP-2004
BP219740 Sugano cDNA library, caudate nucleus Homo sapiens cDNA
LOCUS clone CNR08585, mRNA sequence.
ACCESSION BP219740
VERSION BP219740.1 GI:52092643
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE 1 (bases 1 to 582)
AUTHORS Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES

Location/Qualifiers
1..582

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CNR08985"

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/clone_lib="Sugano cDNA library, caudate nucleus"

ORIGIN

Alignment Scores:

Pred. No.:	8.83e-47	Length:	582
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BP219740 (1-582)

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DB 175 ATGGAAGGGCTCTGACTCTCTGAGCCCTCGGAGAGAGAGCCCTTGGAGACC 234
OY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 235 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACA 294
OY 41 AppSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 295 GATTCCACCACTCTTAAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGCGAGCAG 354
OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 355 TTCTCTCATTAACCTCGAATTTGATGATGATTAATGATCTTAACCAATCTGTCAAGAGGGCT 414
OY 81 ArgGlyValCysSerTyrLeu 87
DB 415 CGAGGGGTGTGTTCTACTTA 435
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RESULT 24

BP261141

LOCUS BP261141 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone HS102606, mRNA sequence.

ACCESSION

BP261141

VERSION BP261141.1 GI:52176372

KEYWORDS EST.

SOURCE

ORGANISM

Homosapiens (human)

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1..582

/organism="Homo sapiens"

ORIGIN

Alignment Scores:

Pred. No.:	8.83e-47	Length:	582
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BP261141 (1-582)

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OY 1 MetGUARGAlAleuAnSerTyrPheGluProProValGluGluSerAlaleuGluArg 20
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OY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 126 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACA 185
OY 41 AppSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 186 GATTCCACCACTCTTAAATCAAGCCCATCTGAAGATCACTCAGCAAGAAATGCGAGCAG 245
OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 246 TTCTCTCATTAACCTCGAATTTGATGATGATTAATGATCTTAACCAATCTGTCAAGAGGGCT 305
OY 81 ArgGlyValCysSerTyrLeu 87
DB 306 CGAGGGGTGTGTTCTACTTA 326
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RESULT 25

BP270415

LOCUS BP270415 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION clone KAR02166, mRNA sequence.

ACCESSION

BP270415

VERSION BP270415.1 GI:52219764

KEYWORDS EST.

SOURCE

ORGANISM

Homosapiens (human)

Homosapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 582)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1..582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="KAR02166"

/tissue_type="small intestine"

/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.: 8.83e-47 Length: 582
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP275810 (1-582)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 158 ATGAAAGGGCTCTGAACCTCTTCACTTCAGAGCTCCGGTGAGAGAGAGCGCTTGAGAGCG 217
QY 21 ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThr 40
DB 218 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 277
QY 41 AAsperThrThSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 278 GATTCACCACTTCTTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATG 337
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 338 TTCTCTCATTAACCTGGAATATGATGATTGATCTTAAACAATCTGTCAAGAGGGCT 397
QY 81 ArgGlyValCysSerTyrLeu 87
DB 398 CGAGGGGTGTCTCTACTTA 418

RESULT 26
BP275810 582 bp mRNA linear EST 16-SEP-2004
LOCUS BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION KDN04583, mRNA sequence.
ACCESSION BP275810
VERSION BP275810.1 GI:52189542
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 582)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
CONTACT: Yutaka Suzuki
DEPARTMENT OF Virology
INSTITUTE OF MEDICAL SCIENCE, UNIVERSITY OF TOKYO
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..582
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KDN04583"
/issue_type="kidney"
/clone_lib="Sugano cDNA library, kidney"

ORIGIN

Alignment Scores:

Pred. No.: 8.83e-47 Length: 582
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP275810 (1-582)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 149 ATGAAAGGGCTCTGAACCTCTTCACTTCAGAGCTCCGGTGAGAGAGAGCGCTTGAGAGCG 208
QY 21 ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThr 40
DB 209 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 268
QY 41 AAsperThrThSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 269 GATTCACCACTTCTTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATG 328
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 329 TTCTCTCATTAACCTGGAATATGATGATTGATCTTAAACAATCTGTCAAGAGGGCT 388
QY 81 ArgGlyValCysSerTyrLeu 87
DB 389 CGAGGGGTGTCTCTACTTA 409

RESULT 27
BP195721 583 bp mRNA linear EST 14-SEP-2004
LOCUS BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION ADB08961, mRNA sequence.
ACCESSION BP195721
VERSION BP195721.1 GI:52039998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.

REFERENCE 1 (bases 1 to 583)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
CONTACT: Yutaka Suzuki
DEPARTMENT OF Virology
INSTITUTE OF MEDICAL SCIENCE, UNIVERSITY OF TOKYO
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADB08961"
/issue_type="brain"
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ORIGIN

Alignment Scores:

Pred. No.: 8.85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP195721 (1-583)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 217 ATGAAAGGGCTCTGAACCTCTTCACTTCAGAGCTCCGGTGAGAGAGAGCGCTTGAGAGCG 276
QY 21 ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThr 40
DB 277 CGACCTGAACCACTCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAGAAACAAC 336

QY 41 ApsSerThrThrSerIleSerProSerGluAapThrGlnGlnGluSerMet 60
|||||
DB 337 GATTCCACCACTTCTAAATCAAGCCATCTGAAGATACACAGAAATGCGACATG 396

QY 61 PheSerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnAsnLeuSerGluArgAla 80
|||||
DB 397 TTCTCTCATTAACCTGGAATATTGATGATTAATCTTAAACAATCTGTCAAGAGGCGCT 456

QY 81 ArgGlyValCysSerTyrLeu 87
|||||
DB 457 CGAGGGGTGTGTTCTACTTA 477

RESULT 28
LOCUS BP262103 583 bp mRNA linear EST 16-SEP-2004
DEFINITION BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HSI05902, mRNA sequence.
ACCESSION BP262103
VERSION BP262103.1 GI:52177334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Hirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HSI05902"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 8,85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP262103 (1-583)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
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DB 94 ATGGAAGAGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAGCGC 153

QY 21 ArgProGluThrIleSerGluProIleSerTyrValAapLeuThrAsnGluGluThrThr 40
|||||
DB 154 CAACCTGAACCATCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACCT 213

QY 41 ApsSerThrThrSerIleSerProSerGluAapThrGlnGlnGluSerMet 60
|||||
DB 214 GATTCCACCACTTCTAAATCAAGCCATCTGAAGATACACAGAAATGCGACATG 273

QY 61 PheSerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnAsnLeuSerGluArgAla 80
|||||
DB 274 TTCTCTCATTAACCTGGAATATTGATGATTAATCTTAAACAATCTGTCAAGAGGCGCT 333

QY 81 ArgGlyValCysSerTyrLeu 87
|||||
DB 334 CGAGGGGTGTGTTCTACTTA 354

RESULT 29
LOCUS BP262741 583 bp mRNA linear EST 16-SEP-2004
DEFINITION BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HSI07919, mRNA sequence.
ACCESSION BP262741
VERSION BP262741.1 GI:52177972
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominae; Homo.
REFERENCE 1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Hirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source 1..583
/organism="Homo sapiens"
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/clone="HSI07919"
/tissue_type="small intestine"
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ORIGIN

Alignment Scores:
Pred. No.: 8,85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP262741 (1-583)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
|||||
DB 30 ATGGAAGAGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAGCGC 89

QY 21 ArgProGluThrIleSerGluProIleSerTyrValAapLeuThrAsnGluGluThrThr 40
|||||
DB 90 CAACCTGAACCATCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACCT 149

QY 41 ApsSerThrThrSerIleSerProSerGluAapThrGlnGlnGluSerMet 60
|||||
DB 150 GATTCCACCACTTCTAAATCAAGCCATCTGAAGATACACAGAAATGCGACATG 209

QY 61 PheSerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnAsnLeuSerGluArgAla 80
|||||
DB 210 TTCTCTCATTAACCTGGAATATTGATGATTAATCTTAAACAATCTGTCAAGAGGCGCT 269

QY 81 ArgGlyValCysSerTyrLeu 87
|||||
DB 270 CGAGGGGTGTGTTCTACTTA 290

RESULT 30
LOCUS BP319548 583 bp mRNA linear EST 17-SEP-2004

DEFINITION BP19548 Sugano cDNA library, pericardium Homo sapiens cDNA clone
PCD11128, mRNA sequence.
ACCESSION BP19548
VERSION BP19548.1 GI:52248523
KEYWORDS EST.
SOURCES
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 583)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,U., Nakai,K. and Sugano,S.
TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PCD11128"
/issue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"
ORIGIN
Alignment Scores:
Pred. No.: 8.85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BP19548 (1-583)
QY 1 MetGuaArgAlaLeuAuaSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 209 ATGGAAAGGGCTGGAACCTCTCACTTCGAGCTCCGGTGGAGAGAGCCGCTTGGAAAGC 268
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 269 GCACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAAGAACCACT 328
QY 41 AAspSerThrThrSerIleSerIleSerProSerGluAAspThrGluGluValAsnGlySerMet 60
Db 329 GATTCACCACTTCTAATAATCAGCCACTGAAAGATCTACGACAAAGAAATGGCAGCATG 388
QY 61 PheSerLeuIleThrTyrPheAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 389 TTCTCTCATTAACCTCGAATATTGATGATTGATTAATCTTAACCAATCTGTCAAGAGGGCT 448
QY 81 ArgGlyValCysSerTyrLeu 87
Db 449 CGAGGGGTGTCTTCTTACTTA 469
RESULT 31
LOCUS BU783229 583 bp mRNA linear EST 11-OCT-2002
DEFINITION In01a08.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6123158
ACCESSION BU783229 5' similar to TF:095551 095551 D3J0K3.3 ;, mRNA sequence.
VERSION BU783229.1 GI:23827207
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 583)
Mellon,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scaerle,M., Brestelli,J., Gradowh,G., Clifton,S.,
Hillier,L., Maria,M., Pape,D., Wylie,T., Martin,J., Bilestein,A.,
Schmitz,A., Treising,B., Ritter,E., Konko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagatahvali,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: In01a08.x1
Contact: Douglas Mellon, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmellon@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gldco
High quality sequence atop: 430.
FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6123158"
/issue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1:
XhoI; Site 2: EcoRI; Constructed with lambda ZAPRI system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas Est project library."
ORIGIN
Alignment Scores:
Pred. No.: 8.85e-47 Length: 583
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x BU783229 (1-583)
QY 1 MetGuaArgAlaLeuAuaSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 158 ATGGAAAGGGCTGGAACCTCTCACTTCGAGCTCCGGTGGAGAGAGCCGCTTGGAAAGC 217
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 218 GCACTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAAGAACCACT 277
QY 41 AAspSerThrThrSerIleSerIleSerProSerGluAAspThrGluGluValAsnGlySerMet 60
Db 278 GATTCACCACTTCTAATAATCAGCCACTGAAAGATCTACGACAAAGAAATGGCAGCATG 337
QY 61 PheSerLeuIleThrTyrPheAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 338 TTCTCTCATTAACCTCGAATATTGATGATTGATTAATCTTAACCAATCTGTCAAGAGGGCT 397

QY 81 ArgGlyValCysSerTyrLeu 87
DB 398 CGAGGGGTGTCTTCTACTTA 418

RESULT 32
BP263059
LOCUS
DEFINITION BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA
ACCESSION BP263059
VERSION BP263059.1 GI:52178290
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 584)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL
PUBMED
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..584
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS110591"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 8,87e-47 Length: 584
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP263059 (1-584)

QY 1 MetGluAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 83 ATGGAAGGGGCTGTGAACCTCTTCCAGCCTCCGGTGGAGAGAGCCCTTGGAAACGC 142

QY 21 ArgPProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 143 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACT 202

QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 203 GATTCACACACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 262

QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 263 TTCTCTCATTAACCTGGAATATGATGATTGAATCAACAACTGTGCAAGAGGGCT 322

QY 81 ArgGlyValCysSerTyrLeu 87
DB 323 CGAGGGGTGTCTTCTACTTA 343

RESULT 33
BP348623
LOCUS
DEFINITION BP348623 Sugano cDNA library, small intestine Homo sapiens cDNA
ACCESSION BP348623
VERSION BP348623.1 GI:52278608
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 584)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL
PUBMED
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
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/organism="Homo sapiens"
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ORIGIN

Alignment Scores:
Pred. No.: 8,87e-47 Length: 584
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP348623 (1-584)

QY 1 MetGluAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 190 ATGGAAGGGGCTGTGAACCTCTTCCAGCCTCCGGTGGAGAGAGCCCTTGGAAACGC 249

QY 21 ArgPProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 250 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACT 309

QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 310 GATTCACACACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 369

QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 370 TTCTCTCATTAACCTGGAATATGATGATTGAATCAACAACTGTGCAAGAGGGCT 429

QY 81 ArgGlyValCysSerTyrLeu 87
DB 430 CGAGGGGTGTCTTCTACTTA 450

RESULT 34
BP236074
LOCUS
DEFINITION BP236074 Sugano cDNA library, coronary artery endothelial cell Homo
ACCESSION BP236074
VERSION BP236074.1 GI:52108984
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

DEFINITION BP348623 Sugano cDNA library, brain Homo sapiens cDNA clone
SZR01143, mRNA sequence.
ACCESSION BP348623
VERSION BP348623.1 GI:52278608
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 584)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL
PUBMED
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
source
1..584
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZR01143"
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ORIGIN

Alignment Scores:
Pred. No.: 8,87e-47 Length: 584
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP348623 (1-584)

QY 1 MetGluAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 190 ATGGAAGGGGCTGTGAACCTCTTCCAGCCTCCGGTGGAGAGAGCCCTTGGAAACGC 249

QY 21 ArgPProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 250 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAACT 309

QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 310 GATTCACACACTTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGAGCATG 369

QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 370 TTCTCTCATTAACCTGGAATATGATGATTGAATCAACAACTGTGCAAGAGGGCT 429

QY 81 ArgGlyValCysSerTyrLeu 87
DB 430 CGAGGGGTGTCTTCTACTTA 450

RESULT 34
BP236074
LOCUS
DEFINITION BP236074 Sugano cDNA library, coronary artery endothelial cell Homo
ACCESSION BP236074
VERSION BP236074.1 GI:52108984
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
AUTHORS Homiidae; Homo.
TITLE (bases 1 to 588)
JOURNAL Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
PUBMED Mizushima-Sugano, J., Nakai, K. and Sugano, S.
COMMENT Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
1534256
JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
CONTACT Contact: Yutaka Suzuki
DEPARTMENT Department of Virology
INSTITUTE Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES
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/organism="Homo sapiens"
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endothelial cell"
ORIGIN
Alignment Scores:
Pred. No.: 8.95e-47 Length: 588
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3
US-10-757-745-2_COPY_54_140 (1-87) x BP236074 (1-588)
QY 1 MetGluArgAlaLeuAenSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 196 ATGGAAAGGGGCTCGAAGCTCTCACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAAAGCG 255
QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThr 40
Db 256 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAGAAACAACACT 315
QY 41 AspSerThrThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 316 GATTCACCACTTCTTAAATCAGCCCATCTGAGAGATCTCAGCAAGAAATGGCAGCAGT 375
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 376 TTCTCTCATTAACCTGGAATATTGATGATTGATTAATCTAAACATCTGTCAAGAGGGCT 435
QY 81 ArgGlyValCysSerTyIleu 87
Db 436 CGAGGGGTGTGTTCTTACTTA 456
RESULT 35
AL703449 602 bp mRNA linear EST 04-SRP-2003
LOCUS DKFZP686G0621.r1.686 (synonym: hlc3) Homo sapiens cDNA clone
DEFINITION
ACCESSION AL703449
VERSION AL703449.1 GI:19668804
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 602)
AUTHORS Anorge, W., Winkler, U., Mewes, W., Weill, B. and Wiemann, S.
TITLE EST (Anorge, W., Winkler, U., Mewes, W., Weill, B. and Wiemann, S.)
JOURNAL Unpublished (1999)

COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de,
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No 5' sequence available.
This clone (DKFZP686G0621) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
SOURCE Location/Qualifiers
1..602
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP686G0621"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlc3)"
/note="vector: pT7D1Ex2; Site_1: SflTA; Site_2: SflTB;
cDNA-collection"
ORIGIN
Alignment Scores:
Pred. No.: 9.23e-47 Length: 602
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 1
DB: 1
US-10-757-745-2_COPY_54_140 (1-87) x AL703449 (1-602)
QY 1 MetGluArgAlaLeuAenSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 161 ATGGAAAGGGGCTCGAAGCTCTCACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAAAGCG 220
QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThr 40
Db 221 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTGACCTAAACCAATGAGAAACAACACT 280
QY 41 AspSerThrThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 281 GATTCACCACTTCTTAAATCAGCCCATCTGAGAGATCTCAGCAAGAAATGGCAGCAGT 340
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 341 TTCTCTCATTAACCTGGAATATTGATGATTGATTAATCTAAACATCTGTCAAGAGGGCT 400
QY 81 ArgGlyValCysSerTyIleu 87
Db 401 CGAGGGGTGTGTTCTTACTTA 421
RESULT 36
CB069952 621 bp mRNA linear EST 21-JAN-2003
LOCUS CB069952
DEFINITION
ACCESSION CB069952
VERSION CB069952.1 GI:27814472
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Mellon, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Seacrest, M., Bresnelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blierstein, A.,

TITLE
JOURNAL
COMMENT

Schmitt, A., Theising, B., Rötter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McMan, R., Cole, R., Teagard, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1631610.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557

Email: dmelton@biochem.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 476.

FEATURES

source

Location/Qualifiers

1..621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5534035"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Alignment Scores:

Pred. No.: 9,616-47 Length: 621
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CB069952 (1-621)

QY 1 MetGUUAGUAlaLeuAsnSerTyrrPheGUUProProValGluGluSerAlaLeuGUUArg 20
DB 166 ATGGAAAGGGCTGTGAACCTCTACTCGAGCTCCGCTGAGAGAGCCCTTGGAAACC 225
QY 21 ATGProGUUThrLisSerGUUProLysThrTyrrValAspLeuThrAsnGUUArg 40
DB 226 CGACCTGAAACCATCTCTGAGCCCAAGACCTTAAGTTCACCTAACCAATGAAGAAACAAC 285
QY 41 AAspSerThrThrSerLysLisSerProSerGUUAspThrGlnGlnGluAsnGlySerMet 60
DB 286 GATTCCACCACTTCTAAATCAAGCCCATCTGAAGATCACTGACCAAGAAAATGGCAGCAG 345
QY 61 PheSerLeuLisThrTrpAsnLisAspGlyLeuAspLeuAsnAsnLeuSerGUUArg 80
DB 346 TTCTCTCATTAACCTGGAATATTTGATGATTAGATCAATCAATCTGTCAAGAGGCGCT 405
QY 81 ArgGlyValCysSerTyrrLeu 87
DB 406 CAGGGGCTGTCTCTACTTA 426
RESULT 37
CB157906 634 bp mRNA linear EST 29-JAN-2003
LOCUS

DEFINITION K-EST0217150 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-5-F06

5', mRNA sequence.

ACCESSION

CB157906

VERSION

CB157906.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 5 row: F column: 06
High quality sequence stop: 634.

FEATURES

source

Location/Qualifiers

1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L18POOL1n1-5-F06"
/cell_line="SN-354+Cho-CK+Cho-CK+HLK-3"
/lab_host="Top10P"
/clone_lib="L18POOL1n1"
/note="Organ: Liver; Vector: pRTT3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was constructed by the Soares
laboratory and it was constructed as described by Bonaldi,
M.F., Lemmon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Alignment Scores:

Pred. No.: 9,886-47 Length: 634
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CB157906 (1-634)

QY 1 MetGUUAGUAlaLeuAsnSerTyrrPheGUUProProValGluGluSerAlaLeuGUUArg 20
DB 112 ATGGAAAGGGCTGTGAACCTCTACTCGAGCTCCGCTGAGAGAGCCCTTGGAAACC 171
QY 21 ATGProGUUThrLisSerGUUProLysThrTyrrValAspLeuThrAsnGUUArg 40
DB 172 CGACCTGAAACCATCTCTGAGCCCAAGACCTTAAGTTCACCTAACCAATGAAGAAACAAC 231
QY 41 AAspSerThrThrSerLysLisSerProSerGUUAspThrGlnGlnGluAsnGlySerMet 60
DB 232 GATTCCACCACTTCTAAATCAAGCCCATCTGAAGATCACTGACCAAGAAAATGGCAGCAG 291
QY 61 PheSerLeuLisThrTrpAsnLisAspGlyLeuAspLeuAsnAsnLeuSerGUUArg 80
DB 232 TTCTCTCATTAACCTGGAATATTTGATGATTAGATCAATCAATCTGTCAAGAGGCGCT 351
QY 81 ArgGlyValCysSerTyrrLeu 87
DB 352 CAGGGGCTGTCTCTACTTA 372
RESULT 38

CV023369
LOCUS 634 bp mRNA linear EST 20-AUG-2004
DEFINITION 288 Full Length cDNA from the Mammalian Gene Collection Homo
sapiens cDNA 5' similar to BC017553, mRNA sequence.
ACCESSION CV023369
VERSION CV023369.1 GI:51481130
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 634)
REFERENCE Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Pench,C.,
Vandenhaute,J., Cusick,M.E., Albaladejo,S., Hill,D.E. and Vidal,M.
Human ORFome Version 1.1: a platform for Reverse Proteomics
Genome Res. (2004) in press
CONTACT: Vidal M
TITLE Marc Vidal Laboratory
JOURNAL Dana Farber Cancer Institute
COMMENT 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc.Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
results from a PCR reaction using an MGC full-length cDNA as
template DNA and ORF specific primers
PCR Primers
FORWARD: ATGAGCTTGGGAGATGCTCTGCA
BACKWARD: TACATATTATATCTAGATGCACAGAG
Insert Length: 634 Std Error: 32.00
Plate: 11008 row: 05 column: F
Seq primer: ACTGCGCGCTGTTTACACGTCGTGACTGGGAAAC
High quality sequence start: 97
High quality sequence stop: 633
POLYA=No.
FEATURES
source location/Qualifiers
1..634
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_id="Full Length cDNA from the Mammalian Gene
Collection"
/note="Vector: mixed; The ORFs were PCR amplified from the
MGC (Mammalian Gene Collection) as of April 2004 and
cloned by recombinational Gateway cloning into pDONR223
Donor Vector. Reference: MGC (Mammalian Gene Collection)
Program Team, Generation and Initial Analysis of more than
15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,
2002, 99(26), 16899-16903"

ORIGIN
Alignment Scores:
Pred. No.: 9.88e-47 Length: 634
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x CV023369 (1-634)
QY 1 MetGUAGGAlaLeuAnSerTYrPheGluPProPovaLgUguSerAlaUguUArg 20
DB 160 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGAGAGCCCTTGAAAGCC 219
QY 21 ArgProGUUThrIleSerGUProLySerThTYrValAAspleuThraAngGUguUThr 40
DB 220 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGACCTTAACAATGAAGAAACAACCT 279

QY 41 AsperThrThrSerTyIleSerProSerGUAspThrGInGUguAnGUySerMet 60
DB 280 GATTCACACCACTTCTAAATCGCCATCTGGAAGATCTCACAGAAAGAAATGCAAGCATG 339
QY 61 PheSerIleuIleThrTTPAsnIleAspGlyLeuAspleuAnSerGUAspAla 80
DB 340 TTCTCTCTCATTCAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATG 359
QY 81 ArgGlyValCySerTyIleu 87
DB 400 CGAGGGGTGGTTCCTACTTA 420
RESULT 39
B133830 644 bp mRNA linear EST 30-JUN-2001
LOCUS 602999339P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141577 5',
DEFINITION mRNA sequence.
ACCESSION B133830
VERSION B133830.1 GI:15018487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 644)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Stransberg, Ph.D.
COMMENT Email: cgabs-remail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Invivo Genomics, Inc.
DNA Sequencing by: Invivo Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
<http://image.jhmi.gov>
Plate: L14M11348 Row: n column: 10
High quality sequence stop: 531.
FEATURES
source location/Qualifiers
1..644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5141577"
/tissue_type="cervical carcinoma cell line"
/lab_note="PM108"
/clone_id="NIH_MGC_12"
/note="Origin: cervical; Vector: pCMV-SPORT6, Site 1: NotI,
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.4 Kb. Library prepared by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. No.: 1.01e-46 Length: 644
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x B133830 (1-644)
QY 1 MetGUAGGAlaLeuAnSerTYrPheGluPProPovaLgUguSerAlaUguUArg 20
DB 147 ATGGAAAGGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGAGAGCCCTTGAAAGCC 206
QY 21 ArgProGUUThrIleSerGUProLySerThTYrValAAspleuThraAngGUguUThr 40
DB 207 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGACCTTAACAATGAAGAAACAACCT 266

QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGlnGluAsnGlySerMet 60
 DB 267 GATTCACACACTTCTAAATATGACCCATCTGAAGATCTACAGCAAGAAATGCGACGATG 326
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 327 TTCTCTCATTAACCTGGAATTTGATGATTAAGATCTTAACCAATCTGTCAAGAGGGCT 386
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 387 CGAGGGGTGTGTCTCTACTTA 407

RESULT 40

LOCUS CR753214 652 bp mRNA linear EST 01-SEP-2004
 DEFINITION DKFZp4691195.1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 DKFZp4691195.5, mRNA sequence.
 CR753214
 ACCESSION CR753214.1 GI:51845629
 VERSION EST
 KEYWORDS

SOURCE

ORGANISM Pongo pygmaeus (orangutan)
 Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Pongo.
 1 (bases 1 to 652)
 Ansoerge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
 Mewes, H.W., Weill, B., Amd, C., Osanger, A., Fobo, G., Han, M. and
 Wiemann, S.
 Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 COMMENT MIPS

TITLE MIPS
 JOURNAL MIPS
 COMMENT MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; lin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp4691195
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/
 FEATURES
 source
 Location/Qualifiers
 1..652
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp4691195"
 /tissue_type="kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="469 (synonym: pkid1)"
 /note="Vector: pSPORT1_Sci; Site_1: SfilA; Site_2: SfilB"

ORIGIN

Alignment Scores:
 Pred. No.: 1,02e-46 Length: 652
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR753214 (1-652)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 177 ATGGAAGAGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAGCGC 236
 QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
 DB 237 CGCCCTGAACCATCTCTGAGCCCAAGACCTAATGTGACCTTAACCAATGAAGAAACAAC 296

QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGlnGluAsnGlySerMet 60
 DB 267 GATTCACACACTTCTAAATATGACCCATCTGAAGATCTACAGCAAGAAATGCGACGATG 356
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 357 TTCTCTCATTAACCTGGAATTTGATGATTAAGATCTTAACCAATCTGTCAAGAGGGCT 416
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 417 CGAGGGGTGTGTCTCTACTTA 437

RESULT 41

LOCUS CN298920 657 bp mRNA linear EST 16-MAY-2004
 DEFINITION 17000600170525 GRN PRENEU Homo sapiens cDNA 5', mRNA sequence.
 CN298920
 ACCESSION CN298920.1 GI:47315334
 VERSION EST
 KEYWORDS

SOURCE

ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 657)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 Transcriptionome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 657 Std Error: 0.00.
 FEATURES
 source
 Location/Qualifiers
 1..657
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cell, retinoic acid and
 mitogen-treated hES cell line H7"
 /clone_lib="GRN PRENEU"
 /note="Oligo dT primed, full-length enriched cDNA library
 from hES cell line H7 (929) maintained in feeder-free
 conditions. Embryoid bodies were generated in the presence
 of all-trans retinoic and mitogens."

ORIGIN

Alignment Scores:
 Pred. No.: 1,03e-46 Length: 657
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN298920 (1-657)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 116 ATGGAAGAGGCTCTGAACCTCTACTTCGAGCTCCGGTGGAGAGAGCGCTTGGAGCGC 175
 QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
 DB 176 CGACCTGAACCATCTCTGAGCCCAAGACCTAATGTGACCTTAACCAATGAAGAAACAAC 235
 QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGlnGluAsnGlySerMet 60

Db 236 GATTCACACCTCTTAAATCAGCCCATCTAAGATCTCAGCAAGAAATGCGAGCATG 295
 Qy 61 Pheserleu1leThrTTPAsn1leAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 Db 296 TTCCTCTCATTAACCTCGAATATGATGATTAATGATTAACAATCTGTCAAGAGGCT 355
 Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 356 CGAGGGGTGTCTCTACTTA 376
 RESULT 42
 Bg719113 678 bp mRNA linear EST 08-MAY-2001
 LOCUS 60269045F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831186 5',
 DEFINITION mRNA sequence.
 ACCESSION Bg719113
 VERSION Bg719113
 KEYWORDS Bg719113.1 GI:13998300
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 1 (bases 1 to 678)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@ds-remail.nih.gov
 Tissue Procurement: Miklos Palkevics, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L14M10753 row: 1 column: 11
 High quality sequence stop: 672.
 Location/Qualifiers
 1..678
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4831186"
 /lab_host="DH10B"
 /clone_1id="NIH_MGC_97"
 /note="Organ: testis; Vector: pBluescriptPR (modified
 pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
 (GTCGAG); Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size selected for average
 insert size 2.2 kb and normalized to R0F 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci in
 preparation). Library constructed by M. Brownstein
 (NIH/NHGRI). National Institutes of Health. Note: this is
 a NIH_MGC Library."
 ORIGIN
 Alignment Scores: 1.08e-46 Length: 678
 Pred. No.: 448.00 Matches: 87
 Score: 448.00
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x Bg719113 (1-678)
 Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
 Db 182 ATGGAAGGAGCTCTGAACTCTACTTCGAGCTCCGATGAGAGAGAGCGCTTGAAAGCG 241

Qy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
 Db 242 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTTAACCAAGAAAGAACT 301
 Qy 41 AspSerThrThrSerLeuIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 Db 302 GATTCACACCTTCTTAAATCAGCCCATCTCGAAGATACACACCAAGAAATGCGAGCATG 361
 Qy 61 Pheserleu1leThrTTPAsn1leAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 Db 362 TTCCTCTCATTAACCTCGAATATGATGATTAATGATTAACAATCTGTCAAGAGGCT 421
 Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 422 CGAGGGGTGTCTCTACTTA 442
 RESULT 43
 CR767236 701 bp mRNA linear EST 23-SEP-2004
 LOCUS DKFZP469E1236_r1 469 (synonym: PK1d1) Pongo pygmaeus cDNA clone
 DEFINITION DKFZP469E1236 5', mRNA sequence.
 ACCESSION CR767236
 VERSION CR767236.1 GI:52609173
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Pongo.
 1 (bases 1 to 701)
 Ansoerge, W., Krieger, S., Regiert, T., Rittmeyer, C., Schwager, B.,
 Mewes, H.W., Well, B., Amdt, C., Oeinger, A., Fobo, G., Han, M. and
 Wiemann, S.
 Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email: s.wiemann@dkfz-heidelberg.de; rlin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZP469E1236
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 Location/Qualifiers
 1..701
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZP469E1236"
 /cissue="Type:Kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1id="469 (synonym: PK1d1)"
 /note="Vector: pSPORT1_Sfi1, Site_1: Sfi1a, Site_2: Sfi1b"
 ORIGIN
 Alignment Scores: 1.13e-46 Length: 701
 Pred. No.: 448.00 Matches: 87
 Score: 448.00
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x CR767236 (1-701)
 Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
 Db 88 ATGGAAGGAGCTCTGAACTCTACTTCGAGCTCCGATGAGAGAGAGCGCTTGAAAGCG 147

QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
 DB 148 CGCCCTGAACCACTCTGAGCCAGACCTATGCTGACTTAACAATGAAGAAACAACACT 207
 QY 41 AASPserThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 208 GATTCACACACTCTTAATCAATCAGCCATCGAAGATCACTCAGCAAGAAATGCGACACTG 267
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 268 TTCTCTCTCATTAACCTGGAATATGATGATGATCAATCAATCTGTCAGAGAGGCGCT 327
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 328 CGAGGGGTGTCTTCTACTTA 348

RESULT 44
 BU661472 710 bp mRNA linear EST 30-SEP-2002
 LOCUS c172d11.z1 Hembase: Erythroid Precursor Cells (LCB:c1 library) Homo
 DEFINITION sapiens cDNA clone c172d11 5', mRNA sequence.
 ACCESSION BU661472.1 GI:23373654
 VERSION BU661472.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 710)
 Gubin,A.N., Lee,Y.T., Bouffard,G.G. and Miller,J.L.
 Gene Expression in Human Erythroid Precursor Cells
 Unpublished (2002)
 Contact: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jmlf@nih.gov
 The 'c1' library was constructed by Alexander Gubin, Ph.D. in the
 Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
 analyses by National Institutes of Health Intramural Sequencing
 Center (NISC). More information available at:
 http://hembase.nidk.nih.gov
 Plate: 72 row: d column: 11
 Seg primer: 5' lambda-TripLpx2 Sequencing Primer.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="c172d11"
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 /cell_type="Erythroid Precursor Cells"
 /cell_line="Primary culture of peripheral Blood
 Mononuclear Cells"
 /dev_stage="Precursor erythroblasts; GPA+"
 /lab_host="DH5alpha"
 /clone_lib="Hembase; Erythroid Precursor Cells (LCB:c1
 library)"
 /notes="Organ: blood; Vector: pTriplEx2; Site:1: SfiI;
 Site:2: SfiI; A complementary DNA (cDNA) library from
 human erythroid precursor cells was constructed using
 SMART PCR (polymerase chain reaction) cDNA library
 Construction Kit (Clontech, Palo Alto, CA) according to
 the manufacturer's directions, but with slight
 modifications. Briefly, reverse transcription was
 performed in the presence of 1 umol/L peptide nucleic acid
 (PNA) oligos
 (N-terminal)-biotin-GTC-CAC-CCG-AGG-CTT-G-(C-terminal) and

(N-terminal)-biotin-C(T/C)T-GAA-GTT-CTC-AGG-A-(C-terminal)
 . Synthesized cDNA was digested with SfiI and
 size-selected on a 1% agarose gel (>800bp). Large-scale
 sequencing of the library was performed by the NIH
 Intramural Sequencing Center (NISC;
 Http://www.nisc.nih.gov/).

ORIGIN

Alignment Scores:
 Pred. No.: 1.15e-46 Length: 710
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_copy_54_140 (1-87) x BU661472 (1-710)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 76 ATGAAAGGGCTGTGAACCTCTACTTCCGAGCTCCGAGAGAGAGAGCGCTTGAAACCC 135
 QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
 DB 136 CGACCTGAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 195
 QY 41 AASPserThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 196 GATTCACACACTCTTAATCAATCAGCCATCGAAGATCACTCAGCAAGAAATGCGACACTG 255
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 256 TTCTCTCTCATTAACCTGGAATATGATGATGATCAATCAATCTGTCAGAGAGGCGCT 315
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 316 CGAGGGGTGTCTTCTACTTA 336

RESULT 45
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 LOCUS CN298923
 DEFINITION 1700600002122 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN298923
 VERSION CN298923.1 GI:47315337
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 711)
 Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murae,J., Flak,G.J.,
 Li,Y., Xu,C., Pang,R., Guejler,K., Rao,M.S., Mandalam,R.,
 Lebkowicz,J. and Stanton,L.W.
 Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert length: 711 Std Error: 0.00.
 Location/Qualifiers
 1..711
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, DMSO-treated H9 cell
 line"

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.txt

Page 30

/clone_11b="GRN PREHEP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:

Prod. No.: 1.15e-46 Length: 711
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN298923 (1-711)

QY 1 MetGUAAGAlaLeuAnSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 125 ATGGAAGAGGCTCTGAATCTTCTGAGCTCCGCTGAGAGAGAGCGCTTGAGACGC 184
QY 21 ArgProGluThrIleSerGluProValThrTYrValAspLeuThrAsnGluGluThr 40
Db 185 CGACCTGAACCATCTCGAGCCCAAGCTATGTTGACCTAACCAAGAAAGAAACAAC 244
QY 41 AapSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 245 GATTCCACCATCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 304
QY 61 PheSerLeuIleThrTPAenlleaSpGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 305 TTCTCTCTCATTAACCGAATATTGATGATGATTAACCACTCTGCAGAGAGGCT 364
QY 81 ArgGlyValCysSerTYrLeu 87
Db 365 CGAGGGGTGTGTCTCTACTTA 385

QY 1 MetGUAAGAlaLeuAnSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 152 ATGGAAGAGGCTCTGAATCTTCTGAGCTCCGCTGAGAGAGAGCGCTTGAGACGC 211
QY 21 ArgProGluThrIleSerGluProValThrTYrValAspLeuThrAsnGluGluThr 40
Db 212 CGACCTGAACCATCTCGAGCCCAAGCTATGTTGACCTAACCAAGAAAGAAACAAC 271
QY 41 AapSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 272 GATTCCACCATCTTAAATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 331
QY 61 PheSerLeuIleThrTPAenlleaSpGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 332 TTCTCTCTCATTAACCGAATATTGATGATGATTAACCACTCTGCAGAGAGGCT 391
QY 81 ArgGlyValCysSerTYrLeu 87
Db 392 CGAGGGGTGTGTCTCTACTTA 412

RESULT 46
CN298922 729 bp mRNA linear EST 16-MAY-2004
LOCUS 17000600077717 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298922
ACCESSION CN298922.1 GI:47315336
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lobkowsky, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_11b="GRN PREHEP"
/note="oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

RESULT 47
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LOCUS 17000424496911 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN298924
ACCESSION CN298924.1 GI:47315338
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 729)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lobkowsky, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
15146197
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 729 Std Error: 0.00.
Location/Qualifiers
1..729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_11b="GRN_ES"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p23),
and H9 (p26) maintained in feeder-free conditions"

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
source

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
FEATURES
source

ORIGIN

Alignment Scores:

Alignment Scores:	1.19e-46	Length:	729
Pred. No.:	448.00	Matches:	87
Score:	100.0%	Conservative:	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CN298924 (1-729)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db ATGGAAGAGGCTCTGAACTCTGAGCCCTCGGTGAGAGAGCGCTTGAGACCC 153
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 154 CGACCTGAACACCATCTGAGCCCAAGACCTAATGTTGACCTAACCAATGAGAAACAACCT 213
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 214 GATTCCACCACTCTTAAATGAGCCCATCTGAAGATACACAGCAAGAAATGCGACGATG 273
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 274 TTCTCTCATTAACCTGGAATATGATGATGATTAACAATCTGTGAGAGAGGCT 333
QY 81 ArgGlyValCysSerTyrLeu 87
Db 334 CGAGGGGTGTGTTCTACTTA 354

RESULT 48

CX760857

LOCUS

AGENCOURT 40963383 NIH_MGC_281 Homo sapiens cDNA clone

IMAGE:7783600 3', mRNA sequence.

ACCESSION

CX760857

VERSION

CX760857.1 GI:58057513

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Hemo

1 (bases 1 to 731)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics / NIH

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Meil Filipo

cDNA Library Preparation: Express Genomics

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov/

Plate: LLM15944 row: b column: 14

High quality sequence stop: 574.

FEATURES

Source

1..731

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:7783600"

/tissue_type="pluripotent cell line derived from

blastocyst inner cell mass"

/lab_host="DH10B Tona"

/clone_idb="NIH_MGC_281"

/note="Organ: Blastocyst; Vector: pExpress-1; Site: 1; EcoRV; Site 2: NotI; RNA obtained from pluripotent cell line derived from blastocyst inner cell mass (cell line HSF-6, NIH Registry designation UC06. Positive for OCT4 expression by rtPCR, positive for SSEA-3, SSEA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence passage 62. cDNA was primed using oligo-dT primer: 5'-pGACTAGTCTAGATCGGAGCGGCCGC(17)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 2.0 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_280) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

Alignment Scores:

Alignment Scores:	1.19e-46	Length:	731
Pred. No.:	448.00	Matches:	87
Score:	100.0%	Conservative:	0
Percent Similarity:	100.0%	Mismatches:	0
Best Local Similarity:	100.0%	Indels:	0
Query Match:	100.0%	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CX760857 (1-731)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 164 ATGGAAGAGGCTCTGAACTCTGAGCCCTCGGTGAGAGAGCGCTTGAGACCC 223
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
Db 224 CGACCTGAACACCATCTGAGCCCAAGACCTAATGTTGACCTAACCAATGAGAAACAACCT 283
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 284 GATTCCACCACTCTTAAATGAGCCCATCTGAAGATACACAGCAAGAAATGCGACGATG 343
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 344 TTCTCTCATTAACCTGGAATATGATGATGATTAACAATCTGTGAGAGAGGCT 403
QY 81 ArgGlyValCysSerTyrLeu 87
Db 404 CGAGGGGTGTGTTCTACTTA 424

RESULT 49

BI258848

LOCUS

60296963P1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109303 5',

mRNA sequence.

ACCESSION

BI258848

VERSION

BI258848.1 GI:14815606

KEYWORDS

EST.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 767)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Office of Cancer Genomics / NIH

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cga@bbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov/

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.rst

Page 32

Plate: L1AM11264 row: m column: 16
High quality sequence stop: 758.
Location/Qualifiers

FEATURES

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1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5109303"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_id="NIH_MGC_12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NCBI Site: 2; Salt: Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.4 kb. Library prepared by Jife Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 1.27e-46 Length: 767
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x B1258848 (1-767)

QY 1 MetG1AAGAlaLeuAnSerTyrPheG1uPProProValG1uG1uSerAlaLeuG1uArg 20
DB 97 ATGGAAGGGCTCTGAACCTCCTACCTCGAGCCCTCGAGAGAGAGCGCTTGGAACGC 156
QY 21 ArgProG1uThr11eSerG1uProLyThrTyValAspLeuThraAng1uG1uThrThr 40
DB 157 CGACCTGAACCATCTCTGAGCCCAAGCCTATGTGACCTAAACCAATGAAGAAACAAC 216
QY 41 AspSerThrTherSerLy11eSerProSerG1uAspThrc1ng1uAnG1ySerMet 60
DB 217 GATTCACACACTTCTAAATATGAGCCCATCTGAATATCTCAGCAAAATAATGGCAGCGCT 276
QY 61 PheSerLeu11eThrTyPasn11eAspG1yLeuAspLeuAnSerG1uArgAla 80
DB 277 TTCTCTCATTAACCTGAATATGATGATTAATCAATCTGTCAAGAGGCGCT 336
QY 81 ArgG1yValCySerTyLeu 87
DB 337 CGAGGGGTGTCTCTACTTA 357

RESULT 50
B1754101 774 bp mRNA linear EST 25-SEP-2001
LOCUS B1754101
DEFINITION 603027659P1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197838 5',
mrna sequence.
ACCESSION B1754101
VERSION B1754101.1 GI:15745679
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 774)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsrbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Invitrogen, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Plate: L1AM11495 row: f column: 15
High quality sequence stop: 756.
Location/Qualifiers

FEATURES

source
1..774
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5197838"
/lab_host="DH10B"
/clone_id="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1; NCBI Site: 2; ECKV (destroyed): RNA source anonymous pool of 6 male brains, age range 21-27 yo. Library is oligo-dt primed and directionally cloned. (ECKV site is destroyed upon cloning). Average insert size 1.5 kb. Insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 1.28e-46 Length: 774
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
US-10-757-745-2_COPY_54_140 (1-87) x B1754101 (1-774)

QY 1 MetG1AAGAlaLeuAnSerTyrPheG1uPProProValG1uG1uSerAlaLeuG1uArg 20
DB 219 ATGGAAGGGCTCTGAACCTCCTACCTCGAGCCCTCGAGAGAGAGCGCTTGGAACGC 278
QY 21 ArgProG1uThr11eSerG1uProLyThrTyValAspLeuThraAng1uG1uThrThr 40
DB 279 CGACCTGAACCATCTCTGAGCCCAAGCCTATGTGACCTAAACCAATGAAGAAACAAC 338
QY 41 AspSerThrTherSerLy11eSerProSerG1uAspThrc1ng1uAnG1ySerMet 60
DB 339 GATTCACACACTTCTAAATATGAGCCCATCTGAATATCTCAGCAAAATAATGGCAGCGCT 398
QY 61 PheSerLeu11eThrTyPasn11eAspG1yLeuAspLeuAnSerG1uArgAla 80
DB 399 TTCTCTCATTAACCTGAATATGATGATTAATCAATCTGTCAAGAGGCGCT 458
QY 81 ArgG1yValCySerTyLeu 87
DB 459 CGAGGGGTGTCTCTACTTA 479

RESULT 51
B6719977 786 bp mRNA linear EST 08-MAY-2001
LOCUS B6719977
DEFINITION 602691335F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823432 5',
mrna sequence.
ACCESSION B6719977
VERSION B6719977.1 GI:13999164
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 786)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgsrbs-remail.nih.gov
Tissue Procurement: Miklos Palcovite, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shizaki
Tohiyuki and Piero Carninci (RIKEN)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM10733 row: f column: 09

High quality sequence stop: 784.

FEATURES
Source
Location/Qualifiers

1..786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4823432"
/lab_host="DH10B"
/clone_id="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(gtcgag); Oligo-dt primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1,31e-46 Length: 786
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG719977 (1-786)

QY 1 MetGluArgAlaLeuAsnSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 305 ATGGAAGAGGCTCTGAACCTCTCACTCGAGCCCTCGTGAGAGAGAGCCCTTGGAACCC 364
QY 21 ArgProGluThrIleSerGluProGluThrTyValAspLeuThrAsnGluGluThr 40
DB 365 CGACCTGAACCATCTCTGAGCCCAAGACTATGTTGACCTAATGAAGAAACAAT 424
QY 41 AppSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 425 GATTCACACCACTCTTAATCAAGCCCATCTGAAGATATCAAGCAAGAAATGACACATG 484
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 485 TTCTCTCATTAACCTGAACCATGATGATTAAGATCTAAACAATGTCTAGAGAGGCT 544
QY 81 ArgGlyValCysSerTyrLeu 87
DB 545 CGAGGGGTGTCTCTACTTA 565

RESULT 52
CX756424 799 bp mRNA linear EST 24-JAN-2005
LOCUS CX756424
DEFINITION IMAGE:7779791 3', mRNA sequence.
ACCESSION CX756424
VERSION CX756424.1 GI:58053080
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 799)
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

JOURNAL COMMENT

Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsabbs-remail.nih.gov
Tissue Procurement: Meri Firpo

CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LLM15934 row: c column: 21
High quality sequence stop: 579.

FEATURES
Source
Location/Qualifiers

1..799
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7779791"
/tissue_type="Pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B Tona"
/clone_id="NIH_MGC_281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site 1:
EcoRV; Site 2: NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-6, NIH Registry designation UC06. Positive for OCT4
expression by rtPCR, positive for SSEA-3, SSEA-4,
Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. CDNA was primed
using oligo-dt primer:
5'-pGACATGTTCTAGATCGGAGCGCCGCCCTT)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
primary library is normalized (non-normalized by Express
library is NIH_MGC_280) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN

Alignment Scores:

Pred. No.: 1,34e-46 Length: 799
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CX756424 (1-799)

QY 1 MetGluArgAlaLeuAsnSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 177 ATGGAAGAGGCTCTGAACCTCTCACTCGAGCCCTCGTGAGAGAGAGCCCTTGGAACCC 236
QY 21 ArgProGluThrIleSerGluProGluThrTyValAspLeuThrAsnGluGluThr 40
DB 237 CGACCTGAACCATCTCTGAGCCCAAGACTATGTTGACCTAATGAAGAAACAAT 296
QY 41 AppSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 297 GATTCACACCACTCTTAATCAAGCCCATCTGAAGATATCAAGCAAGAAATGACACATG 356
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 357 TTCTCTCATTAACCTGAACCATGATGATTAAGATCTAAACAATGTCTAGAGAGGCT 416
QY 81 ArgGlyValCysSerTyrLeu 87
DB 417 CGAGGGGTGTCTCTACTTA 437

RESULT 53

CX166335 810 bp mRNA linear EST 23-DEC-2004
 LOCUS HPG2_39_B09_g1_A035 NIH_MGC_258 Homo sapiens cDNA clone
 DEFINITION IMAGE:7459923.5, mRNA sequence.
 ACCESSION CX166335
 VERSION CX166335.1 GI:56796415
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo

REFERENCE 1 (bases 1 to 810)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@nci-remail.nih.gov
 Tissue Procurement: BresaGen, Inc.
 CDNA Library Preparation: Express Genomics, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
 University of Georgia
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM15771 row: d column: 17
 Seq primer: JENREV (CAGGAACGCTATGACC)
 High quality sequence stop: 810.

FEATURES
 source
 1..810
 Location/Qualifiers

1..810
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:7459923"
 /sex="male"
 /tissue_type="human embryonic stem cells differentiated to
 an early endodermal cell type"
 /cell_line="human embryonic stem cells"
 /cell_line="BG01"
 /lab_host="DH10B-T1 phage-resistant E. coli"
 /clone_idb="NIH_MGC_258"
 /note="Vector: pEXpress-1; Site 1: NotI; Site 2: EcoRV;
 RNA obtained from human embryonic stem cells isolated from
 the inner cell mass of blastocyst stage embryos and
 differentiated to an early endodermal cell type. Cell line
 id and NIH Registry designation is BG01. Positive for AFP
 expression. Passage number 40. cDNA primed using oligo-dT
 primer: 5'-DGAAGTTCAGTCCGCGCGCCGCC(T)25-3' and
 cloned into the EcoRV/NotI sites of pEXpress-1. This
 primary library is non-normalized (normalized primary
 library is NIH_MGC_259). It was constructed by Express
 Genomics (Frederick, MD). Sequence ends have been trimmed
 to exclude vector and regions below phred quality 16.
 Three-prime sequences are presented as their reverse
 complement and have been trimmed to exclude polyA. Note:
 this is a Mammalian Gene Collection library."

ORIGIN

Alignment Scores:
 Pred. No.: 1,36e-46 Length: 810
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 8 Gaps: 0

US-10-757-745-2_copy_54_140 (1-87) x CX166335 (1-810)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 117 ATGGAAGAGGCGCTCTAACCCTCACTTGAACCCCGGTGAGAGAGCGCTTGAAGCGC 176
 QY 21 ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThrThr 40
 DB 177 CGACCTGAAGAACCATCTCGAGGCCAGACCATGTTGACCTTAACCAATGAAGAAACAAC 236
 QY 41 AspSerThrThrSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 237 GATTCCACCACTTCTTAATATCAGCCCATCTGAAGATACACAGCAAGAAATGCGACGATG 296
 QY 61 PheSerLeuIleThrTyrPasnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 DB 297 TTCTCTCATTAACCTGGAATATGATGATGATCTTAACATCTGTCAAGAGGCGCT 356
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 357 CGAGGGGTGTGTTCTCACTTA 377

RESULT 54
 BI908925 838 bp mRNA linear EST 16-OCT-2001
 LOCUS 603067028F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215926.5',
 DEFINITION mRNA sequence.
 ACCESSION BI908925
 VERSION BI908925.1 GI:16172029
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo

REFERENCE 1 (bases 1 to 838)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@nci-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM11542 row: h column: 07
 High quality sequence stop: 773.

FEATURES

source
 1..838
 Location/Qualifiers
 1..838
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5215926"
 /tissue_type="leukocyte"
 /lab_host="DH10B"
 /clone_idb="NIH_MGC_118"
 /note="Vector: pCMV-SK076; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN
 Alignment Scores:
 Pred. No.: 1,42e-46 Length: 838
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x B1908925 (1-838)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaleuGluArg 20
DB 161 ATGAAAGGGCTCTGAACCTCTGAGCTCCGGTGGAGAGAGCCCTTGAGAGCC 220
QY 21 ArgProGluThrIleSerGluProLyThrTyrValAspLeuThrAsnGluGluThr 40
DB 221 CGACCTGAACACCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACACT 280
QY 41 AspSerThrThrSerLyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 281 GATTCACACCACTCTTAAATCAAGCCCATCTGAGATCACTACAGCAAGAAATGCGACATG 340
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 341 TTCTCTCATTAACCTGGAATTTGATGATGATTAACATCTGTCAAGAGGGCT 400
QY 81 ArgGlyValCysSerTyrLeu 87
DB 401 CGAGGGGTGTGTTCTACTTA 421

RESULT 55

CR765451

LOCUS CR765451 846 bp mRNA linear EST 23-SEP-2004
DEFINITION DKFZP469E2434.r1.469 (synonym: pkid1) Pongo pygmaeus CDNA clone
ACCESSION CR765451
VERSION CR765451.1 GI:52605526

KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pongo

AUTHORS 1 (bases 1 to 846)
Ostenwelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,
Mewes, H.W., Weill, B., Amd, C., Osanger, A., Fobo, G., Han, M. and
Wieman, S.

TITLE Pongo pygmaeus mRNA (Ostenwelder, B., Obermaier, B.,
Deutschenbaur, S., et al.)
JOURNAL Unpublished (2004)

COMMENT MIPS
Contact: MIPS

Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wieman,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wieman@dkfz-heidelberg.de; sequenced by Medigenomix
(Matisriedt/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFZP469E2434) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZP469E2434
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
source

1..846
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP469E2434"
/issue_type="Kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:
Pred. No.:

1.44e-46

Length:

846

Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR765451 (1-846)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaleuGluArg 20
DB 63 ATGAAAGGGCTCTGAACCTCTGAGCTCCGGTGGAGAGAGCCCTTGAGAGCC 122
QY 21 ArgProGluThrIleSerGluProLyThrTyrValAspLeuThrAsnGluGluThr 40
DB 123 CGCCCTGAACACCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACACT 182
QY 41 AspSerThrThrSerLyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 183 GATTCACACCACTCTTAAATCAAGCCCATCTGAGATCACTACAGCAAGAAATGCGACATG 242
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 243 TTCTCTCATTAACCTGGAATTTGATGATGATTAACATCTGTCAAGAGGGCT 302
QY 81 ArgGlyValCysSerTyrLeu 87
DB 303 CGAGGGGTGTGTTCTACTTA 323

RESULT 56

BE784416

LOCUS BE784416 853 bp mRNA linear EST 20-OCT-2000
DEFINITION 601473891P1 NIH_MGC_68 Homo sapiens CDNA IMAGE:3876862.5',
mRNA sequence.

ACCESSION BE784416
VERSION BE784416.1 GI:10205614
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

AUTHORS 1 (bases 1 to 853)
NIH-MGC http://mgc.nci.nih.gov/
Tissue Procurement: DCM/DMP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov

Plate: L1AM9638 row: e column: 23
High quality sequence stop: 660.

FEATURES
source

1..853
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3876862"
/issue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPOrt6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.:

1.46e-46

Length:

853

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.fst

Page 36

Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BF784416 (1-853)

OY 1 MetGUARGAlaLeuAenSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 164 ATGGAAAGGAGCTCTGAACCTCTGACCTCCGAGTGAAGAGAGCGCTTGAAACGC 223
OY 21 ArgProGluThrTlleSerGluProValTyrValAlaPleuThrAenGluGluThr 40
DB 224 CGACCTGAAACCATCTGACCCAGACCACTATGTTGACCTTACCAATGAAAGAAACACT 283
OY 41 AppSerThrThrSerTyrIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
DB 284 GATTCCACCACTTCTAAATCATGCCCATCTGAAGATCATGACAAAGAAATGCGACATG 343
OY 61 PheSerLeuIleThrTTPAenIleAapGlyLeuAapLeuAenAenLeuSerGluArgAla 80
DB 344 TTCTCTCATTAACCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 403
OY 81 ArgGlyValCysSerTyrLeu 87
DB 404 CGAGGGGTGTGTCTACTTA 424

RESULT 57 858 bp mRNA linear EST 05-SEP-2001
LOCUS B1553412 60193358F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5264582 5',
DEFINITION mRNA sequence.

ACCESSION B1553412
VERSION B1553412.1 GI:15440724

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..858
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5264582"
/issue_type="hippocampus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_95"
/note="Organ brain; Vector: pBluescriptR (modified pBluescript KS+), Site: 1 BamHI, Site 2: SalI-XhoI (5'-ATTTCCTCATTAACCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGAT-3' and normalized to R05. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in

Preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 1,478-46 Length: 858
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x B1553412 (1-858)

OY 1 MetGUARGAlaLeuAenSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 180 ATGGAAAGGAGCTCTGAACCTCTGACCTCCGAGTGAAGAGAGCGCTTGAAACGC 239
OY 21 ArgProGluThrTlleSerGluProValTyrValAlaPleuThrAenGluGluThr 40
DB 240 CGACCTGAAACCATCTGACCCAGACCACTATGTTGACCTTACCAATGAAAGAAACACT 299
OY 41 AppSerThrThrSerTyrIleSerProSerGluAspThrGlnGlnGluAenGlySerMet 60
DB 300 GATTCCACCACTTCTAAATCATGCCCATCTGAAGATCATGACCAAGAAATGCGACATG 359
OY 61 PheSerLeuIleThrTTPAenIleAapGlyLeuAapLeuAenAenLeuSerGluArgAla 80
DB 360 TTCTCTCATTAACCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGAT 419
OY 81 ArgGlyValCysSerTyrLeu 87
DB 420 CGAGGGGTGTGTCTACTTA 440

RESULT 58

LOCUS B6740396

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4779449"
/lab_host="DH10B (T1 phage-resistance)"
/clone_lib="NCI CGAP_Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

ORIGIN

Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

Alignment Scores:

Pred. No.:	1.49e-46	Length:	870
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BG740396 (1-870)

QY 1 MetGUAGAlaLeuAsnSerTyRheGluProProValGluGluSerAlaLeuGluArg 20

DB 71 ATGGAAAGGGCTGTGAACCTCACTCGAGCCTCCGGTGAAGAGAGCGCCTTGGAACGC 130

QY 21 ATGProGUThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40

DB 131 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACACT 190

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

DB 191 GATTCCACCATCTTAAATATCAAGCCCATCTGAAGATACACAGAAAGAAATGCGAGCATG 250

QY 61 PheSerIleuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80

DB 251 TTCTCTCATTAACCTGGAATATGATGATTAGATTAACAATCTGTCAAGAGAGGCT 310

QY 81 ArgGlyValCysSerTyrLeu 87

DB 311 CGAGGGGTGTCTCTACTTA 331

RESULT 59

LOCUS BUI59911

DEFINITION AGENCOURT_7913863 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6144208

5', mRNA sequence.

ACCESSION BUI59911

VERSION BUI59911.1 GI:22673821

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homniidae; Homo.

1 (bases 1 to 870)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM13468 row: n column: 17

High quality sequence stop: 677.

Location/Qualifiers

1.870

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6144208"

/tissue_type="retinoblastoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_67"

/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

ORIGIN

Average insert size 1.75 kb. Library constructed by Life Technologies."

Alignment Scores:

Pred. No.:	1.49e-46	Length:	870
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BUI59911 (1-870)

QY 1 MetGUAGAlaLeuAsnSerTyRheGluProProValGluGluSerAlaLeuGluArg 20

DB 95 ATGGAAAGGGCTGTGAACCTCACTCGAGCCTCCGGTGAAGAGAGCGCCTTGGAACGC 154

QY 21 ATGProGUThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40

DB 155 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAACACT 214

QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60

DB 215 GATTCCACCATCTTAAATATCAAGCCCATCTGAAGATACACAGAAAGAAATGCGAGCATG 274

QY 61 PheSerIleuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80

DB 275 TTCTCTCATTAACCTGGAATATGATGATTAGATTAACAATCTGTCAAGAGAGGCT 334

QY 81 ArgGlyValCysSerTyrLeu 87

DB 335 CGAGGGGTGTCTCTACTTA 355

RESULT 60

LOCUS BUI69945

DEFINITION AGENCOURT_7913097 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6024760

5', mRNA sequence.

ACCESSION BUI69945

VERSION BUI69945.1 GI:22683929

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homniidae; Homo.

1 (bases 1 to 883)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DP/Gapzar

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM13235 row: m column: 17

High quality sequence stop: 413.

Location/Qualifiers

1.883

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6024760"

/tissue_type="large cell carcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_68"

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.fasta

Page 38

ORIGIN Average insert size 1.8 kb. Library constructed by Life Technologies. "

Alignment Scores:

Pred. No.: 1.52e-46 Length: 883
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BU169945 (1-883)

OY 1 MetGUArgAlaLeuAseSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 40 ATGGAAAGGGCTCTGAACCTCTACCTTCGAGCCTCGGGTGGAGAGAGCGCTTGAAAGCG 99
OY 21 ArgProGluThrIleSerGluProIleThrTYrValAspLeuThrAsnGluGluThrThr 40
DB 100 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGCTTGCCTAACCAATGAGAAACAACCT 159
OY 41 AspSerThrTherSerIleSerProSerGluAspThrGluGluGluAsnGlySerMet 60
DB 160 GATTCACCACTTCTTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGCGAGCATG 219
OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 220 TTCTCTCATTAACCTGGAATATTGATGATTAGATCTTAAACATCTGTCAAGAGGGCT 279
OY 81 ArgGlyValCysSerTYrLeu 87
DB 280 CGAGGGGTGTCTTCTTACTTA 300

RESULT 61

BU179107 883 bp mRNA linear EST 04-SEP-2002
LOCUS BU179107
DEFINITION AGENCOURT 7984768 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6174958

5' mRNA sequence.

ACCESSION BU179107

VERSION BU179107.1 GI:22693091

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source
1
883
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="6174958"
/feature_type="leiomysarcoma"
/lab_host="DH10B (phage resistant)"
/clone_lib="NIH MGC_71"
/notes="Organ: Uterus; Vector: pCMV-SPORT6; Site: 1: Nof1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dir.

ORIGIN Average insert size 2.1 kb. "

Alignment Scores:

Pred. No.: 1.52e-46 Length: 883
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BU179107 (1-883)

OY 1 MetGUArgAlaLeuAseSerTYrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 18 ATGGAAAGGGCTCTGAACCTCTACCTTCGAGCCTCGGGTGGAGAGAGCGCTTGAAAGCG 77
OY 21 ArgProGluThrIleSerGluProIleThrTYrValAspLeuThrAsnGluGluThrThr 40
DB 78 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGCTTGCCTAACCAATGAGAAACAACCT 137
OY 41 AspSerThrTherSerIleSerProSerGluAspThrGluGluGluAsnGlySerMet 60
DB 138 GATTCACCACTTCTTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGCGAGCATG 197
OY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 198 TTCTCTCATTAACCTGGAATATTGATGATTAGATCTTAAACATCTGTCAAGAGGGCT 257
OY 81 ArgGlyValCysSerTYrLeu 87
DB 258 CGAGGGGTGTCTTCTTACTTA 278

RESULT 62

CD251503 906 bp mRNA linear EST 22-MAY-2003
LOCUS CD251503
DEFINITION AGENCOURT 14212105 NIH MGC 179 Homo sapiens cDNA clone

IMAGE:30385385 5' mRNA sequence.

ACCESSION CD251503

VERSION CD251503.1 GI:31011969

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source
1
906
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="30385385"
/feature_type="pilocytic"
/lab_host="DH10B (non 71 and 75 phage resistances)"
/clone_lib="NIH_MGC_79"

FEATURES
source

Location/Qualifiers
1. .948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDBK007YK05"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.67e-46 Length: 948
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AL555333 (1-948)

QY 1 MetGluArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 179 ATGGAAAAGGCTCTGAACTCTGAACTCTGAGCCTCCGGTGGAGAGAGCGCCCTTGGAAAGC 238
QY 21 ArgProGluThrIleSerGluProGluThrTyValAspLeuThrAsnGluGluThr 40
Db 239 CGACCTGAAACCATCTCTGAGCCCAAGACCATGTGACCTAAACCATGAGAAACAAC 298
QY 41 AspSerThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 239 GATTCACCACTCTTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGGCAGCATG 358
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 359 TTCTCTCATTAACCTGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 418
QY 81 ArgGlyValCysSerTyLeu 87
Db 419 CGAGGGGTGTCTCTACTTA 439

RESULT 65
B1161201 959 bp mRNA linear EST 05-JUL-2001
LOCUS B1161201
DEFINITION 60286565921 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019639 5',
mRNA sequence.
ACCESSION B1161201
VERSION B1161201.1 GI:14621202
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 959)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LICM1835 row: e column: 16
High quality sequence stop: 551.

FEATURES
source

Location/Qualifiers
1. .959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5019639"
/issue="IMAGE:5019639"
/issue_type="epithelioid carcinoma cell line"
/lab_host="VH10B (phage-resistant)"
/clone_lib="NIH_MGC_42"
/note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald W. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 1.7e-46 Length: 959
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x B1161201 (1-959)

QY 1 MetGluArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 178 ATGGAAAAGGCTCTGAACTCTGAACTCTGAGCCTCCGGTGGAGAGAGCGCCCTTGGAAAGC 237
QY 21 ArgProGluThrIleSerGluProGluThrTyValAspLeuThrAsnGluGluThr 40
Db 238 CGACCTGAAACCATCTCTGAGCCCAAGACCATGTGACCTAAACCATGAGAAACAAC 297
QY 41 AspSerThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
Db 298 GATTCACCACTCTTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGGCAGCATG 357
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 358 TTCTCTCATTAACCTGGATATGATGATGATGATGATGATGATGATGATGATGATGAT 417
QY 81 ArgGlyValCysSerTyLeu 87
Db 418 CGAGGGGTGTCTCTACTTA 438

RESULT 66
BM468826 972 bp mRNA linear EST 05-FEB-2002
LOCUS BM468826
DEFINITION 6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154
5', mRNA sequence.
ACCESSION BM468826
VERSION BM468826.1 GI:18517868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 972)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LLM12356 row: d column: 03
 High quality sequence stop: 707.
 Location/Qualifiers

FEATURES

1..972
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5587154"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_11b="NIH_MGC_92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	1.73e-46	Length:	972
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BM468826 (1-972)

QY 1 MetGUAAGAlaLeuAnsSerTyrrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 55 ATGGAAAGGGCTCTGAACCTCTACTCGAGCCTCCGCTGAGAGAGCCCTTGGAAACC 114
 QY 21 ATGProGluThrIleSerGluProGlyThrTyrrValAspLeuThraSngluGluThrThr 40
 DB 115 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTTAACCAATGAAGAAACAAC 174
 QY 41 AApSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 175 GATTCACACCTCTTAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGCGACGATG 234
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 235 TTCTCTCATTAACCTGGAATATGATGATTAAGATCAACATCTGTGAGAGAGGCT 294
 QY 81 ATGGLyValCyseSerTyrrLeu 87
 DB 295 CGAGGGGTGTCTTCTACTTA 315

RESULT 67
 LOCUS BX338160 981 bp mRNA linear EST 08-APR-2004
 DEFINITION BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1056YC23.5-PRIME, mRNA sequence.
 ACCESSION BX338160
 VERSION BX338160.2 GI:46283046
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 981)
 REFERENCE 1 Li, W.-B., Gruber, C., Jesse, J., and Polayes, D.
 AUTHORS Full-length cDNA libraries and normalization
 TITLE Unpublished (2001)
 JOURNAL On May 2, 2003 this sequence version replaced gi:30345671.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segre@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna78/CS0D1056AB12QPlc=3474.r>.
 Location/Qualifiers

FEATURES

1..981
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1056YC23"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_11b="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	1.75e-46	Length:	981
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BX338160 (1-981)

QY 1 MetGUAAGAlaLeuAnsSerTyrrPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 173 ATGGAAAGGGCTCTGAACCTCTACTCGAGCCTCCGCTGAGAGAGCCCTTGGAAACC 232
 QY 21 ATGProGluThrIleSerGluProGlyThrTyrrValAspLeuThraSngluGluThrThr 40
 DB 233 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTGACCTTAACCAATGAAGAAACAAC 292
 QY 41 AApSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 293 GATTCACACCTCTTAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGCGACGATG 352
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 353 TTCTCTCATTAACCTGGAATATGATGATTAAGATCAACATCTGTGAGAGAGGCT 412
 QY 81 ATGGLyValCyseSerTyrrLeu 87
 DB 413 CGAGGGGTGTCTTCTACTTA 433

RESULT 68
 LOCUS BE892886 995 bp mRNA linear EST 20-OCT-2000
 DEFINITION 601435730F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3920790 5', mRNA sequence.
 ACCESSION BE892886
 VERSION BE892886.1 GI:10353510
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 995)
 REFERENCE NIH-MGC <http://mhc.nci.nih.gov/>.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1998)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC/DC/DTP
 cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
<http://image.lnl.gov>
Plate: L1M9752 row: 1 column: 07
High quality sequence stop: 573.

FEATURES
source

1. 995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3920790"
/issue_type="metastatic melanoma"
/lab_host="DH108 (phage-resistant)"
/clone_lib="NIH-MGC_12"
/note="Organ: SKIN; Vector: PCW-SPORT6; Site: 1: NotI,
Site 2: SalI. Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 1.78e-46 Length: 995
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BB992886 (1-995)

QY 1 MetGluArgAlaLeuAerSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 189 ATGGAAAGGGCTCTGAACCTCTACTCTGAGCCTCGGAGGAGGAGACCGCTTGAAACCC 248
QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
Db 249 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAAGAACACT 308
QY 41 AspSerThrSerTyIleSerProSerGluAapThrGluGluGluAsnGlySerMet 60
Db 309 GATTCACCACTCTTAAATCAGCCCATCTCAAGATCTCAGCAAGAAATGGCAGCATG 368
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAapLeuAenAenLeuSerGluArgAla 80
Db 369 TTCTCTCATTAACCTGGAATATGATGATTGATTAACCAATCTGTCAAGAGGCT 428
QY 81 ArgGlyValCysSerTyLeu 87
Db 429 CGAGGGGTGTGTTCTTACTTA 449

RESULT 69
BX337141 1018 bp mRNA linear EST 07-APR-2004
LOCUS BX337141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION Clone CSOD1036Y02 5-PRIME, mRNA sequence.
ACCESSION BX337141
VERSION BX337141.2 GI:46271144
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 2, 2003 this sequence version replaced gi:3037585.
Genoscope - Centre National de Sequencage
Contact: Genoscope
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCWSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdnats=CSOD1036E01QPlc=3474.r>.

FEATURES
source

1. 1018
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1036Y02"
/issue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the PCWSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 1.84e-46 Length: 1018
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX337141 (1-1018)

QY 1 MetGluArgAlaLeuAerSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
Db 150 ATGGAAAGGGCTCTGAACCTCTACTCTGAGCCTCGGAGGAGGAGACCGCTTGAAACGC 209
QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
Db 210 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAAGAACACT 269
QY 41 AspSerThrSerTyIleSerProSerGluAapThrGluGluGluAsnGlySerMet 60
Db 270 GATTCACCACTCTTAAATCAGCCCATCTCAAGATCTCAGCAAGAAATGGCAGCATG 329
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAapLeuAenAenLeuSerGluArgAla 80
Db 330 TTCTCTCATTAACCTGGAATATGATGATTGATTAACCAATCTGTCAAGAGGCT 389
QY 81 ArgGlyValCysSerTyLeu 87
Db 390 CGAGGGGTGTGTTCTTACTTA 410

RESULT 70
BM554324 1035 bp mRNA linear EST 20-FEB-2002
LOCUS BM554324
DEFINITION AGENCOUT 6546794 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742466
5', mRNA sequence.
ACCESSION BM554324
VERSION BM554324.1 GI:18793827
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo (1035)

REFERENCE
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gsab@remail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
 Plate: LLM12760 row: k column: 11
 High quality sequence stop: 738.

FEATURES

source

Location/Qualifiers

1..1035
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742466"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /clone_1ib="NIH_MGC_119"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 1,88e-46 Length: 1035
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BMS54324 (1-1035)

QY 1 MetGUAAGAlaLeuAnsSerTyRPhGluProProValIGluSerAlaLeuGluArg 20
 DB 332 ATGGAAGGGCTCTGAACCTCACTTCGAGCTCCGGTGAAGAGAGCCCTTGGAACCC 391
 QY 21 ATGProGluThrIleSerGluProLysThrTyRValAspLeuThrAsnGluGluThrThr 40
 DB 392 CCACTGGAACCATCTCTAGCCCAAGACCTATGTTGACCTTAACATAGAGAACACT 451
 QY 41 AppSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 452 GATTCACCACTTCTTAATCAAGCCCATCTGAAGATCACTCAAGAAATGGAGCATG 511
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 512 TTCTCTCATTAACCTGAATATGATGATTAGATTAAACAATCTGTCAAGAGGGCT 571
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 572 CGAGGGGTGTCTCTACTTA 592

RESULT 71

LOCUS BX337905 1067 bp mRNA linear EST 07-APR-2004
 DEFINITION BX337905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 clone CS0D1052YNI3 5-PRIME, mRNA sequence.
 ACCESSION BX337905
 VERSION BX337905.2 GI:46273926
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1067)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE

JOURNAL

COMMENT

Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30339657.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r

FEATURES

source

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0D1052CG07QPL&c=3474.r>.

ORIGIN

Alignment Scores:

Pred. No.: 1,95e-46 Length: 1067
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX337905 (1-1067)

QY 1 MetGUAAGAlaLeuAnsSerTyRPhGluProProValIGluSerAlaLeuGluArg 20
 DB 184 ATGGAAGGGCTCTGAACCTCACTTCGAGCTCCGGTGAAGAGAGCCCTTGGAACCC 243
 QY 21 ATGProGluThrIleSerGluProLysThrTyRValAspLeuThrAsnGluGluThrThr 40
 DB 244 CCACTGGAACCATCTCTAGCCCAAGACCTATGTTGACCTTAACCAATGAAGAAACAAC 303
 QY 41 AppSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 304 GATTCACCACTTCTTAATCAAGCCCATCTGAAGATCACTCAAGAAATGGAGCATG 363
 QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 364 TTCTCTCATTAACCTGAATATGATGATTAGATTAAACAATCTGTCAAGAGGGCT 423
 QY 81 ArgGlyValCysSerTyrLeu 87
 DB 424 CGAGGGGTGTCTCTACTTA 444

RESULT 72

LOCUS BX444691 1081 bp mRNA linear EST 04-MAY-2004
 DEFINITION BX444691 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 CS0DN005YNO2 5-PRIME, mRNA sequence.
 ACCESSION BX444691
 VERSION BX444691.2 GI:47009162
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1081)
 AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

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us-10-757-745-2_copy_54_140.rst

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AUTHORS
Li, W.B., Gruber, C., Jesses, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30780264.
COMMENT

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CSODN05DQ01Q1&c=3474.r.
FEATURES
Location/Qualifiers
1..1081
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN05YNO2"
/cissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_1ib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.:	1..99e-46	Length:	1081
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BX444691 (1-1081)

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QY      1  MetGluArgAlaLeuAseSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
DB      186  ATGGAAGAGGCTCTGAACCTCTACTTCAGCCCTCCGCTGAGAGAGAGCCCTTGGAACGC 245
QY      21  ArgProGluThrIleSerGluProIleThrTyValAspLeuThrAsnGluGluThr 40
DB      246  CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAACACT 305
QY      41  AspSerThrThSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB      306  GATTCACACCACTCTAAATCAAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATG 365
QY      61  PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnIleuSerGluArgAla 80
DB      366  TTCTCTCATTAACCTGGAATATGATGATTGATTGAATCTAAACAATCTGTCAGAGAGGCT 425
QY      81  ArgGlyValCysSerTyIleu 87
DB      426  CGAGGGGTGTGTTCTTACTTA 446
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RESULT 73
LOCUS DQ049205 1089 bp DNA linear GSS 02-JUN-2005
DEFINITION Homo sapiens TTRAP gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ049205
VERSION DQ049205.1 GI:66902404
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
1 (bases 1 to 1089)
Nielsen, R., Buettmann, C., Clark, A.G., Gnanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(et) Plos Biol. 3 (6), E170 (2005)
2 (bases 1 to 1089)
Nielsen, R., Buettmann, C., Clark, A.G., Gnanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-May-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES

Location/Qualifiers
1..1089
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
1..>1089
/gene="TTRAP"
/locus_tag="HC17203"

ORIGIN

Alignment Scores:

Pred. No.:	2.01e-46	Length:	1089
Score:	448.00	Matches:	87
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x DQ049205 (1-1089)

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QY      1  MetGluArgAlaLeuAseSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
DB      160  ATGGAAGAGGCTCTGAACCTCTACTTCAGCCCTCCGCTGAGAGAGAGCCCTTGGAACGC 219
QY      21  ArgProGluThrIleSerGluProIleThrTyValAspLeuThrAsnGluGluThr 40
DB      220  CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAACACT 279
QY      41  AspSerThrThSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB      280  GATTCACACCACTCTAAATCAAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCATG 339
QY      61  PheSerLeuIleThrTTPAsnIleAspGlyLeuAspLeuAsnIleuSerGluArgAla 80
DB      340  TTCTCTCATTAACCTGGAATATGATGATTGATTGAATCTAAACAATCTGTCAGAGAGGCT 399
QY      81  ArgGlyValCysSerTyIleu 87
DB      400  CGAGGGGTGTGTTCTTACTTA 420
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RESULT 74
LOCUS BM555041 1103 bp mRNA linear EST 20-FEB-2002
DEFINITION AGNCOURT_6545705 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737150
5', mRNA sequence.
ACCESSION BM555041
VERSION BM555041.1 GI:18795166
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 1103)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strusberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Place: LNL12746 row: m column: 23
 High quality sequence stop: 678.
 Location/Qualifiers
 1..1103

FEATURES
 source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5737150"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_88"
 /note="Organ: small intestine; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 2,04e-46 Length: 1103
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BM555041 (1-1103)

QY 1 MetGUAAGAlaLeuAenSerTyRheGluProProValAGluGluSerAlaLeuGluArg 20
 DB 189 ATGAAAGGGCTCTGAACCTCTACTTCAGGCTCCGGTGAAGAGAGCGCTTGAAAGCC 248
 QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
 DB 249 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGACTTAACCAATGAAGAAACAAC 308
 QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 309 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACATG 368
 QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 369 TTCCTCTCATTAACCTGGAATATGATGATTAATCAATCAATCTGTCAAGAGGGCT 428
 QY 81 ArgGlyValCysSerTyLeu 87
 DB 429 CGAGGGGTGTGTCTCTACTTA 449

RESULT 75
 LOCUS CR601303 1168 bp mRNA linear HTC 21-JUL-2004
 DEFINITION full-length cDNA clone CS0DN005YN02 of Adult brain of Homo sapiens (human).
 ACCESSION CR601303
 VERSION CR601303.1 GI:50482110
 KEYWORDS HTC; cDNA; cDNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1168)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Feng Liang Email: fling@life.technet.com URL: <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Paraday Avenue
 2 (bases 1 to 1168)
 Genoscope.
 Direct Submission

REFERENCE 2 (bases 1 to 1168)
 AUTHORS Genoscope.
 TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: segreg@genoscope.cns.fr)
 JOURNAL - Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

COMMENT

FEATURES
 source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DN005YN02"
 /tissue_type="Adult brain"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
 Pred. No.: 2.2e-46 Length: 1168
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR601303 (1-1168)

QY 1 MetGUAAGAlaLeuAenSerTyRheGluProProValAGluGluSerAlaLeuGluArg 20
 DB 185 ATGAAAGGGCTCTGAACCTCTACTTCAGGCTCCGGTGAAGAGAGCGCTTGAAAGCC 244
 QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrThr 40
 DB 245 CGACCTGAACCACTCTGAGCCCAAGACCTATGTGACTTAACCAATGAAGAAACAAC 304
 QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 305 GATTCACCACTCTTAATAATCAGCCCATCTGAAGATCTCAGCAAGAAATGCGACATG 364
 QY 61 PheSerLeuIleThrTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 365 TTCCTCTCATTAACCTGGAATATGATGATTAATCAATCAATCTGTCAAGAGGGCT 424
 QY 81 ArgGlyValCysSerTyLeu 87
 DB 425 CGAGGGGTGTGTCTCTACTTA 445

RESULT 76
 LOCUS BM553049 1192 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT 6542413 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742798 5', mRNA sequence.
 ACCESSION BM553049
 VERSION BM553049.1 GI:18791437
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

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US-10-757-745-2_copy_54_140.rst

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REFERENCE 1 (bases 1 to 1192)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L1AM12761 row: 1 column: 07
High quality sequence stop: 747.

FEATURES
source
1..1192
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742798"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_11b="NIH_MGC_119"
/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 2,266-46 Length: 1192
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BM553049 (1-1192)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 217 ATGAAAGGGCTGAACTCTTAACCTTCGAGCTCCGGTGGAGAGAGCCCTTGGAAAGC 276
QY 21 ArgProGluThrIleSerGluProValThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 277 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAGAAACAAC 336
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGln 60
DB 337 GATTCACACACTTCTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGGCAGCATG 396
QY 61 PheSerLeuIleThrTyrPheIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 397 TTCTCTCATTAACCTCGAATATTAATGATTAAGTCTAAACCAATGTCGAGAGGGCT 456
QY 81 ArgGlyValCysSerTyrLeu 87
DB 457 CAGAGGGGTGTGTTCTACTTA 477

RESULT 77
CR592636 1620 bp mRNA linear HTC 21-JUL-2004
LOCUS CR592636
DEFINITION Full-length cDNA clone CS0DM007YB11 of Fetal liver of Homo sapiens (human)
ACCESSION CR592636
VERSION CR592636.1 GI:50473443
KEYWORDS HTC; CNSLT_CDNA.

SOURCE
ORGANISM Homo sapiens (human)
Homosapiens
Sukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 1620)

REFERENCE 1 (bases 1 to 1620)
AUTHORS Li, W.B., Gruber, C., Jeesee, J. and Polyses, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Peng Liang Email: fliang@life.uchicago.edu
<http://fulllength.invitrogen.com/> invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1620)

REFERENCE
AUTHORS Genoscope,
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequencage@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the PCMVSPORT 6 vector Library
was normalized. Library was constructed by Life Technologies, a
division of invitrogen.

FEATURES
source
1..1620
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YB11"
/tissue_type="fetal liver"
/plasmid="PCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 3,386-46 Length: 1620
Score: 448.00 Matches: 87
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR592636 (1-1620)

QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 103 ATGAAAGGGCTGAACTCTTAACCTTCGAGCTCCGGTGGAGAGAGCCCTTGGAAAGC 162
QY 21 ArgProGluThrIleSerGluProValThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 163 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAGAAACAAC 222
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGlnGlnGlnGlnGlnGln 60
DB 223 GATTCACACACTTCTAAATCAGCCCATCTGAGATCTCAGCAAGAAATGGCAGCATG 282
QY 61 PheSerLeuIleThrTyrPheIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 283 TTCTCTCATTAACCTCGAATATTAATGATTAAGTCTAAACCAATGTCGAGAGGGCT 342
QY 81 ArgGlyValCysSerTyrLeu 87
DB 343 CAGAGGGGTGTGTTCTACTTA 363

RESULT 78
CR597293 1894 bp mRNA linear HTC 21-JUL-2004
LOCUS CR597293
DEFINITION Full-length cDNA clone CS0DK007YK05 of HeLa cells Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNSLT_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1894)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1894)

REFERENCE 2 (bases 1 to 1894)
 AUTHORS Direct Submission
 TITLE Genoscope.
 JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage: BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
 source Location/Qualifiers
 1..1894

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK007YK05"
 /tissue_type="Hela cells Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
 Pred. No.: 4.14e-46 Length: 1894
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR597293 (1-1894)

QY 1 MetGUATGAlaLeuanserTyrPhegluProProvalgluGluserAlaLeuGluaarg 20
 DB 178 ATGGAAGGGCTCTGAACCTCTTCACTTCGAGCTCCGGTGAAGAGAGGCCCTTGAAGCC 237
 QY 21 ArgProgluThrIleSerGluprolysthrTyValaspLeuThrasngluThrThr 40
 DB 238 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAACCAATGAGAAACAAC 297
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluasnGlyserMet 60
 DB 238 GATTCACCACTTCAAAATCAGCCCATCTGAAGATCTACAGCAAGAAATGCGAGCAG 357
 QY 61 PheSerLeuIleThrTAsnIleaspGlyLeuaspLeuAsnAsnLeuSerGluArgala 80
 DB 358 TTCTCTCATTAACCTGGAATATTGATGATTAAGATCTAAACAATCTGCAAGAGGGCT 417
 QY 81 ArgGlyValCysSerTyrIleu 87
 DB 418 CGAGGGGTGTGTTCTACTTA 438

RESULT 79

LOCUS CR595644 1909 bp mRNA linear HTC 21-JUL-2004
 DEFINITION full-length cDNA clone CSOD1052YN13 of Placenta Cot 25-normalized of Homo sapiens (human).
 ACCESSION CR595644
 VERSION CR595644.1 GI:50476451
 KEYWORDS HTC, CNSUT_cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 581)
 AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 1909)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1909)

REFERENCE 2 (bases 1 to 1909)
 AUTHORS Direct Submission
 TITLE Genoscope.
 JOURNAL Submitted (20-JUN-2004) Genoscope - Centre National de Sequencage: BP 191 91006 Evry cedex - FRANCE (E-mail: sequef@genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES
 source Location/Qualifiers
 1..1909

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSOD1052YN13"
 /tissue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
 Pred. No.: 4.19e-46 Length: 1909
 Score: 448.00 Matches: 87
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR595644 (1-1909)

QY 1 MetGUATGAlaLeuanserTyrPhegluProProvalgluGluserAlaLeuGluaarg 20
 DB 184 ATGGAAGGGCTCTGAACCTCTTCACTTCGAGCTCCGGTGAAGAGAGGCCCTTGAAGCC 243
 QY 21 ArgProgluThrIleSerGluprolysthrTyValaspLeuThrasngluThrThr 40
 DB 244 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTTGACCTAAACCAATGAGAAACAAC 303
 QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluasnGlyserMet 60
 DB 304 GATTCACCACTTCAAAATCAGCCCATCTGAAGATCTACAGCAAGAAATGCGAGCAG 363
 QY 61 PheSerLeuIleThrTAsnIleaspGlyLeuaspLeuAsnAsnLeuSerGluArgala 80
 DB 364 TTCTCTCATTAACCTGGAATATTGATGATTAAGATCTAAACAATCTGCAAGAGGGCT 423
 QY 81 ArgGlyValCysSerTyrIleu 87
 DB 424 CGAGGGGTGTGTTCTACTTA 444

RESULT 80

LOCUS AV717253 581 bp mRNA linear EST 16-OCT-2000
 DEFINITION AV717253 DCB Homo sapiens cDNA clone DCBMA04 5', mRNA sequence.
 ACCESSION AV717253
 VERSION AV717253.1 GI:10814405
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 581)
 AUTHORS Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J.,
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

TITLE
JOURNAL
COMMENT
Seng, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X.,
Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Cheng, Z., and Han, Z.
Homo sapiens cDNA DB clones
Unpublished (2000)
Contract: Zengang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhongjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
Source
Location/Qualifiers

1..581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBMA04"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_id="DCB"
/note="Vector: pTRIPlex2; Site_1: sf1A; Site_2: sf1B"

ORIGIN

Alignment Scores:
Pred. No.: 2,13e-46 Length: 581
Score: 445.00 Matches: 86
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 98.9% Mismatches: 0
Query Match: 99.3% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AV1717253 (1-581)

QY 1 MetGUAAGAlaleuAenSerTYRPhgIuPProProValAGluGluSerAlaleuGluArg 20
Db 3 ATGGAAGGCTCTCGAAGCTCTCTGAGCTCCGCGGAGGAGAGCGCTTGGAAGCG 62
QY 21 ArgProGluThrIleSerGluProLysThrTYRValAAspLeuThrAengGluThrThr 40
Db 63 CGACCTGAAACCATCTCTGAGCCAGACCTTGTGACCTTAACCAATGAAAGAAACAAC 122
QY 41 AAspSerThrThrSerIleSerProSerGluAAspThrGluGluGluAengIysSerMet 60
Db 123 GATCCACCACTTCTTAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGAGCAG 182
QY 61 PhsSerLeuIleThrTPAenIleAAspGlyLeuAAspLeuAenAenSerGluArgAla 80
Db 183 TTCTCTCATTTACCTGGAATATTGATGATTAATCTTAACCAATCTGTCAAGAGGCGT 242
QY 81 ArgGlyValCysSerTYRLeu 87
Db 243 CGAGGGGTGTGTTCTTACTTA 263

RESULT 81

BP234218 582 bp mRNA linear EST 15-SEP-2004
LOCUS BP234218 Sugano cDNA library, coronary artery endothelial cell Homo
DEFINITION sapiens cDNA clone HCR02378, mRNA sequence.
ACCESSION BP234218
VERSION BP234218.1 GI:52107128
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 582)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous

JOURNAL
PUBMED
COMMENT
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ime.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
Source

1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR02378"
/issue_type="coronary artery"
/cell_type="endothelial cell"
/clone_id="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN

Alignment Scores:
Pred. No.: 2,87e-46 Length: 582
Score: 444.00 Matches: 86
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 98.9% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP234218 (1-582)

QY 1 MetGUAAGAlaleuAenSerTYRPhgIuPProProValAGluGluSerAlaleuGluArg 20
Db 187 ATGGAAGGCTCTCGAAGCTCTCTGAGCTCCGCGGAGGAGAGCGCTTGGAAGCG 246
QY 21 ArgProGluThrIleSerGluProLysThrTYRValAAspLeuThrAengGluThrThr 40
Db 247 CGACCTGAAACCATCTCTGAGCCAGACCTTGTGACCTTAACCAATGAAAGAAACAAC 306
QY 41 AAspSerThrThrSerIleSerProSerGluAAspThrGluGluGluAengIysSerMet 60
Db 307 GATTCACCACTTCTTAATCAGCCCATCTGAAGATACCTCAGCAAGAAATGCGAGCAG 366
QY 61 PhsSerLeuIleThrTPAenIleAAspGlyLeuAAspLeuAenAenSerGluArgAla 80
Db 367 TTCTCTCATTTACCTGGAATATTGATGATTAATCTTAACCAATCTGTCAAGAGGCGT 426
QY 81 ArgGlyValCysSerTYRLeu 87
Db 427 CGAGGGGTGTGTTCTTACTTA 447

RESULT 82

BP233592 582 bp mRNA linear EST 15-SEP-2004
LOCUS BP233592 Sugano cDNA library, coronary artery endothelial cell Homo
DEFINITION sapiens cDNA clone HCR00774, mRNA sequence.
ACCESSION BP233592
VERSION BP233592.1 GI:52106502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 582)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yszuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. .582
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_xref="HCR00774"
/tissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN

Alignment Scores:

Pred. No.:	3,85e-46	Length:	582
Score:	443.00	Matches:	86
Percent Similarity:	98.9%	Conservative:	0
Best Local Similarity:	98.9%	Mismatches:	1
Query Match:	98.9%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BP233592 (1-582)

QY 1 MetGUAAGAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 175 ATGGAAAGGGCTCTGAACCTCTACTCGAGCCTCCGCTGAGAGAGCCCTTGGAACCC 234
QY 21 ATGProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 225 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAAGAACACT 294
QY 41 AAppSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 295 GATTCACACACTCTCTAAATCAGCCCATCTGAAGATCTCAGCAAGAAACGACGACATG 354
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 355 TTCTCTCATTAACCTGGAATATGATGATTAGATCAACCAATCTGCAGAGAGGGCT 414
QY 81 ATGGLYValCySeSerTyrLeu 87
DB 415 CGAGGGGTGTGTCTCTACTTA 435

RESULT 83

BP262485

LOCUS BP262485 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION clone HS107111, mRNA sequence.

ACCESSION BP262485.1 GI:52177716

VERSION BP262485.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 572)

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki

DEPARTMENT Department of Medical Science, University of Tokyo

ADDRESS 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

EMAIL Email: yszuzuki@ims.u-tokyo.ac.jp.

LOCATION/Qualifiers

1. .572

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
/clone_xref="HS107111"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.:	9.11e-46	Length:	572
Score:	440.00	Matches:	85
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	98.8%	Mismatches:	0
Query Match:	98.2%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BP262485 (1-572)

QY 2 GUAGAAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 21
DB 119 CAGAGGGCTCTGAACCTCTACTCTGAGCCTCCGCTGAGAGAGCCCTTGGAACCCCA 178
QY 22 ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAsp 41
DB 179 CCGAAGACATCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAAAGAAACAATGAT 238
QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
DB 239 TCTCATTAACCTGGAATATGATGATTAGATCAACCAATCTGCAGAGGGCTCGA 298
QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
DB 299 TTCTCATTAACCTGGAATATGATGATTAGATCAACCAATCTGCAGAGGGCTCGA 358
QY 82 GLYValCySeSerTyrLeu 87
DB 359 GGGGTGTGTCTCTACTTA 376

RESULT 84

BP263516

LOCUS BP263516 Sugano cDNA library, small intestine Homo sapiens cDNA

DEFINITION clone HS11929, mRNA sequence.

ACCESSION BP263516.1 GI:52178747

VERSION BP263516.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE 1 (bases 1 to 582)

AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.TITLE Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki

DEPARTMENT Department of Medical Science, University of Tokyo

ADDRESS 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

EMAIL Email: yszuzuki@ims.u-tokyo.ac.jp.

LOCATION/Qualifiers

1. .582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_xref="HS11929"

/tissue_type="small intestine"

/clone_lib="Sugano cDNA library, small intestine"

Alignment Scores: Pred. No.: 9.32e-46 Length: 582

Score: 440.00 Matches: 85
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 98.8% Mismatches: 0
 Query Match: 98.2% Indels: 0
 Gaps: 0
 DB: 3

US-10-757-745-2_COPY_54_140 (1-87) x BP263516 (1-582)

QY 2 GUAAGALALEUANSERTYRPHGLUPROPROVALGUGLUSERALALEUAGUATGATG 21
 DB 129 CAGAGGGCTGGAACCTCTACTCTGAGCCCTCCGGTGAGAGAGAGCCCTTGGAACCCCGA 188
 QY 22 PROGLUTHTLIESERGLUPROLYERTHTYRVALAASPLEUTHRAENGUGLUTHTHRAAP 41
 DB 189 CCGAAGAACCATCTCGAGCCCAAGACCTATGTTGACCTAACCAATGGAAGAAACAACTGAT 248
 QY 42 SERTHTHSETYSLIESERPROSERGLUAAPTHTNGINGINGUAENGISERMETPHE 61
 DB 249 TCACACACCTCTAAATACGCCCATCTGAAGATGACTGACGAGAAATGGCAGCATGTTCC 308
 QY 62 SETLEUHTHTTPAANILEASPGIYLEUASPLEUASPLEUASERGLUATGATGATG 81
 DB 309 TCTCTCATTTACCTGGAATATGATGATTAAGATCTTAACAATCTGTGAGAGAGGCTCGA 368
 QY 82 GIYVALCYSESTYRLEU 87
 DB 369 GGGGTGTGTCTCTACTTA 386

RESULT 85
 LOCUS BF977971 626 bp mRNA linear EST 22-JAN-2001
 DEFINITION 602148451P1 NIH_MGC_62 Homo sapiens CDNA clone IMAGE:4307317 5',
 mRNA sequence.
 VERSION BF977971
 KEYWORDS BF977971.1 GI:12345186
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 626)
 NIH-MGC http://mgs.nci.nih.gov/.
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: ATCC/DCTD/DTF
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLNL at:
 http://image.llnl.gov
 Plate: ILCM1177 row: e column: 14
 High quality sequence stop: 614.

FEATURES
 Location/Qualifiers

source

1..626
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4307317"
 /tissue_type="melanotic melanoma, high MDR"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH MGC 62"
 /note="Organ: skin; Vector: pDNR-LIB (Clontech); Site 1:
 SfiI (ggcgccctcgcc); Site 2: SfiI (ggccatcgcc)
 Double-stranded cDNA was prepared from cell lysate RNA. 5'
 and 3' adaptors were used in cloning as follows:
 adaptor sequence: 5'-CACGCGCATTTAGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCCGACGCGCCACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies

ORIGIN

contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA)."

Alignment Scores:

Pred. No.: 1,02e-45 Length: 626
 Score: 440.00 Matches: 85
 Percent Similarity: 100.0% Conservative: 2
 Best Local Similarity: 97.7% Mismatches: 0
 Query Match: 96.2% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BF977971 (1-626)

QY 1 METGLUAXALALEUANSERTYRPHGLUPROPROVALGUGLUSERALALEUAGUATG 20
 DB 174 ATGGAAGGGCTCTGAACCTCTACTCTGAGCCCTCCGGTGAGAGAGAGCCCTTGGAACCC 233
 QY 21 AXPPTGLUTHTLIESERGLUPROLYERTHTYRVALAASPLEUTHRAENGUGLUTHTH 40
 DB 234 CGACCTGGAACCATCTCGAGCCCAAGACCTATGTTGACCTTAACCAATGGAAGAAACAACT 293
 QY 41 AASPTHTHSETYSLIESERPROSERGLUAAPTHTNGINGINGUAENGISERMET 60
 DB 294 GATTCACACCTCTAAATACGCCCATCTGAAGATGACTGACGAGAAATGGCAGCATGTTCC 353
 QY 61 PHESERLEUHTHTTPAANILEASPGIYLEUASPLEUASPLEUASERGLUATGATGATG 80
 DB 354 TTTCTCTCATTTACCTGGAATATGATGATTAAGATCTTAACAATCTGTGAGAGGCT 413
 QY 81 ARGGLVALCYSESTYRLEU 87
 DB 414 CGAGGGTGTGTCTCTACTTA 434

RESULT 86
 LOCUS BX358707 942 bp mRNA linear EST 08-APR-2004
 DEFINITION BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
 clone CS0D1042YL19 5-PRIME, mRNA sequence.
 VERSION BX358707
 KEYWORDS BX358707.2 GI:46306560
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 942)
 I. N. B. Grueter, C. J. Jassie, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 5, 2003 this sequence version replaced gi:30378261.
 Contact: Genoscope
 Genoscope - Centre National de Séquençage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seq@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-Cligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0D1042CFL0P1ac=3474.r.

FEATURES
 Location/Qualifiers

source

1..942
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1042YL19"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_id="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ALIGNMENT SCORES:

Pred. No.:	1,75e-45	Length:	942
Score:	440.00	Matches:	85
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	98.8%	Mismatches:	0
Query Match:	98.2%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BM358707 (1-942)

QY 2 GUAAGALALEUANSERYTPHEGUAUPROVALGUGLUSERALALEUGUARG 21
 DB 32 CAGAGGGCTCTGAACCTCTACTCGAGCTCCGGTGAAGAGAGCGCTTGAGAGCCGA 91
 QY 22 PROGUHTRILLESERGLUPROLYSTHRTYRVALASPLEUTHASGLUGLUTHRAAP 41
 DB 92 CCGAAGACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAATGAT 151
 QY 42 SERTHTRSERLYSIESERPROSERGLUAPTRHNGINGLUASNGLYSERMETPHE 61
 DB 152 TCCACCACTTCTTAATACGCCCATCTGAAGATCTCAGCAGAAAGAAATGGCAGCATGTC 211
 QY 62 SERLEUILEHTRTPASNILEASPGIYLEUASPLEUASNAUSLEUSERGLUARG 81
 DB 212 TCTCATTAACCTGGAATATGATGATTAGATCTTAACAATCTGTCAAGAGGGCTGCA 271
 QY 82 GYVALCYSESTYTLU 87
 DB 272 GGGGTGTCTCTACTTA 289

RESULT 87
 BM926092 1046 bp mRNA linear EST 12-MAR-2002
 LOCUS AGENCOURT_6649780 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5764440
 DEFINITION 5', mRNA sequence.

ACCESSION BM926092
 VERSION BM926092.1 GI:19376471
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

FEATURES

source 1. 1046
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5764440"
 /lab_host="DH10B"
 /clone_1ib="NIH_MGC_114"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."

ALIGNMENT SCORES:

Pred. No.:	2.01e-45	Length:	1046
Score:	440.00	Matches:	85
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	98.8%	Mismatches:	0
Query Match:	98.2%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BM926092 (1-1046)

QY 2 GUAAGALALEUANSERYTPHEGUAUPROVALGUGLUSERALALEUGUARG 21
 DB 36 CAGAGGGCTCTGAACCTCTACTCGAGCTCCGGTGAAGAGAGCGCTTGAGAGCCGA 95
 QY 22 PROGUHTRILLESERGLUPROLYSTHRTYRVALASPLEUTHASGLUGLUTHRAAP 41
 DB 96 CCGAAGACCATCTGAGCCCAAGACCTATGTTGACCTAACCAATGAGAAACAATGAT 155
 QY 42 SERTHTRSERLYSIESERPROSERGLUAPTRHNGINGLUASNGLYSERMETPHE 61
 DB 156 TCCACCACTTCTTAATACGCCCATCTGAAGATCTCAGCAGAAAGAAATGGCAGCATGTC 215
 QY 62 SERLEUILEHTRTPASNILEASPGIYLEUASPLEUASNAUSLEUSERGLUARG 81
 DB 216 TCTCATTAACCTGGAATATGATGATTAGATCTTAACAATCTGTCAAGAGGGCTGCA 275
 QY 82 GYVALCYSESTYTLU 87
 DB 276 GGGGTGTCTCTACTTA 293

RESULT 88
 CR602029 1743 bp mRNA linear HTC 21-JUL-2004
 LOCUS Full-length cDNA clone CS001042Y119 of Placenta Cot 25-normalized
 DEFINITION of Homo sapiens (human).

ACCESSION CR602029
 VERSION CR602029.1 GI:50482836
 KEYWORDS HTC; CNSLT_cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

REFERENCE NIH-MGC http://mgi.nci.nih.gov/
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
 TITLE Unpublished (1999)
 JOURNAL Contact: Robert Strausberg, Ph.D.
 COMMENT Email: cga@bbs-rmail.nih.gov

FEATURES

Location/Qualifiers

source

1..1743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS001047113"
/issue_type="placenta"
/issue_type="placenta"
/plasmid="PCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.: 3.92e-45 Length: 1743
Score: 440.00 Matches: 85
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 98.8% Mismatches: 0
Query Match: 98.2% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CRE02029 (1-1743)

QY 2 GUARGALAEUAASerTYrPheGluProProVALGluGluSerAlaLeuGluArg 21
Db 32 CAGAGGGCTCTGAACCTCTAATCGAGCTCCGGTGAAGAGAGAGCGCTTGAAACCGCA 91
QY 22 ProGluThrIleSerGluProLYrThrTYrValAspLeuThrAsnGluGluThrAsp 41
Db 92 CCGAAGACATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAAGAAACATGAT 151
QY 42 SerThrThrSerLYrIleSerProSerGluAspThrGluGluGluAsnGlySerMetPhe 61
Db 152 TCACACACTTCTAAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATGTTT 211
QY 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg 81
Db 212 TCTCTCATTAACCTGGAATATGATGATTAAGATCTTAAACATCTGTCAAGAGCGCTCGA 271
QY 82 GlyValCysSerTYrLeu 87
Db 272 GGGGTGTCTCTACTTA 289

RESULT 89
AUI39147 752 bp mRNA linear EST 02-AUG-2002
LOCUS AUI39147 PLACE1 Homo sapiens cDNA clone PLACE1010031 5', mRNA
DEFINITION AUI39147 PLACE1 Homo sapiens cDNA clone PLACE1010031 5', mRNA
ACCESSION AUI39147
VERSION AUI39147
KEYWORDS AUI39147.1 GI:11000668
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 752)
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Isegai, T.

REFERENCE
AUTHORS
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isegai
Genomics Laboratory
Helix Research Institute
153-3 Yana, Kiasarezu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'- and one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

1..752
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="PLACE1010031"
/issue_type="placenta"
/clone_type="placenta"
/note="vector: pM18SFJ3"

ORIGIN

Alignment Scores:
Pred. No.: 1.75e-45 Length: 752
Score: 439.00 Matches: 86
Percent Similarity: 98.9% Conservative: 0
Best Local Similarity: 98.9% Mismatches: 1
Query Match: 98.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AUI39147 (1-752)

QY 1 MetGluArgAlaLeuAsnSerTYrPheGluProProVALGluGluSerAlaLeuGluArg 20
Db 160 ATGGAAGGCTCTGAACCTCTAATCGAGCTCCGGTGAAGAGAGAGCGCTTGAAACCGC 219
QY 21 ArgProGluThrIleSerGluProLYrThrTYrValAspLeuThrAsnGluGluThrAsp 40
Db 220 CGACCTGAAACATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAAGAAACAACT 279
QY 41 AspSerThrThrSerLYrIleSerProSerGluAspThrGluGluGluAsnGlySerMetPhe 60
Db 280 GATTCACACATCTTAAATCAAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGCATG 339
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 340 TTTCTCTCATTAACCTGGAATATGATGATTAAGATCTTAAACATCTGTCAAGAGCGCT 399
QY 81 ArgGlyValCysSerTYrLeu 87
Db 400 CGAGGGGTGTCTCTACTTA 420

RESULT 90
BX365835 783 bp mRNA linear EST 08-APR-2004
LOCUS BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
ACCESSION BX365835
VERSION BX365835
KEYWORDS BX365835.2 GI:46288859
SOURCE EST.
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 783)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization.
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NciI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Nci I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

For more information about this cluster, see
http://www.genoscope.cns.fr/cdnats-CSIDB0022R03Plac=3474.r.
location/Qualifiers

FEATURES

1..783
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DB007YB11"

/issue_type="NEUROBLASTOMA_COT_10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA_COT_10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.:	1,84e-45	Length:	783
Score:	439.00	Matches:	85
Percent Similarity:	98.9%	Conservative:	1
Best Local Similarity:	97.7%	Mismatches:	0
Query Match:	98.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x BX365835 (1-783)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 172 ATGAAAGAGGCTTGAAGCTCTGAGCTCCGATGAGAGAGCGCTTGGAAACG 231
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 232 CGACCTGAACCATCTCTGAGCCCAACCTATKTTGACCTAACATGAGAAACAACT 291
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 292 GATTCCACACCTCTTAAATCAGCCCATCTGAGAAATCAGCAAAAATGACACAT 351
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 352 TTCTCTCATTAACCTGGAATATGATGATTAATCAATCTGTACAGAGGGCT 411
QY 81 ArgGlyValCysSerTyrLeu 87
DB 412 CGAGGGGTGTGTTCTACTTA 432

RESULT 91

CR791801

LOCUS

DEFINITION CR791801 739 bp mRNA linear EST 01-OCT-2004

DKFZP468J1522.x1.468 (synonym: phr11) Pongo pygmaeus cDNA clone

CR791801

DKFZP468J1522.5', mRNA sequence.

CR791801.1

GI:53710641

EST.

Pongo pygmaeus (orangutan)

Pongo pygmaeus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Pongo.

1 (bases 1 to 739)

Outenwelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,

Mewes, H.W., Weill, B., Amid, C., Oesanger, A., Fobo, G., Han, M. and

Wiemann, S.

Pongo pygmaeus mRNA (Outenwelder, B., Obermaier, B.,

Deutschenbaur, S., et al.)

Unpublished (2004)

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ);

Email: s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix

(Martinsried/Germany) within the cDNA sequencing consortium of the

German Genome Project. This clone (DKFZP468J1522) is available at

the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in

Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/ci.cgi?cloneid=DKFZP468J1522

Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..739

Location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.:	2.3e-45	Length:	739
Score:	438.00	Matches:	85
Percent Similarity:	97.7%	Conservative:	0
Best Local Similarity:	97.7%	Mismatches:	2
Query Match:	97.8%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x CR791801 (1-739)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 178 ATGAAAGAGGCTTGAAGCTCTGAGCTCCGATGAGAGAGCGCTTGGAAACG 237
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 238 CGCCCTGAACCATCTCTGAGCCCAACCTATGTTGACCTAACATGAGAAACAACT 297
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 298 GATTCCACACCTCTTAAATCAGCCCATCTGAGAAATCAGCAAAAATGACACAT 357
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 358 TTCTCTCATTAACCTGGAATATGATGATTAATCAATCTGTACAGAGGGCT 417
QY 81 ArgGlyValCysSerTyrLeu 87
DB 418 CGAGGGGTGTGTTCTACTTA 438

RESULT 92

T26956

LOCUS

DEFINITION T26956 310 bp mRNA linear EST 12-JUN-1996

11d155proj Clontech adult human fat cell library HU1108A Homo

sapiens cDNA clone 11d155, mRNA sequence.

T26956

T26956.1 GI:575899

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

1 (bases 1 to 310)

Bouilland, F.

Study of expressed sequences tags in adipose tissue 1994

Unpublished (1994)

On Nov 17, 1994 this sequence version replaced gi:624970.

Contact: Frederic Bouilland

Centre de Recherche sur l'Endocrinologie moleculaire et le

Developpement

CNRS

9, Rue Jules Hetzel, Meudon Bellevue, 92190 France

Tel: 33 1 45 07 52 87

Fax: 33 1 45 07 58 90

Email: bouilland@infobiogen.fr

Southern blot human DNA EcoRI : 2 major bands 3.1, 2.3 Kb and 2

weak : 4.2 and 1.9 Kb (wash 0.5xSSC).

Location/Qualifiers

1..310

/organism="Homo sapiens"

FEATURES

source

/mol_type="mRNA"

Location/Qualifiers

/strain="Caucasian"
/db_xref="taxon:9606"
/clone="11d155"
/clone_lib="Clontech adult human fat cell library H1108A"
/note="Vector: lambda gt10; Site 1: EcoRI;
dev-stage=adult; tissue-type=adipose tissue;
lab host=Bacteriophage lambda; first strand priming with
random and poly-d(T) oligonucleotides."

ORIGIN

Alignment Scores:

Pred. No.:	9,876-46	Length:	310
Score:	437.00	Matches:	85
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	97.5%	Indels:	0
DB:	8	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) x T26956 (1-310)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaIleuGluArg 20
DB 56 ATGGAAAGGGCTCTGAACCTCTTCTGACCTCCGGTGGAGAGAGCGCTTGGAAACGC 115
QY 21 ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThrThr 40
DB 116 CGACCTGAACCATCTCGAACCCCAACCTATGTGACCTACCAAGAAAGAAACAACT 175
QY 41 AspSerThrThrSerIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 176 GATTCACCACTCTTAATACGCCCATCTGAGAACTCAGCAAGAAATGGCAGCATG 235
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnIleuSerGluArgAla 80
DB 236 TTCTCTCATTAACCTGGAATTTGATTAATGATTAATGATTAATGATTAATGATTAATG 295
QY 81 ArgGlyValCysSer 85
DB 296 CGAGGGGTGTCTTCTTCC 310

RESULT 93

BX374579

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLES

JOURNAL

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

COMMENT

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ORIGIN /clone_lib="Sugano cDNA library, small intestine"

Alignment Scores:
 Pred. No.: 4.04e-45 Length: 580
 Score: 435.00 Matches: 87
 Percent Similarity: 98.9% Conservative: 0
 Best Local Similarity: 98.9% Mismatches: 0
 Query Match: 97.1% Indels: 1
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP261787 (1-580)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 94 ATGGAAAGGGCTGTGAACCTCTACTCGAGCCTCCGGTGGAGAGAGCCCTTGGAAACCC 153
 QY 21 ATGProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
 Db 154 CCACTGAAACCATCTCTGAGCCCAAGACCTTATGTTGACCTTAACCAATGAAGAAACACT 213
 QY 41 AppSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 Db 214 GATTCACACCACTTCTTAAATCAGCCCATCTGAAGTACTCAGCAAGAAATGGCAGCAT 273
 QY 60 PheSerLeuIleThrTPAanIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAl 80
 Db 274 GTTCTCTCTCATCTACCTGGAATATGATGATTAGATCTTAAACAATCTCTCAGAGGGGC 333
 QY 80 aArgGlyValCysSerTyrLeu 87
 Db 334 TCGAGGGGTGTCTTCTACTTA 355

RESULT 95
 LOCUS BG119064 927 bp mRNA linear EST 30-JAN-2001
 DEFINITION 602347589F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4442399 5',
 mRNA sequence.
 ACCESSION BG119064
 VERSION BG119064.1 GI:12612570
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM10215 row: a column: 24
 High quality sequence stop: 676.

FEATURES
 source
 1..927
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4442399"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_90"
 /note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; NciI;
 Site: 2; SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.7 kb. Library enriched for

ORIGIN

full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

Alignment Scores:
 Pred. No.: 1.35e-44 Length: 927
 Score: 433.00 Matches: 84
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 96.7% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG119064 (1-927)

QY 4 AlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArgProGlu 23
 Db 1 GCTTGAACCTCTACTCTGAGCCTCCGGTGAAGAGAGCGCTTGAAGCGCAGACTGAA 60
 QY 24 ThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThAspSerThr 43
 Db 61 ACCATCTCTGAGCCCAAGACCTATGTGACCTTAACAATGAAGAAACAATGATTCAC 120
 QY 44 ThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 63
 Db 121 ACTTCTAATATCAGCCCATCTGAAGATCTCAGCAAGAAATGGCAGATGTTCTCTTC 180
 QY 64 ILeThrTPAanIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgIVal 83
 Db 181 ATTACCTGGAATATGATGATTAGATCTTAAACAATCTGTGAGAGGGCTCGAGGGGTG 240
 QY 84 CysSerTyrLeu 87
 Db 241 TGTCTCTACTTA 252

RESULT 96
 LOCUS B1334820 704 bp mRNA linear EST 30-JUL-2001
 DEFINITION 602998939F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141193 5',
 mRNA sequence.
 ACCESSION B1334820
 VERSION B1334820.1 GI:15019477
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM11347 row: n column: 10
 High quality sequence stop: 704.

FEATURES
 source
 1..704
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5141193"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site: 1; NciI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.4 kb. Library prepared by Life Technologies."

Alignment Scores:

Pred. No.:	1,36e-44	Length:	70
Score:	432.00	Matches:	86
Percent Similarity:	98.9%	Conservative:	1
Best Local Similarity:	97.7%	Mismatches:	0
Query Match:	96.4%	Indels:	1
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) X BI334820 (1-704)

Oy	1	WetGluValAlaLeuAlaMetSerTyrPheGluProProValGluGluSerAlaLeuGluArg	20
Oy			
Db	147	ATGAAAGAGCTCTGAACCTCTACTTCAGGCTCCGGTGGAGGAGAGCGCCCTGGAAAGC	206
Oy			
Oy	21	ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluThrThr	40
Db	207	CGACCTGAACCATCTCTGAGCGCAAGACCTTGTTCCTACCTAACCAATGAAGAAACACT	266
Oy			
Oy	41	AspSerThrThrSerIleSerProSerGluAspArgGluGluGluGlySerMet	60
Db	267	GATTCACACACTCTCAAAATCAGCCCATCTGAATATCTGCGACACAAATGCGACAT	326
Oy			
Oy	60	cPheSerLeuIleThrTyrPheAlaAspGlyLeuAspLeuAspLeuSerGluValArgAl	80
Db	327	GATCTCTCTCAATCCCGGAATATATGATGATTAACATCTTCAACATCTCTCAGAGGCGC	386
Oy			
Oy	80	aArgGlyValCysSerTyrIleu	87
Db	387	TCAGGGGAGTGCTTCACTTA	408

RESULT	97
BPI99948	
Locus	561 bp mRNA linear EST 14-SEP-2004
Definition	BPI99948 Sugano cDNA library, amygdala Homo sapiens cDNA clone
	AMR00446, mRNA sequence.

```

FEATURES
  source
    location/Qualifiers
      1..581
        /organism="Homo sapiens"
        /db="ncbi"
        /db_type="taxon.19606"
        /accession="AMR00446"
        /citation_type="amygdala"
        /clone_lib="Sugano cDNA library, amygdala"

```

Best Local Similarity:	96.6%	Mismatches:	3
Query Match:	96.2%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) X BP199948 (1-581)

Qy	1	WetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluValx	20
Qy			
Db	196	ATGAAAGGGCTCTGAACCTCTACTGGAGCTCCGGTGGAGAGAGCGCTTTGGAACGC	255
Qy	21	ArgProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThrThr	40
Db	256	CAACTGAAACACTCTCTGAGCCCAAGACCTATGTTGACCTAACCAAGAAAGAAACAAC	315
Qy	41	AspSerThrThrSerTyrIleSerProSerGluAspThrGluGluAsnGluSerMet	60
Db	316	GATTCACACACTCTTAAATACAGCCCACTGAAATACCTACAGAAAGAAATGGCAGCATG	375
Qy	61	PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla	80
Db	376	TTCTCTCTCATTAACCTGGAAATATATAGATTAATGATTAACATCTGTCAAGAGAGCTC	435
Qy	81	ArgGlyValCysSerTyrLeu	87
Db	436	GGGGGAGNGGTGTTCTTAACTTA	456

RESULT 98	BP348796	568 bp	mRNA	linear	EST 17-SEP-2004
LOCUS	BP348796				
DEFINITION	BP348796 Sugano cDNA library, brain Homo sapiens				
ACCESSION	SZRO1880				cdna clone
VERSION	BP348796				
KEYWORDS	BP348796.1				GI:52278781
SOURCE	EST				
ORGANISM	Homo sapiens				
	Homo sapiens (human)				

Alignment Scores:		
Pired. No.:	1,8e+44	Length:
Score:	930.50	Align:
Percent Similarity:	93.0%	Conservative:
Identical Similarity:	87.7%	Mismatches:
Query Match:	96.0%	Indels:
Gaps:	0	

US-10-757-745-2_COPY_54_140 (1-87) x BP348796 (1-568)

US-10-757-743-2_COPY_54_140 (1-87) X BP348796 (1-588)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProGluValGluSerAlaLeuGluArg 20

DB 187 ATGAAAGGGCTGTGACTCTTACTTGCAGCCTCCGGTGAGAGAGCGCTTGAGAGCC 246
QY 21 ATGPRGGLuThrIleSerGluProLyThrTyValAspLeuThrAsnGluThrThr 40
DB 247 GCACCTGAAACCATCTCTGAGCCCAAGACCTATGTTGACCTAACCAATGAAACCAACT 306
QY 41 AAspSerThrThrSerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 307 GATTCACACACTTCTTAAATCAGCCCATTTGAAAGATCTACAGCAAGAAATGGCAGCATG 366
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 367 TTCTCTCATTAACCTGGAATATGATGATTAGATCTTAACAATCTGTCAAGAGGGCT 426
QY 81 Arg-GlyValCysSerTyrLeu 87
DB 427 CGAGGGGGTGTTCTTACTTA 448

RESULT 99

BG740339 932 bp mRNA linear EST 15-MAY-2001
LOCUS BG740339

DEFINITION 602635289P1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4780318 5',
mRNA sequence.

ACCESSION BG740339.1 GI:14050992

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 932)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M10639 row: a column: 23
High quality sequence stop: 759.
Location/Qualifiers
1..932
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4780318"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NCI;
Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 4,416-44 Length: 932
Score: 429.00 Matches: 83
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 95.8% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG740339 (1-932)

QY 5 LeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArgArgProGluThr 24
DB 3 CTGAACCTCTTACTTGAACCTCCGGTGAGAGAGCGCTTGAGAGCGGCACTGAAACG 62

QY 25 ILeSerGluProLyThrTyValAspLeuThrAsnGluThrThrAspSerThrThr 44
DB 63 ATCTCTGAGCCCAAGACCTATGTTGACCTTAACAATGAAACCAACTGATTCACCACT 122
QY 45 SerTyIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu 64
DB 123 TCTTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGGCAGCATGTTCTCTCAT 182
QY 65 ThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCys 84
DB 183 ACCTGGAATATGATGATTGATCTTAACAATCTGTCAAGAGGGCTGAGGGGTGTCT 242
QY 85 SerTyrLeu 87
DB 243 TCTTACTTA 251

RESULT 100

DQ049206 1089 bp DNA linear GSS 02-JUN-2005
LOCUS DQ049206

DEFINITION Pan troglodytes TTRAP gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.

ACCESSION DQ049206

VERSION DQ049206.1 GI:66902405

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

1 (bases 1 to 1089)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubsiz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeillo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A scan for positively selected genes in the genomes of humans and
chimpanzees
(er) Plos Biol. 3 (6), E170 (2005)
15869325
2 (bases 1 to 1089)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubsiz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeillo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
Location/Qualifiers
1..1089
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1089
/gene="TTRAP"
/locus_tag="Hc17203"

FEATURES

source

gene

ORIGIN

Alignment Scores:

Pred. No.: 5,46-44 Length: 1089
Score: 429.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 3
Query Match: 95.8% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x DQ049206 (1-1089)

QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
DB 160 ATGAAAGGGCTGTGACTCTTACTTGAAGCTCCGGTGAGAGAGCGCTTGAGAGCG 219
QY 21 ArgProGluThrIleSerGluProLyThrTyValAspLeuThrAsnGluThrThr 40

Db 220 CGACCTGAACCATCTCTGAGCCGANNNNNNNTTGTACCTAACCATAGAAACAACCT 279
Qy 41 AapSerThrThSerIylIeSerProSerGluAepThrGInGInGluAaNGlySerMet 60
Db 280 GATTCACACACTCTTAATAATCAGCCATCTACATCTCAGAAATAATATGCGACATG 339
Qy 61 PhaeSerLeuIleThrTTPasnlIaAapGlyLeuAapLeuAaAsnLeuSerGluArgAla 80
Db 340 TTCTCTCTCATTAACCTGGAAATATGATGATTAATCAATCTGTCAGAGAGGACT 399
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 400 CGAGGGGTGTGTCTACTTA 420

RESULT 101
BX422491 904 bp mRNA linear EST 03-MAY-2004
LOCUS BX422491 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM007YE11 5-PRIME, mRNA sequence.
ACCESSION BX422491
VERSION BX422491.2 GI:46955237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
AUTHORS Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30766188.
CONTACT: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the PCWSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna78=CS0DM007AC06P1kc=3474.r.
FEATURES
source location/Qualifiers
1..904
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/class_type="FETAL LIVER"
/dev_stage="fetal"
/clone_1lb="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: PCWSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the PCWSPORT 6
vector. Library was not normalized."

ORIGIN
Alignment Scores:
Pred. No.: 5.68e-44 Length: 904
Score: 428.00 Matches: 84
Percent Similarity: 96.6% Conservative: 0
Best Local Similarity: 96.6% Mismatches: 3
Query Match: 95.5% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BX422491 (1-904)
Qy 1 MetGluArgAlaLeuAaSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
|||||

Db 103 ATGGAAAGGCGCTCTGAACCTCTTACTTGTGAGCTCCGGTGGAGAGAGCGCTTGAAACG 162
Qy 21 ArgProGluThrIleSerGluProGlyThrTyrValAapLeuThaAsnGluGluThr 40
Db 163 CGACCTGAACCATCTCTGAGCCGANNNNNTTGTACCTAACCATAGAAACAACCT 222
Qy 41 AapSerThrThSerIylIeSerProSerGluAepThrGInGInGluAaNGlySerMet 60
Db 223 GATTCACACACTCTTAATAATCAGCCATCTACATCTCAGAAATAATATGCGACATG 282
Qy 61 PhaeSerLeuIleThrTTPasnlIaAapGlyLeuAapLeuAaAsnLeuSerGluArgAla 80
Db 283 TTCTCTCTCATTAACCTGGAAATATGATGATTAATCAATCTGTCAGAGAGGACT 342
Qy 81 ArgGlyValCysSerTyrLeu 87
Db 343 CGAGGGGTGTGTCTACTTA 363

RESULT 102
BP243301 556 bp mRNA linear EST 15-SEP-2004
LOCUS BP243301 Sugano cDNA library, liver HepG2 Homo sapiens cDNA clone
DEFINITION BP243301, mRNA sequence.
ACCESSION BP243301
VERSION BP243301.1 GI:52116211
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
AUTHORS Mizushima-Sugano, J., Nakai, K. and Sugano, S.
JOURNAL Sequence comparison of human and mouse genes reveals a homologous
PUBMED block structure in the promoter regions
15342556 Genome Res. 14 (9), 1711-1718 (2004)
CONTACT: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
FEATURES
source location/Qualifiers
1..556
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP19431"
/class_type="liver"
/cell_line="HepG2"
/clone_1lb="Sugano cDNA library, liver HepG2"
/note="hepatoma"

ORIGIN
Alignment Scores:
Pred. No.: 4.04e-44 Length: 556
Score: 427.00 Matches: 83
Percent Similarity: 98.9% Conservative: 3
Best Local Similarity: 95.4% Mismatches: 1
Query Match: 95.3% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP243301 (1-556)
Qy 1 MetGluArgAlaLeuAaSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
Db 188 ATGGAAAGGCGCTCTGAACCTCTTACTTGTGAGCTCCGGTGGAGAGAGCGCTTGAAACG 247
Qy 21 ArgProGluThrIleSerGluProGlyThrTyrValAapLeuThaAsnGluGluThr 40
Db 248 CGACCTGAACCATCTCTGAGCCGANNNNNTTGTACCTAACCATAGAAACAACCT 307
|||||

Qy 41 AepSerThrSerIleSerProSerGluAspThrGlnGluAsnGlySerMet 60
 Db 308 GATTCCACCACTTCTTAATCACTGATCTGAAGATCTCAGCAGAAATGGACCATG 367
 Qy 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 80
 Db 368 TTCTCATTAATACCGAATATGATGATTAGATCTAAACATCTGTGCAGAGGGCT 427
 Qy 81 ArgGlyValCysSerTyrLeu 87
 Db 428 CGAGAGTGGCTTCTACTTA 448

RESULT 103
 BM172060 570 bp mRNA linear EST 04-DEC-2001
 LOCUS imagec3_2001/sml293bdf41.xl NIH_MGC_76 Homo sapiens cDNA clone
 DEFINITION IMAGE:4700059 5', mRNA sequence.
 ACCESSION BM172060
 VERSION BM172060.1 GI:17311623
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 570)
 REFERENCE Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and
 AUTHORS Prange,C.K.
 TITLE The I.M.A.G.E. Consortium quality control effort: clone
 JOURNAL resequencing for verification
 COMMENT Unpublished (2001)
 Other ESTs: BG533717
 Contact: Prange CK
 The I.M.A.G.E. Consortium
 Lawrence Livermore National Laboratory
 Livermore, CA, USA
 Email: help@image.llnl.gov
 This read has been verified (found to hit its original self in the
 correct orientation), as part of the I.M.A.G.E. Consortium quality
 control effort. High quality sequence is defined as having 100 or
 more base pairs with a phred quality value of 20 or greater, where
 a sliding window of 4 base pairs with a phred quality value of 15
 or greater marks the beginning and end of the sequence. For
 information on obtaining this clone, please contact
 info@image.llnl.gov.
 Place: LNCM1533 Row: a column: 20
 Seq primer: -21m13
 High quality sequence stop: 570.
 Location/Qualifiers
 1..570
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4700059"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_host="NIH_MGC_76"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site: 1:
 S11 (ggcgcgcgcgcgc); Site 2: S11 (ggcctatcgcc); 5' and
 3' adaptors were used in cloning as follows: 5' adaptor
 sequence: 5'-CACGCGCATATGAGC-3' and 3' adaptor sequence:
 5'-ATTCTAGAGCGCGAGCGCGCATG-dT(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.85
 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

Alignment Scores:
 Score: 4.17e-44 Length: 570
 Percent Similarity: 427.00 Matches: 83
 Percent Similarity: 97.7% Conservative: 1
 Best Local Similarity: 96.5% Mismatches: 2

Query Match: 95.3% Indels: 0
 Db: 3 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x BM172060 (1-570)

Qy 2 GlnArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 21
 Db 15 CAGAGGGCTCTGAATCTCTACTTCAGCCTCCGGGAGAGAGCGCCTTGAAACGCCA 74
 Qy 22 ProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluThrThrAsp 41
 Db 75 CCTGAACACACTCTTTATCCCAAGACCTATGTTGACCTAACCAATGAAGAAACAATGAT 134
 Qy 42 SerThrThrSerIleSerProSerGluAspThrGlnGluAsnGlySerMetPhe 61
 Db 135 TTCACCACTCTTAATAATAGCCCATCTGAAGTACTCAGCAGAAATGGCAGCATGTTTC 194
 Qy 62 SerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 81
 Db 195 TTCTCATTAATACCGAATATGATGATTAGATCTTAACATCTGTGCAGAGGGCTCGA 254
 Qy 82 GlyValCysSerTyrLeu 87
 Db 255 GCGGTGTGTTCTACTTA 272

RESULT 104
 BP274942 584 bp mRNA linear EST 16-SEP-2004
 LOCUS BP274942 Sugano cDNA library, kidney Homo sapiens cDNA clone
 DEFINITION KDN02414, mRNA sequence.
 ACCESSION BP274942
 VERSION BP274942.1 GI:52188674
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 584)
 REFERENCE Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 AUTHORS Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 JOURNAL block structure in the promoter regions
 COMMENT PUBMED
 15342556
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1..584
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KDN02414"
 /tissue_type="kidney"
 /clone_lib="Sugano cDNA library, kidney"

Alignment Scores:
 Pred. No.: 2.52e-43 Length: 584
 Score: 421.00 Matches: 83
 Percent Similarity: 95.4% Conservative: 0
 Best Local Similarity: 95.4% Mismatches: 4
 Query Match: 94.0% Indels: 0
 Db: 3 Gaps: 0
 US-10-757-745-2_COPY_54_140 (1-87) x BP274942 (1-584)

Qy 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 Db 127 ATGGAAGGGCTCTGAATCTCTACTTCGAGCCTCCGGTGGAGAGAGCGCCTTGGAACGC 186

QY 21 ArgProGluThrlIleSerGluProLysThrTyrValAspLeuThraAsnGluGluThr 40
DB 187 CGACCTGAACACCTCTGAGCCAGACCTATGTGACCTAACCAATGAGAAACAACT 246
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 247 GATTCCACACCTCTTAAACACGCTATCTGAGATCTCAGCAAGAAATGCGACGCT 306
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 307 TTCTCTCATTAACCTGGAATATGATGATTAATCTTAAACAATCTGCCAGAGAGGCT 366
QY 81 ArgGlyValCysSerTyrLeu 87
DB 367 CGAGGGGAGAGTACTACTTA 387
RESULT 105
BI760756 757 bp mRNA linear EST 25-SEP-2001
LOCUS 603044763F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:518534 5'
DEFINITION mRNA sequence.
ACCESSION BI760756
VERSION BI760756.1 GI:15752334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 757)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11462 row: m column: 15
High quality sequence start: 6
High quality sequence stop: 755.
High quality sequence
Location/Qualifiers
1..757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5185334"
/lab_host="DH10B"
/clone_1lb="NIH_MGC_116"
/note="Organ: Pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 3,54e-43 Length: 757
Score: 421.00 Matches: 86
Percent Similarity: 98.9% Conservative: 0
Best Local Similarity: 98.9% Mismatches: 1
Query Match: 94.0% Indels: 1

DB: 3 Gaps: 0
UC-10-757-745-2_copy_54_140 (1-87) x BI760756 (1-757)
QY 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
DB 69 ATGAAAGAGGCTCTGAACTCTTCACTTCGACCTCCGATGAGAGAGAGCC-CTGAAAGC 127
QY 21 ArgProGluThrlIleSerGluProLysThrTyrValAspLeuThraAsnGluGluThr 40
DB 128 CGACCTGAACACCTCTGAGCCAGACCTATGTGACCTAACCAATGAGAAACAACT 187
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 188 GATTCCACACCTCTTAAACATCAGCCCAATCTGAGATCTCAGCAAGAAATGCGACGCT 247
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
DB 248 TTCTCTCATTAACCTGGAATATGATGATTAATCTTAAACAATCTGCCAGAGAGGCT 307
QY 81 ArgGlyValCysSerTyrLeu 87
DB 308 CGAGGGGAGAGTACTACTTA 328
RESULT 106
BS337046 889 bp mRNA linear EST 03-APR-2001
LOCUS 602565130F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4689919 5'
DEFINITION mRNA sequence.
ACCESSION BS337046
VERSION BS337046.1 GI:13528594
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 889)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Clontech Laboratories, Inc.
cDNA Library Preparation: Clontech Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM1506 row: k column: 08
High quality sequence start: 525.
High quality sequence
Location/Qualifiers
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4689919"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1lb="NIH_MGC_77"
/note="Organ: Lung; Vector: pDNR-LTB (Clontech); Site 1:
SfiI (ggccgcctcgcc); Site 2: SfiI (ggccatctggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGACC-3' and 3' adaptor sequence:
5'-ATTCTTAGAGCGCGAGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 4,378-43 Length: 889
 Score: 421.00 Matches: 86
 Percent Similarity: 98.9% Conservative: 0
 Best Local Similarity: 98.9% Mismatches: 1
 Query Match: 94.0% Indels: 1
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG537046 (1-889)

QY 1 MetGUArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
 DB 176 ATGGAAGAGGGCTGTGAACCTCTACTCGAGCCCTCGGTGAGAGAGCGCCCTTGAAGCC 235
 QY 21 ArgProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThr 40
 DB 236 CCACTCGAAGACCATCTCTAGCGCCAGACCTATGTTGACCTTAACCAATGAGAAACAACCT 295
 QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 DB 296 GATTCACACCACTTCTAAATCAAG-CCATCTGAAGATCTCAGCAAGAAATGCGACCATG 354
 QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
 DB 355 TTCTCTCATTAACCTGGAATATGATGATTAGATCTTAACAATCTGTCAAGAGAGGCT 414
 QY 81 ArgGlyValCysSerTyLeu 87
 DB 415 CGAGGGGTGTGTTCTACTTA 435

RESULT 107

BP264149 581 bp mRNA linear EST 16-SEP-2004
 LOCUS BP264149 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION clone HS114850, mRNA sequence.
 ACCESSION BP264149
 KEYWORDS BP264149.1 GI:52179380
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 REFERENCE 1 (bases 1 to 581)
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source
 1..581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS114850"
 /issue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.: 1,478-42 Length: 581
 Score: 415.00 Matches: 81
 Percent Similarity: 96.5% Conservative: 2
 Best Local Similarity: 94.2% Mismatches: 0
 Query Match: 92.6% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP264149 (1-581)

QY 2 GUArgAlaLeuAnsSerTyPheGluProProValGluGluSerAlaLeuGluArg 21
 DB 129 CAGAGGGCTGTGAACCTCTACTCGAGCCCTCGGTGAGAGAGCGCCCTTGAAGCCCA 188
 QY 22 ProGluThrIleSerGluProLysThrTyValAspLeuThrAsnGluGluThrAsp 41
 DB 189 CCGAAGACCATCTCTAGCGCCAGACCTATGTTGACCTTAACCAATGAGAAACAACCTGAT 248
 QY 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
 DB 249 TCACACCACTTCTAAATCAAGCCCTCTGAAGATCTCAGCAAGAAATGCGACGCTTTC 308
 QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 81
 DB 309 TCTCATTAACCTGGAATATGATGATTAGATCTTAACAATCTGTCAAGAGAGGCTGCG 368
 QY 82 GlyValCysSerTyLeu 87
 DB 369 GGGGTGTGTGCTGCTTG 386

RESULT 108

CN641671 1090 bp mRNA linear EST 12-MAY-2004
 LOCUS CN641671 ILLUMIGEN_MCO_5159 Katze_MBR Macaca mulatta cDNA clone IB1W:570
 DEFINITION 5', similar to bases 11 to 990 highly similar to human TTRAP
 (Hs.210628), mRNA sequence.
 ACCESSION CN641671
 KEYWORDS CN641671.1 GI:47152681
 SOURCE EST.
 ORGANISM Macaca mulatta (rhesus monkey)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecoidea; Macaca.
 REFERENCE 1 (bases 1 to 1090)
 AUTHORS Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
 Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
 Iadonato, S.P.
 TITLE Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 JOURNAL Genome Biol. 6 (7), R60 (2005)
 PUBMED 15998449
 COMMENT Contact: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2003.12.04, 732 Q20 bases.
 PCR Primers
 FORWARD: CCTCCTAATGAGGAGCAACAAA
 BACKWARD: CACTATAGCGCAATTGGCTA
 Insert Length: 1090 Std Error: 0.00
 Plate: C1000043 row: E column: 07
 Seq primer: CCTCCTAATGAGGAGCAACAAA
 POLYA=No.

FEATURES

source
 1..1090
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IB1W:5970"
 /sex="female"
 /dev_stage="adult"
 /lab_host="E. coli SOLR"
 /clone_lib="Katze_MBR"
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
 Site 2: Xho I; Created from StrataGene ZAP-cDNA synthesis
 kit (catalog #200400) and ZAP-CDNA Gigapack III Gold
 Cloning Kit (catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.: 3,34e-42 Length: 1090
Score: 415.00 Matches: 81
Percent Similarity: 93.1% Conservative: 0
Best Local Similarity: 93.1% Mismatches: 6
Query Match: 92.6% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN61671 (1-1090)

OY 1 MetGUARGALaleuanserTTPheGUPProPovaIGUIGUserAlaleuGUARG 20
DB 32 ATGAAAGGCTCTCAACCTCTCACTCTGAGCCCTCCGATGAGAGAGCGCTTGAGACGC 91
OY 21 AAGPGGUTHThIleSerGUPProLYThTYValAPleuThraNGUIGUThThr 40
DB 92 CGCCGAAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAAGAAACAAT 151
OY 41 AAGSerThThSerLYleSerProSerGUAPThThGInGInGUAGLYSerMet 60
DB 152 GATTCCACCACTTCAAAATCAAGCCCATCTGAAGATCTCAGAGAAATGACAGCATG 211
OY 61 PhaserleuIleThThPAsnIleAPGlyleuAPleuAAsnleuSerGUARGAla 80
DB 212 TTCTGCTCAATACCTGGAATATGATGATTAATCAATCTGTCAGAGAGGCT 271
OY 81 ArgGlyValCyseSerTYrleu 87
DB 272 CGAGGGGTGTGTCTTACTTA 292

RESULT 109

CV805216 827 bp mRNA linear EST 15-NOV-2004
LOCUS CV805216
DEFINITION AGENCOURT_36377305 NIH_MGC_280 Homo sapiens cDNA clone
IMAGE:7504495 5', mRNA sequence.

ACCESSION CV805216
VERSION CV805216.1 GI:55748182

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 827)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Meri Filipo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLT at:
<http://image.llnl.gov>
Plate: ILNLT5875 row: e column: 05
High quality sequence start: 291.
Location/Qualifiers
1..827
location="Homo sapiens"
mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7504495"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B"
/clone_id="NIH_MGC_280"

FEATURES

source

1..827
location="Homo sapiens"
mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7504495"
/tissue_type="pluripotent cell line derived from
blastocyst inner cell mass"
/lab_host="DH10B"
/clone_id="NIH_MGC_280"

ORIGIN

Alignment Scores:

Pred. No.: 1.83e-41 Length: 827
Score: 408.00 Matches: 79
Percent Similarity: 95.3% Conservative: 3
Best Local Similarity: 91.9% Mismatches: 4
Query Match: 91.1% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CV805216 (1-827)

OY 1 MetGUARGALaleuanserTTPheGUPProPovaIGUIGUserAlaleuGUARG 20
DB 194 ATGAAAGGCTCTGAACTCTCACTCTGAGCCCTCCGATGAGAGAGCGCTTGAAACGC 253
OY 21 AAGPGGUTHThIleSerGUPProLYThTYValAPleuThraNGUIGUThThr 40
DB 254 CGACCTGAACCATCTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAAGAAACAAT 313
OY 41 AAGSerThThSerLYleSerProSerGUAPThThGInGInGUAGLYSerMet 60
DB 314 GATTCCACCACTTCAAAATCAAGCCCATCTGAAGATCTCAGAGAAATGACAGCATG 373
OY 61 PhaserleuIleThThPAsnIleAPGlyleuAPleuAAsnleuSerGUARGAla 80
DB 374 TTCTGCTCAATACCTGGAATATGATGATTAATCAATCTGTCAGAGAGGCT 433
OY 81 ArgGlyValCyseSerTYr 86
DB 434 CGAGGGGTGTGTCTTACTTA 451

RESULT 110

B1915865 915 bp mRNA linear EST 16-OCT-2001
LOCUS B1915865
DEFINITION 603184527F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5248495 5',
mRNA sequence.

ACCESSION B1915865
VERSION B1915865.1 GI:16179808

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 915)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLT)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLT at:
<http://image.llnl.gov>

Plate: L1AM1627 row: e column: 08
High quality sequence stop: 696.
Location/Qualifiers

FEATURES
Source

1..915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5248495"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 4,36e-41 Length: 915
Score: 405.50 Matches: 83
Percent Similarity: 95.5% Conservative: 2
Best Local Similarity: 93.3% Mismatches: 2
Query Match: 90.5% Indels: 2
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x B1915865 (1-915)

QY 1 MetGUAAGAlaLeuAnsSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 167 ATGGAAGGGCTGTGAACCTCTACTCGAGCTCCGGTGAAGAGAGCGCTTGAACGC 226
QY 21 ArgProGluThrIleSerGluProIysThrTyValAspLeuThrAsnGluThrThr 40
DB 227 CGACCTGAAACCACTCTGAGCCCAAGACCTAGTGAACCTAACCAATGAAGAAACACT 286
QY 41 AspSerThrThrSerIysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 287 GATTCCACCACTTCTTAATATCAAGCCATCTGAAGATCACTACAGAAATATGGCAGCAG 346
QY 61 PheSerLeuIleThrTrpAsnIleAsp-GlyLeuAspLeuAsnLeuSer---GluArg 79
DB 347 TTCTCTCTCATTAACCTGGAATATGATCGATTAGATCTAAACAATCTCTCAGACGAGG 406
QY 79 GAlaArgGlyValCysSerTyrLeu 87
DB 407 CTCGACGGGGCTGTGTTCTCTACTTA 431

RESULT 111
BQ787387 352 bp mRNA linear EST 26-JUL-2002
LOCUS BQ787387
DEFINITION im09c09.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:6034553
5' similar to TR:095551 095551 DJ30M3.3 ; mRNA sequence.
ACCESSION BQ787387
VERSION BQ787387.1 GI:21995859
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS
TITLE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 352)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K., Lemisha, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A., Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, H., Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium

JOURNAL COMMENT

Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.p.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: 40RP from Gibco.

FEATURES

source
Location/Qualifiers

1..352
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6034553"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1: XhoI, Site 2: EcoRI. Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:
Pred. No.: 1.45e-41 Length: 352
Score: 405.00 Matches: 79
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 90.4% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BQ787387 (1-352)

QY 1 MetGUAAGAlaLeuAnsSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 115 ATGGAAGGGCTGTGAACCTCTACTCGAGCTCCGGTGAAGAGAGCGCTTGAACGC 174
QY 21 ArgProGluThrIleSerGluProIysThrTyValAspLeuThrAsnGluThrThr 40
DB 175 CGACCTGAAACCACTCTGAGCCCAAGACCTATGTGACCTAACCAATGAAGAAACCACT 234
QY 41 AspSerThrThrSerIysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 235 GATTCCACCACTTCTTAATATCAAGCCATCTGAAGTACTCAGCAAGAAATGGCGCAGT 294
QY 61 PheSerLeuIleThrTrpAsnIleAspGlyLeuAspLeuAsnLeuSerGluArg 79
DB 295 TTCTCTCTCATTAACCTGGAATATGATGATTAGATCTTAACAATCTCTCAGACGAG 351

RESULT 112

CN801806 922 bp mRNA linear EST 26-MAY-2004
LOCUS CN801806
DEFINITION ILLUMIGEN MCQ 37066 Kaczke MBR Macaca mulatta cDNA clone IBTUP:15450 5' similar to Bases 18 to 922 highly similar to human TTPAP (Hs:210628), mRNA sequence.
ACCESSION CN801806
VERSION CN801806.1 GI:47697782
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.rtf

Page 64

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 922)
Magnes, C.L., Fellin, P.C., Thomas, M.J., Korh, M.J., Agy, M.B.,
Proli, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.
Analysis of the Macaca mulatta transcriptome and the sequence
divergence between Macaca and human
Genome Biol. 6 (7), R60 (2005)
1599449
Contact: C. Magnes
illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagnes@illumigen.com
Sequenced on 2004.05.13. 514 Q20 bases.
PCR Primers
FORWARD: CCTCACTTAAGGGAACAAA
BACKWARD: CACTATAGGGGGAATTGGGA
Insert Length: 922 Std Error: 0.00
Plate: C0000291 row: H column: 09
Seq primer: CCTCACTTAAGGGAACAAA
POLYA=No.

FEATURES
SOURCE

1..922
Location/Qualifiers
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBIUM.15450"
/sex="female"
/dev_stage="adult"
/lab_host="E. coli SOLR"
/clone_lib="Katze, MMBR"
/note="Organ: brain; Vector: Uni-ZAP XR; Site: 1; Ecor I;
Site 2: Xho I; Created from StrataGene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning Kit (catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.: 1,660-40 Length: 922
Score: 401.00 Matches: 80
Percent Similarity: 93.1% Conservative: 1
Best Local Similarity: 92.0% Mismatches: 6
Query Match: 89.5% Indels: 0
Gaps: 0
DB: 7

US-10-757-745-2_COPY_54_140 (1-87) x CN801806 (1-922)

QY 1 MetGluArgAlaLeuGlnSerTyrPheGluProProValGluGluGluSerAlaLeuGluArg 20
DB 42 ATGACACAGGCTCTGATCTCTGATTCAGCTCCGCTGAGAGAGCCGCTTGAGAGCC 101
QY 21 ArgProGluThrIleSerGluProValSerThrTyrValAspLeuThrIleGluGluThr 40
DB 102 CCGCTTAACCACTCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAGAAACAAT 161
QY 41 AspSerThrThrSerValIleSerProSerGluAspThrGluGluGluGluSerMet 60
DB 162 GATTCACCACTCTTAATTCACCCATCTGAAGATCTGACGAGAGAAATGACACAG 221
QY 61 PheSerLeuIleThrTyrPheGluValAspLeuAspLeuAspLeuSerGluValGala 80
DB 222 TTCCTTCATTTACCTGGAATATTGATGATTAATCTTAACCAATCTGTACAGAGAGCT 281
QY 81 ArgGluValCysSerTyrIleu 87
DB 282 CAGGAGGTGTCTCTACTTA 302
RESULT 113

BU070378/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU070378 347 bp mRNA linear EST 27-AUG-2002
IM09C09.x1 Human insulinoma Homo sapiens cDNA IMAGE:6034553
3' similar to TR:095551 O95551 D30M3.3 ; mRNA sequence.
BU070378.1 GI:22511567
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 347)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradow, G., Gilton, S.,
Hiller, L., Maira, M., Pape, D., Wylie, T., Martin, J., Bilezikian, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCam, R., Cole, R., Tsagaris, V., R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: im09c09.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biolp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pInscrypt SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.

FEATURES
SOURCE

1..347
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6034553"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pInscrypt SK-; Site: 1;
XhoI; Site 2: EcorI; Constructed with lambda ZAPIT system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pInscrypt SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110. Note: This
is a Washington University Pancreas Est project library."

ORIGIN

Alignment Scores:

Pred. No.: 6,196-41 Length: 347
Score: 400.00 Matches: 78
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 89.3% Indels: 0
Gaps: 0
DB: 5

US-10-757-745-2_COPY_54_140 (1-87) x BU070378 (1-347)

QY 1 MetGluArgAlaLeuGlnSerTyrPheGluProProValGluGluGluSerAlaLeuGluArg 20
DB 234 ATGAAAGGCTCTGAACTCTCACTTCAAGCTCCGCTGAGAGAGAGCCCTTGAGAGCC 175
QY 21 ArgProGluThrIleSerGluProValSerThrTyrValAspLeuThrIleGluGluThr 40

QY 20 gATGpGCGUu-ThrIleSerGUp-olYerThrYrValaApleu--ThraAnglUGluTh 39
 |||||
 Db 219 CCGACCTGTAACCACTCTCTAGCCCAAGACCTATGTTAGCTTAGACCAAGAGAAAC 278
 |||||
 QY 39 rTThaPSeThrThrSerIleIleSerProSeGUAaSPThGInGInGUAaNGIySe 59
 |||||
 Db 279 AACTGATTCACACACTCTCAAAATCAGCCCACTCAAGATCACTCAAGAAATGGAG 338
 |||||
 QY 59 MetPheSerIleuIleThrTPaenIleAaGlyLeuAaPleuAaSerIleuSerGUA 79
 |||||
 Db 339 CATGTCCTCTCATTAACCTGGAATATGATGATGATCACTAAACAATCTGTCAAGAG 398
 |||||
 QY 79 gAlaArgGlyValCySeSerTyrIleu 87
 |||||
 Db 399 GGCCTGAGGGGTGTGTCTCTACTTA 423
 |||||

RESULT 116

BG391295 770 bp mRNA linear EST 12-MAR-2001
 LOCUS 602417344F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4536634 5'
 DEFINITION mRNA sequence.
 ACCESSION BG391295
 VERSION BG391295.1 GI:13284743
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 770)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L1AM10460 row: h column: 11
 High quality sequence stop: 693.
 Location/Qualifiers

FEATURES

1..770
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4536634"
 /tissue_type="embryonal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_92"
 /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 2.5 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
 Pred. No.: 2.63e-38 Length: 770
 Score: 383.00 Matches: 84
 Percent Similarity: 93.4% Conservative: 1
 Best Local Similarity: 92.3% Mismatches: 2
 Query Match: 85.5% Indels: 4
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG391295 (1-770)

QY 1 MetGUaRGAlaLaAuAaSerTYrPheGUpProPo-ValGInGInSerAlaLeuGInUar 20
 |||||
 Db 167 ATGAAAGGGCTGAACTCTCTAGCCCTCCGTGTGAGAGAGAGAGCGCCTTGGAGG 226
 |||||

QY 20 gATGpGCGUuThrIleSerGUpPolYerThrYrValaApleuThraAnglUGluTh 40
 |||||
 Db 227 CCGACCTTAACCACTCTCTAGCCCAAGACCTATGTTAGCTTAGACCAATGAAGAAACAGC 286
 |||||
 QY 40 rAaPSeThrThrSerIleIleSer-ProSeGUAaSPThGInGInGUAaNGIy-Ser 59
 |||||
 Db 287 TGAATCCACACTCTTAATAATCAATGTCATCGAAGATCACTAGCAAGAAAATGGCAGAC 346
 |||||
 QY 60 MetPheSerIleuIleThrTPaenIleAaGlyLeuAaPleuAaSerIleuSerGUA 79
 |||||
 Db 347 ATGTCCTCTCATTAACCTGGAATATGATGATGATCACTAAACAATCTGTCAAGAG 406
 |||||
 QY 79 gAlaArgGlyValCySeSerTyrIleu 87
 |||||
 Db 407 GGCCTGAGGGGTGTGTCTCTACTTA 431
 |||||

RESULT 117

BM507091 582 bp mRNA linear EST 15-FEB-2002
 LOCUS 1124901.y1 Human insulinoma Homo sapiens cDNA 5' similar to
 DEFINITION TR:095551 095551 DJ30M3.3 ;, mRNA sequence.
 ACCESSION BM507091
 VERSION BM507091.1 GI:18678234
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 582)
 Melton/D., Brown/J., Kenty/G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Scaerle,M., Breckell,J., Graddon,G., Clifton,S.,
 Hillier,L., Maira,M., Pape,D., Wylie,R., Martin,J., Blissett,A.,
 Schmitz,A., Theising,B., Ritzer,B., Komko,I., Bennett,J.,
 Cardenas,M., Gibbons,M., McGann,R., Cole,R., Teagarden,Y., R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: 1124901.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Harvard Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept. Of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmellon@lobp.harvard.edu
 Library was constructed by Dr. J. Ferrer in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
 University Genome Sequencing Center for information on obtaining a
 clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 See primer: -40RP from Gibco
 High quality sequence stop: 269.
 Location/Qualifiers

FEATURES

1..582
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="insulinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Human insulinoma"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
 XhoI; Site_2: EcoRI; Constructed with lambda ZAPIT system
 (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
 pBluescript SK- by Dr. H. Inoue following the Washington
 University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further
 laboratory on this library (Metabolism Division, Permutt
 Laboratory, Washington University School of Medicine, Box
 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
 is a Washington University Pancreas Est project library."

ORIGIN

Alignment Scores:

Pred. No.: 3,65e-36 Length: 582
 Score: 365.00 Matches: 70
 Percent Similarity: 100.0% Conservative: 3
 Best Local Similarity: 95.9% Mismatches: 0
 Query Match: 81.5% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BMS07091 (1-582)

QY 15 GUGSRAALAUAGUAGRARGRPROGUTHTRIESEGULUPROLYETHRTYRVALASPEN 34
 DB 4 CAAGGCGCTGTGAAGCCGACCTGAAACCATCTGAGCCCAAGACCTATGTGACCTA 63
 QY 35 THAASGLUGLUATHRTTHASPSERTHTHRTSERLYLIESERPROSERGLUASPTHTGIN 54
 DB 64 ACCAATGAAAGAAACAACATGATTCACCACTTCTAATAATAGCCCATCTGAATCTCAG 123
 QY 55 GINGUASERGLYSEMEPHESESERLEUIETHRTTPASNILEASPGLYLEUASPLEUAN 74
 DB 124 CAGAAATGCGAGCATGTTCTCTCATTAACCTGGAATATTGATGATTAACTAAAC 183
 QY 75 AANLEUSERGLUAGLAARGGLYVALCYSERTYRLEU 87
 DB 184 AATCTGTGAGAGGCGCTGAGGCGTGTCTCTACTTA 222

RESULT 118

BP375391

LOCUS BP375391 Sugano cDNA library, uterus Homo sapiens cDNA clone 548 bp mRNA linear EST 21-SEP-2004

DEFINITION WMC00495, mRNA sequence.

ACCESSION BP375391

VERSION BP375391.1 GI:52404205

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 548)

REFERENCE Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. 548

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="WMC00495"

/tissue_type="uterus"

/clone_lib="Sugano cDNA library, uterus"

ORIGIN

Alignment Scores:

Pred. No.: 6.08e-36 Length: 548
 Score: 363.00 Matches: 74
 Percent Similarity: 85.1% Conservative: 0
 Best Local Similarity: 85.1% Mismatches: 13
 Query Match: 81.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP375391 (1-548)

QY 1 METGUATGALAUASERTYRPHGULUPROVALIGUGLSERLALAUGLUARG 20
 DB 94 ATGGAAGGCGCTCGAAGCTCTACTTCAGAGCTCGGTGAGAGAGGCCCTTGAGAGCG 153
 QY 21 ARGPFGUHTHTRIESEGULUPROLYETHRTYRVALASPENUTHTASGLUGLUATHR 40
 DB 154 CGACCTGAAACCATCTGAGCCCAAGACCTATGNGACCTTAACCAATGAAACAACT 213
 QY 41 AASPETHRTHTSERLYLIESERPROSERGLUASPTHTGINGLUASNGLYSERMET 60
 DB 214 GATTCACCACTTCTAATAATCAGCCCATCTGAAATGATCTCAGCAAGAAATGNCAGCATG 273
 QY 61 PHESELEUIETHRTTPASNILEASPGLYLEUASPLEUANASERGLUARGLA 80
 DB 274 TNCCTTCATTAACCTGGAATATNNATGATTAGACTTAACAAATNNNNNAGAGGCT 333
 QY 81 ARGGLYVALCYSERTYRLEU 87
 DB 334 NNAGNNNNNNNNCTACTTA 354

RESULT 119

AL516230

LOCUS AL516230 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone 816 bp mRNA linear EST 23-MAR-2004

DEFINITION CSODA005YK22 5-PRIME, mRNA sequence.

ACCESSION CSODA005YK22

VERSION AL516230.3 GI:45652882

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 816)

REFERENCE Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 13, 2001 this sequence version replaced gi:30490655.

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 3474.r

For more information about this cluster see

http://www.genoscope.cns.fr/cdna?b=CSODA005BF11QPI&c=3474.r.

Location/Qualifiers

1. 816

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODA005YK22"

/tissue_type="NEUROBLASTOMA"

/clone_lib="Homo sapiens NEUROBLASTOMA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with NotI and cloned into

the NotI and EcoRV sites of the pCMVSPORT 6 vector.

ORIGIN

Alignment Scores:

Pred. No.: 1.85e-35 Length: 816
 Score: 361.00 Matches: 81
 Percent Similarity: 92.3% Conservative: 3
 Best Local Similarity: 89.0% Mismatches: 2
 Query Match: 80.6% Indels: 5
 DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AL516230 (1-816)

QY 2 GUUAGAlaleuanserTyrPheGluProProValGluGluSerAlaLeuGluValArgAr 21
DB 194 GAAAGGGCTCTGACTCTGACCTCCGCTGAGAGAGAGCGCTTGAGAAAGGCGCG 253
QY 21 GPROGluTnTt 41
DB 254 ACCTGAACCATCTCTGAGCCAGACCTATGTTGACCTTAACCAATGAAGAAACACCTGA 313
QY 41 PserTnTt 60
DB 314 TTCACCATCTCTAAATCAGCCATCTGAGATGAGCTCAGCAAGAAATGCGACGAT 373
QY 60 CpheSerLeuTt 80
DB 374 GTCTCTCTCATTAAGCTGGAATATGATGATTAGTCTAAACATCTGTCAGAGGCG 453
QY 80 laArgGlyValCysSerTyrLeu 87
DB 434 CTCGAGGGGTGTCTCTCTCTTA 456

RESULT 120

AV61333 394 bp mRNA linear EST 16-JAN-2002
LOCUS AV61333 GLC Homo sapiens cDNA clone GICGRD01 3', mRNA sequence.
DEFINITION AV61333
ACCESSION AV61333.1 GI:9882347
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 394)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,W., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL

COMMENT
PUBMED
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzegzhgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

source
1..394
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GICGRD01"
/tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Alignment Scores:
Pred. No.: 2,31e-35 Length: 394
Score: 357.00 Matches: 69
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 79.7% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x AV61333 (1-394)

QY 19 GUUAGATGProGluTnTt 38
DB 2 GAAGCCGACCTGGAACCATCTCTGAGCCAGACCTATGTTGACCTTAACCAATCTGAGAG 61
QY 39 TnTt 58
DB 62 ACACATGATTCACCATCTCTAAATCAGCCATCTGAGATGAGTCTTAACCAATCTGAGAG 121
QY 59 SerMetPheSerLeuTt 78
DB 122 AGCATGTTCTCTCATTAACCTGGAATATGATGATTAGTCTTAACCAATCTGAGAG 181
QY 79 ArgAlaArgGlyValCysSerTyrLeu 87
DB 182 AGGGCTCGAGGGGTGTCTCTCTTA 208

RESULT 121

T31666 325 bp mRNA linear EST 06-SEP-1995
LOCUS T31666
DEFINITION EST316732 Human Embryo Homo sapiens cDNA 5' end similar to None,
mRNA sequence.
ACCESSION T31666
VERSION T31666.1 GI:613764
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 325)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulton,R.A.,
Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chui,M.-W.,
Clayton,R.A., Cline,R.T., Cotton,M.D., Barle-Hughes,J., Fite,L.D.,
FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Georgiades,N.S.M.,
Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley,P.S.,
Killey,J.M., Klinek,K.M., Kelley,J.C., Liu,J.-I., Maturo,S.M.,
Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T.,
Pallergino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L.,
Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utechtack,T.R.,
Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A.,
Coleman,T.A., Collins,E.-J., Dinke,D., Feng,P., Ferrite,A.,
Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M.,
Gruber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Li,H., Li,H.,
Matsener,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wang,J., Xu,C.,
Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A.,
Haseeltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial Assessment of Human Gene Diversity and Expression Patterns
Based Upon 83 Million Basepairs of cDNA Sequence
Nature 377, 3-174 (1995)

JOURNAL

COMMENT
PUBMED
Contact: Venter, JC
The Institute for Genomic Research
932 Clopper Rd, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: tdbinfo@tdb.tigr.org
For clone availability, additional sequence and expression
information related to this EST, please contact the TIGR Database
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse

FEATURES

source
1..325
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (Inhost):101908"
/db_xref="taxon:9606"
/tissue_type="embryo"
/clone_lib="Human Embryo"

ORIGIN

Alignment Scores:

Pred. No.: 4,84e-33 Length: 325
 Score: 338.00 Matches: 68
 Percent Similarity: 98.6% Conservative: 1
 Best Local Similarity: 97.1% Mismatches: 0
 Query Match: 75.4% Indels: 1
 DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x T31666 (1-325)

QY 1 MetGUARGAlaleuanserTyrPheglupProProValGluGluSerAlaleuGluArg 20
 |||||
 DB 116 ATGGAAGAGGGCTCTGAACTCTTCTGAGCTCCGCTGAGAGAGAGCGCTTGAGAGCC 175
 QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
 |||||
 DB 176 CGACCTGAACCATCTCTAAGCCGACCTAATGTAACCTAACCAATGAGAGAACT 235
 QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 |||||
 DB 236 GATTCCACACCTCTTAAATCAAGCCCATCTGAAAGATACACAGCAAGAAATGACACATG 295
 QY 61 PheSerLeuIleThrTyrAsnIleAsp 69
 |||||
 DB 296 TTCTCTCTAATTAACCTGGAATTTGAT 323

RESULT 122

LOCUS CN791432 674 bp mRNA linear EST 26-MAY-2004
 DEFINITION 4126159 BARC 8BOV Bos taurus cDNA clone 8BOV_42E11 5', mRNA
 sequence.

ACCESSION CN791432
 VERSION CN791432.1 GI:47687412
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 674)
 Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and

AUTHORS

Matkunnali,L.K.
 Construction and Analysis of a cDNA Library Generated From

Intestinal Muscle and Epithelial Tissues of Holstein Cattle

Unpublished (2004)

CONTACT: Richard G. Baumann
 Bovine Functional Genomics Lab

JOURNAL

COMMENT

ANRI BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
 Tel: 3015048604
 Fax: 3015048744

Email: rbaumann@anri.barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt '' -trim fasta. Vector identified
 by cross match using options -mismatch 12 -minscore 18
 Place: 42 row: 8 column: 11
 Seq primer: CCTATTAGCTACACTATAGAAC

High quality sequence stop: 674.
 Location/Qualifiers

1..674
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="8BOV_42E11"
 /sex="Female"
 /tissue_type="Epithelial, Muscle"
 /dev_stage="Lactating, Neonatal"
 /lab_host="DH10B TONa"
 /clone_11b="BARC 8BOV"
 /note="Organ: Intestine; Vector: pCMVSPORT6.1; Site: 1;
 Note1: Site_2: Score1: Normalized cow cDNA intestinal

FEATURES

source

ORIGIN

library in pCMVSPORT6.1, constructed from equimolar mRNA
 pools derived from 5 sources, 4 lactating intestinal, 1
 neonatal intestinal 4/5 lactating, proximal duodenal,
 jejunum, distal ileum, colon, 1/5 neonatal, proximal
 duodenum, jejunum, distal ileum"

Alignment Scores:

Pred. No.: 9.89e-32 Length: 674
 Score: 331.00 Matches: 67
 Percent Similarity: 83.1% Conservative: 7
 Best Local Similarity: 75.3% Mismatches: 13
 Query Match: 73.9% Indels: 2
 DB: 7 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x CN791432 (1-674)

QY 1 MetGUARGAlaleuanserTyrPheglupProProValGluGluSerAlaleuGluArg 20
 |||||
 DB 61 ATGGAAGAGGGCTCTGAACTCTTCTGAGCTCCGCTGAGAGAGAGCGCTTGAGAGCC 120
 QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
 |||||
 DB 121 CGTCCGAGTCCCTCTGAGCTCGGTCTGTGACCTAACCAAGAGAAACAAT 180
 QY 41 AspSerThrThrSerLysIleSerProSerGluAsp-----ThGlnGlnGluAsnGly 58
 |||||
 DB 181 GATTCCATTAGTCTTAAACCAACCATCTGAAAGATTAAGTGTTCAGCAAGAGATGCG 240
 QY 59 SerMetPheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnIleuSerGlu 78
 |||||
 DB 241 AGTGAATCTCTTTCATTACCTGGAATATGATGATGATGATGATGATGATGATGATGATGAT 300
 QY 79 ArgAlaArgGlyValCysSerTyrLeu 87
 |||||
 DB 301 AGGCTCGAGGGGTGTGTTCCATTTA 327

RESULT 123

LOCUS AV659558 388 bp mRNA linear EST 16-JAN-2002
 DEFINITION AV659558 GLC Homo sapiens cDNA clone GLCFYD04 3', mRNA sequence.

ACCESSION AV659558
 VERSION AV659558.1 GI:9880572
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo
 1 (bases 1 to 388)
 Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
 Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
 Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
 Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level
 by comparing gene expression profiles of hepatocellular carcinoma
 with those of corresponding noncancerous liver
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

TITLE

JOURNAL PUBMED
 11752456
 Contact: Zenguan Han
 Chinese National Human Genome Center at Shanghai
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
 201203, P. R. China
 Tel: 86-21-50801919(ex. 45)
 Fax: 86-21-50801922
 Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

FEATURES

source

1..388
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCFYD04"

/tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="c14t1"
 /lab_host="SCLR"
 /clone_id="GIC"
 /note="Vector: pBluescript sk(-), Site_1: EcoRI, Site_2:
 XhoI"

ORIGIN

Alignment Scores:
 Pred. No.: 8,65e-32 Length: 388
 Score: 329.00 Matches: 68
 Percent Similarity: 79.3% Conservative: 1
 Best Local Similarity: 78.2% Mismatches: 0
 Query Match: 73.4% Indels: 18
 DB: 1 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x AV659558 (1-388)

Oy 1 MetGluArgAlaLeuAsnSerTyrPheGluProValGluGluSerAlaLeuGluArg 20
 Db 96 ATGAAAGAGGCTCTGAACTCTGAGCTCCGCTGAGAGAGAGGCGCTTGAAGCG 155
 Oy 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
 Db 156 CGACCTGAAACCATCTCGAGCCCAAGACCTAGTGTGACCTTAACCAATGAAGAAACAAC 215
 Oy 41 AspSerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 Db 216 GATTCCACCACTTCAAAATCAGCCCACTGAGAGATCTCAGCAAGAC----- 263
 Oy 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
 Db 264 -----AATCTGTCAAGAGAGGCT 281
 Oy 81 ArgGlyValCysSerTyrLeu 87
 Db 282 CGAGGGGTGTGTCTCACTTA 302

RESULT 124
 BP349936 581 bp mRNA linear EST 17-SEP-2004
 LOCUS BP349936 Sugano cDNA library, brain Homo sapiens cDNA clone
 DEFINITION SZR06923, mRNA sequence.
 ACCESSION BP349936
 VERSION BP349936.1 GI:52279921
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 581)
 Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.
 Location/Qualifiers
 1..581
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SZR06923"
 /tissue_type="brain"
 /clone_lib="Sugano cDNA library, brain"

FEATURES

ORIGIN
 Alignment Scores:
 Pred. No.: 1,99e-31 Length: 467
 Score: 327.00 Matches: 64
 Percent Similarity: 86.2% Conservative: 11
 Best Local Similarity: 73.6% Mismatches: 12

Alignment Scores:
 Pred. No.: 1,47e-31 Length: 581
 Score: 329.00 Matches: 64
 Percent Similarity: 98.5% Conservative: 0
 Best Local Similarity: 98.5% Mismatches: 1
 Query Match: 73.4% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BP349936 (1-581)

Oy 23 GluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThrAspSer 42
 Db 3 GAAACCATCTCTGAGCCCAANACCTATGTTGACCTTAACCAATGAAGAAACAACGATTC 62
 Oy 43 ThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSer 62
 Db 63 ACCACTTTCAAAATCAGCCCATCTGAGAAATCTCAGCAAGAAATGCGACGATGTTCTCT 122
 Oy 63 LeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluArgAlaArgGly 82
 Db 123 CTCATTTACCTGAAATATTGATGATTGATTCATTAACCAATCTGTCAAGAGAGGCTCGAGG 182
 Oy 83 ValCysSerTyrLeu 87
 Db 183 GGTGTGTCTCACTTA 197

RESULT 125
 CF788416 467 bp mRNA linear EST 21-OCT-2003
 LOCUS CF788416 860384 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
 DEFINITION CF788416.1 GI:37792977
 ACCESSION CF788416.1 GI:37792977
 VERSION
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae; Suidae;

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 467)
 Smith, T.F., Fekling, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
 Noneman, D.J., May, J.E. and Keale, J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)
 Contact: Smith TF
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390

EMAIL: smith@ma.ars.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_aln option. Vector identified with
 cross_match v0.990329.
 Plate: TWM8003 Row: J Column: 8
 Seq primer: GMAATACGACGACATATGAGG.
 Location/Qualifiers
 1..467
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4P1G"
 /note="Vector: pCDNA3.1, Site_1: EcoRI, Site_2: NotI;
 library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:
 Pred. No.: 1,99e-31 Length: 467
 Score: 327.00 Matches: 64
 Percent Similarity: 86.2% Conservative: 11
 Best Local Similarity: 73.6% Mismatches: 12

Query Match: 73.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CF788416 (1-467)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaleuGluArg 20
DB 179 ATGAAAGAGCCCTGAACTCTTCTGAGCCGCCGTGAGAGAAAGCCTTTAAAGT 238
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 239 CCGCTGAGACCCCAATGAGCCGAGCTCTGTGTTGACTTAACCAAGAGAAACAAGT 298
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 299 GATTCCTTAGTGTGTAACCAAGACATCTGAAATGTTACAGCAAGAAAGATGCGAGTGTG 358
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 359 TTCTCTTCATTAACCTGGAATATGATGATGATGACTTAACCAAGATGCTGCTCGAGAGGCT 418
QY 81 ArgGlyValCysSerTyrLeu 87
DB 419 CGAGGGGTGTGTTCTATTTA 439

RESULT 126

LOCUS DN122208 798 bp mRNA linear EST 15-FEB-2005
DEFINITION 1122397 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION DN122208
VERSION DN122208.1 GI:59816487
KEYWORDS EST
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE 1 (bases 1 to 798)
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
Nonneman,D.J., Wray,J.E. and Keele,J.W.
TITLE Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alit option. Vector identified with
cross_match v0.990329.
Plate: HHY8024 row: L column: 17
Seq primer: GTAATGCACTCACTATAGG.
Location/Qualifiers

FEATURES
source 1..798
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 4P1G"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN

Alignment Scores:

Pred. No.: 4.01e-31 Length: 798
Score: 327.00 Matches: 64
Percent Similarity: 86.2% Conservative: 11
Best Local Similarity: 73.6% Mismatches: 12
Query Match: 73.0% Indels: 0

DB: 8 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x DN122208 (1-798)

QY 1 MetGUARGAlaleuanserTyrPheGluProProValGluGluSerAlaleuGluArg 20
DB 180 ATGAAAGAGCCCTGAACTCTTCTGAGCCGCCGTGAGAGAAAGCCTTTAAAGT 239
QY 21 ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThr 40
DB 240 CCGCTGAGACCCCAATGAGCCGAGCTCTGTGTTGACTTAACCAAGAGAAACAAGT 299
QY 41 AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
DB 300 GATTCCTTAGTGTGTAACCAAGACATCTGAAATGTTACAGCAAGAAAGATGCGAGTGTG 359
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
DB 360 TTCTCTTCATTAACCTGGAATATGATGATGATGACTTAACCAAGATGCTGCTCGAGAGGCT 419
QY 81 ArgGlyValCysSerTyrLeu 87
DB 420 CGAGGGGTGTGTTCTATTTA 440

RESULT 127

LOCUS CF764797 648 bp mRNA linear EST 17-OCT-2003
DEFINITION CF764797 Bos taurus skin cDNA library Bos taurus cDNA clone
ACCESSION CF764797
VERSION CF764797.1 GI:37714016
KEYWORDS EST
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 648)
AUTHORS Wang,Y.H., McWilliam,S. and Lehnert,S.
TITLE Transcription profiling of cattle skin
JOURNAL Unpublished (2003)
COMMENT Contact: Dr Yonhong Wang
Functional Genomics lab
CSIRO Livestock Industries
Level 5, Queensland Biosciences Precinct, University of Queensland,
306 Carmody Road St. Lucia QLD Australia
Tel: 07 3214 2445
Fax: 07 3214 2685
Email: Yonhong.Wang@csiro.au
Plate: 41 row: G column: 05.
Location/Qualifiers

FEATURES
source 1..648
/organism="Bos taurus"
/mol_type="mRNA"
/strain="Hereford Shorthorn"
/db_xref="taxon:9913"
/clone="CCL003181"
/sex="female"
/tissue_type="pooled"
/dev stage="Adult"
/lab_host="XLI-BlueMRF strain"
/clone_lib="Bos taurus skin cDNA library"
/note="Organ: skin; Vector: Uni-ZAPXR; Site 1: EcoRI;
Site 2: Xho I; Library made from pooled skin of adult
female Hereford-Shorthorn."

ORIGIN

Alignment Scores:

Pred. No.: 5.5e-31 Length: 648
Score: 325.00 Matches: 66
Percent Similarity: 82.0% Conservative: 7
Best Local Similarity: 74.2% Mismatches: 14
Query Match: 72.5% Indels: 2

DB: 6 Gaps: 1
US-10-757-745-2_COPY_54_140 (1-87) x CF764797 (1-648)

QY 1 MetGluArgAlaLeuAsnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
DB 68 ATGAAAGAGCCCTAACTCTGACCCGCGCGAGAGAGAGCGCTTCAGAAAGC 127
QY 21 ArgProGluThrIleSerGluProLeuThrTyValAspLeuThrAsnGluGluThr 40
DB 128 CGTCCGAGTCCCTCTGAGCCGCGCTGTTGACCTAACCAAGAGAAACAAT 187
QY 41 AspSerThrThrSerLeuIleSerProSerGluAsp-----ThrGlnGlnGluAsnGly 58
DB 188 GATTCATTAGTCTTAAACCAACGACATCTGAGATTAAGATGTTTCAGCAAGAAAGATGC 247
QY 59 SerMetPheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGlu 78
DB 248 AGTGATGTCTTCTTCACTTACCTGGAATTTGATGATGACATGAACATCTCTAGAG 307
QY 79 ArgAlaArgGlyValCysSerTyLeu 87
DB 308 AGGCTCGAGGGGTGTGTTCTATTTA 334

RESULT 128

CN789157 683 bp mRNA linear EST 26-MAY-2004
LOCUS 4123581 BBOV Bos taurus cDNA clone 8BOV_37N03 5', mRNA
DEFINITION Sequence.

ACCESSION CN789157
VERSION CN789157.1 GI:47685137
KEYWORDS EST.

SOURCE Bos taurus (cow)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 683)
AUTHORS Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassell, C.P. and Matukumalli, L.K.

TITLE Construction and Analysis of a cDNA Library Generated From Intestinal Muscle and Epithelial Tissues of Holstein Cattle

JOURNAL Unpublished (2004)

COMMENT Contact: Richard G. Baumann
Bovine Functional Genomics Lab

ANR1 BLDG 162; BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744

EMAIL: rbaumann@anr1.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt '-trim fasta. Vector identified
by cross match using options -mismatch 12 -minscore 18

Plate: 37 row: N column: 03
Seq primer: CCTATTAGGTGACACTATAGAAC
High quality sequence stop: 683.

Location/Qualifiers
1..683

FEATURES
source

/organism="Bos taurus"
/mol_type="mRNA"
/strain="Holstein"
/db_xref="taxon:9913"
/clone="8BOV_37N03"
/sex="Female"

/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TONa"
/clone_id="BARC_8BOV"

/note="Organ: Intestine; Vector: pCMVSPORT6.1; Site: 1;
Not; Site 2: EcorI; Normalized cow cDNA intestinal
library in pCMVSPORT6.1, constructed from equimolar mRNA

pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,

ORIGIN

Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum

Alignment Scores:
Pred. No.: 5,89e-31 Length: 683
Score: 325.00 Matches: 66
Percent Similarity: 82.0% Conservative: 14
Best Local Similarity: 74.2% Mismatches: 2
Query Match: 72.5% Indels: 1
DB: 7 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x CN789157 (1-683)

QY 1 MetGluArgAlaLeuAsnSerTyPheGluProProValGluGluSerAlaLeuGluArg 20
DB 55 ATGAAAGAGCCCTAACTCTGACCCGCGCGAGAGAGAGCGCTTCAGAAAGC 114
QY 21 ArgProGluThrIleSerGluProLeuThrTyValAspLeuThrAsnGluGluThr 40
DB 115 CGTCCGAGTCCCTCTGAGCCGCGCTGTTGACCTAACCAAGAGAAACAAT 174
QY 41 AspSerThrThrSerLeuIleSerProSerGluAsp-----ThrGlnGlnGluAsnGly 58
DB 175 GATTCATTAGTCTTAAACCAACGACATCTGAGATTAAGATGTTTCAGCAAGAAAGATGC 234
QY 59 SerMetPheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGlu 78
DB 235 AGTGATGTCTTCTTCACTTACCTGGAATTTGATGATGACATGAACATCTCTAGAG 294
QY 79 ArgAlaArgGlyValCysSerTyLeu 87
DB 295 AGGCTCGAGGGGTGTGTTCTATTTA 321

RESULT 129

B1181461 750 bp mRNA linear EST 10-JUL-2001
LOCUS B1181461
DEFINITION UNL-P-FN-ak-a-12-0-UNL.g1 UNL-P-FN Sus scrofa cDNA clone

UNL-P-FN-ak-a-12-0-UNL 3', mRNA sequence.

ACCESSION B1181461
VERSION B1181461.1 GI:14655870
KEYWORDS EST.

SOURCE Sus scrofa (pig)
ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
Sus.

REFERENCE 1 (bases 1 to 750)
AUTHORS Caetano, A.R., Johnson, R.K. and Pomp, D.

TITLE Generation and sequence characterization of a normalized cDNA
library from swine ovarian follicles

JOURNAL Mamm. Genome 14 (1), 65-70 (2003)
PUBMED 12532269

COMMENT Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincoln
Lincoln, NE 68583-0908, USA

Tel: 402 472 6416
Fax: 402 472 6362
Email: dpomp@unl.edu

Oligo-dt track not found. Not I site shown in beginning of sequence
is likely internal to the message.

Seq primer: M13 -29

POLYA=No.

Location/Qualifiers
1..750

FEATURES
source

/organism="Sus scrofa"
/mol_type="mRNA"
/strain="University of Nebraska, Lincoln Swine Selection
Lines"

/db_xref="taxon:9823"
/clone="UNL-P-FN-ak-a-12-0-UNL"
/dev_stage="ADULT"

/lab host="EDH10B (Life Technologies)"
 /clone lib="UNL-P-FN"
 /note="Vector: pUT7AD-Pac (Pharmacia) with a modified
 polylinker. Site_1: Not I; Site_2: Eco RI; The UNL-P-FN
 library is a normalized library representing porcine
 ovarian follicles, ranging between 2.0 to 10.0 mm in
 diameter, collected during 7 days of the follicular phase
 of the pig estrous cycle. This library was derived from
 the library UNL-P-FP. The tag is a string of 5-6
 nucleotides present between the Not I site and the
 oligo-dT track. The library was constructed as described
 by Bonaldi, Lennon and Soares, Genome Research 6:
 791-806, 1996.
 TAG_SEQ=None Found"

The following treatments: 1) no treatment, 2) *Salmonella choleraesuis* vaccine strain SC-54, 3) phorbol myristate acetate, concanavalin A, and 8-bromo-cyclic AMP, and 4) lipopolysaccharide and cholera toxin. Each treatment was performed in the presence and absence of cycloheximide. Purified poly A⁺ RNA from each of the treated tissues (2-4) was combined together, reverse transcribed, and cloned in to pCMVSPORT6 to make a library of approximately 530,000 recombinant clones with an average insert size of 1.0 kbp. Poly A⁺ RNA from freshly isolated and non-treated tissue from an Ussing chamber (treatment 1) was cloned in the same manner to produce an unstimulated cDNA library of approximately 900,000 clones with an average insert size of 1.5 kbp. Equal portions of the two libraries were pooled and then subtracted with porcine ST fibroblast RNA to create a subtracted porcine Peyer's patch library of approximately 6,000 clones with an average insert size of 1.0 kbp."

ORIGIN

Alignment Scores:	
Pred. No.:	2,19e-29
Score:	312.00
Percent Similarity:	85.7%
Best local Similarity:	72.6%
Query Match:	69.6%
DB:	6
	Gaps:
	0

US-10-757-745-2_COPY_54_140 (1-87) × CB286391 (1-581)

QY	4	AlaLeuAnaSerTyrPheGluProProValGluGluSerAlaLeuGluArgArgProGlu	23
Db	1	GGCGTGAACCTCCTATTGAGCGGGGCCGTGGAGAGAACGCTTTAAAAAGTCCTCTGAG	60
QY	24	ThrIleSerGluProIleThrTyrValAspLeuThrAsnGluGluThrThrAspSerThr	43
Db	61	ACCCCGCATGAGCCCGAGCTCGTGTGTGACTTAAACCAAGAGAAACAAGTATTCCTT	120
QY	44	ThrSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeu	63
Db	121	AGTTGTAAACCGACACATCTTAAAAATGTTCCAGCAAGAAAGATGGCAGTGTCTCTTTC	180
QY	64	IleThrTyrPasnIleAspGlyLeuAspLeuAsnAsnLeuSerGluIaArgIaArgIaVal	83
Db	181	ATTACCTGGAATATGATGATGATGGACCTTAACACAGCTCTCGAGAGGGCTCGAGGGGTG	240
QY	84	CysSerTyrLeu	87
Db	241	TGTTCCATTTTA	252

LOCUS	BP270589	581 bp	mRNA	linear	EST 17-SEP-2000
DEFINITION	BP270589 Sugano cDNA library, small intestine Homo sapiens cDNA clone KAR02706, mRNA sequence.				

KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 581)
AUTHORS	Suzuki, Y., Yamashita, R., Shiroya, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo

4-6-1, Shitukanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ins.n-tokyo.ac.jp.
Location/Qualifiers
1. 581

FEATURES

Source

ORIGIN

Alignment Scores:	
Pred. No.:	3,95e-29
Score:	31.00
Percent Similarity:	98.5%
Best Local Similarity:	98.5%
Query Match:	69.2%
DB:	3
Length:	581
Matches:	64
Conservative:	0
Mismatches:	0
Indels:	1
Gaps:	0

US-10-757-745-2_COPY_54_140 (1-87) X BP270589 (1-581)

QY	1	MeGIARAlAAlenAAsuSerTyrzheGluProProValGluGluSerAlAlenGluArg	20
Db	388	ATGGAAGAGGCTCTGAATCCCTCACTTCAGAGCTCCGGTGGAGGAGAGCGCCTTGGAAAGC	447
QY	21	ArgProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrThr	40
Db	448	CGACCTGAAACCATCTCTGAGCCCAAGACTATGTGGACCTAACCAATGAAAGAAACAAC	507
QY	41	AspSerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsn-GlySerMe	60
Db	508	GATTCACCACTCTCAAAATCAGCCCACTGAAAGATCACTCAGCAAGAAAAATGGCGACAT	567
QY	60	tpheSerLeuIle64	
Db	568	GTTCCTCTCAATT580	

RESULT	134
EX433489/c	
LOCUS	952 bp mRNA linear EST 04-MAY-2004
DEFINITION	BX433489 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
ACCESSION	C60DN005YN02.3-PRIME, mRNA sequence.
VERSION	BX433489
KEYWORDS	BX433489.2 GI:47002503
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
	Hominidae; Homo.
REFERENCE	1 (bases 1 to 952)
AUTHORS	L1,M.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	On May 15, 2003 this sequence version replaced gi:30775195.

Genoscope - Centre National de Séquençage
2 rue Gaston Crémieux, CP 5706 - 91057 Evry cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primed
ends enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BAI056ZD12_CS05372_1&c=3474.r

FEATURES

```
FEATURES
  source
    Location/Qualifiers
      1..952
      /organism="Homo sapiens"
      /mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="CS0DN005YN02"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: Brain; Vector: PCWSPORT_6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the PCWSPORT 6
vector. Library was not normalized."

```

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:
Score: 7.55e-29	952	68
Percent Similarity: 90.8%	Conservative: 1	6
Best Local Similarity: 89.5%	Mismatches: 2	0
Query Match: 5	Gaps: 0	

US-10-757-745-2_COPY_54_140 (1-87) x BK433489 (1-952)

QY 13 ValGluGluSerAlaLeuGluArgArgProGluThrIleSerGluProGlyThrTyVal 32
 DB 948 GTGGAGGAGAGCGGCTTGGACGCCGAACTGAAACCTCTCTGAGCCCAAGACTATGT- 890

QY 33 AspleuthraAngluGluThr-Thr-AspSerThrThrSerIleSerProSerGluAs 52
 DB 889 GACCTAACCAATGAGAAACAACACTGATTCACACTTCTAAATCAGCCCACTGAGAA 830

QY 52 PThrGlnGlnGluAnglySerMetPheSerIleuIleThrTrpAsnIleAspGlyLeuAs 72
 DB 829 TACTGAGCAAGAAATGCGAGCATGTCTCTCTCATTAACCGAATATGATGATGATTGA 770

QY 72 PleuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrlleu 87
 DB 769 TCTAAACATCTGTCAAGAGAGGCTGAGAGGCTGTGTCTCTACTTA 724

RESULT 135

CN803230 965 bp mRNA linear EST 26-MAY-2004
 LOCUS ILLUMIGEN MCQ 32551 Katze MMR Macaca mulatta cDNA clone
 DEFINITION IBIW:12605 5' similar to Bases 1 to 965 highly similar to human
 TTRAP (Hs.210628), mRNA sequence.

ACCESSION CN803230
 VERSION CN803230
 KEYWORDS EST.
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.
 1 (bases 1 to 965)
 MAGNESSE, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
 Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
 Iadonato, S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 1598449
 CONTACT: C. Magnesse
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagnesse@illumigen.com
 Sequenced on 2004.04.02. 780 Q20 bases.
 PCR Primers
 FORWARD: CCTCCTAAAGGAGACAAA
 BACKWARD: CACTATAGGCGCAATTGGTA
 Insert length: 965 Std Error: 0.00
 Plate: C1000288 row: D column: 11
 Seq primer: CCTCCTAAAGGAGACAAA

FEATURES
 source POLVA=No.
 Location/Qualifiers
 1..965
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBIW:12605"
 /sex="female"
 /dev_stage="adult"
 /lab_host="E. coli SOLR"
 /clone_lib="Katze MMR"
 /note="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
 Site 2: Xho I; Created from Stratasene ZAP-cDNA Synthesis
 Kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
 Cloning Kit (catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.:	Length:	Matches:
Score: 3.35e-28	965	59
Percent Similarity: 305.00	Conservative: 0	95.24
Best Local Similarity: 95.24	Mismatches: 3	0
Query Match: 68.14	Indels: 0	
DB: 7	Gaps: 0	

US-10-757-745-2_COPY_54_140 (1-87) x CN803230 (1-965)

QY 26 SerGluProGlyThr-TyValAspLeuThrAsnGluGluThrThrAspSerThrThrSer 45
 DB 2 TCTGAGCCCAAGACCTATGTTGACCTTAACCAATGAGAAACAACGATTCACACCTTCT 61

QY 46 LysIleSerProSerGluAspThrGlnGlnGluAnglySerMetPheSerIleuIleThr 65
 DB 62 AAATAGCCCATCTGGAAGATATCTACAGCAAGAAAGACGATGTCTGCTCATTAACC 121

QY 66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85
 DB 122 TGGAAATTTGATGATGATGATCTTAACATCTGTCAAGAGAGGCTGAGAGGCTGTGTTC 181

RESULT 136

CR767008 365 bp mRNA linear EST 23-SEP-2004
 LOCUS DKEZp469G2436_r1_469 (synonym: pklid) Pongo pygmaeus cDNA clone
 DEFINITION DKEZp469G2436_5', mRNA sequence.

ACCESSION CR767008
 VERSION CR767008
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Pongo.
 1 (bases 1 to 365)
 ANSORGE, W., Krieger, S., Regiert, T., Rittmuller, C., Schwager, B.,
 Mewes, H.W., Weill, B., Aml, C., Oesinger, A., Fobo, G., Han, M. and
 Wiemann, S.
 Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 CONTACT: MIPS

MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ),
 Email: s.wiemann@dkfz-heidelberg.de, rlin, Germany. Please contact
 DKFZ for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKEZp469G2436
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.

FEATURES
source

Location/Qualifiers
1.365
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP469G2436"
/tissue_type="Kidney"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pSPORT1; Site_1: SfilA; Site_2: SfilB"

ORIGIN

Alignment Scores:

Pred. No.: 7.37e-28 Length: 365
Score: 298.00 Matches: 60
Percent Similarity: 95.2% Conservative: 0
Best Local Similarity: 95.2% Mismatches: 3
Query Match: 66.5% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CR767008 (1-365)

QY 1 MetGUArgAlaLeuAnsSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 176 ATGGAAGAGCGCTCTGAACCTCTACTTCGAGCCCTCGGTGAGAGNAGCCCTTGAACGC 235
QY 21 ArgProGluThrIleSerGluProIleThrTyValAspLeuThrAsnGluThrThr 40
DB 236 CCCCCGAAACCATCTCTGAGCCCAAGACCTATGTCTTACCTAACCAATGAGAAACACT 295
QY 41 AspSerThrThrSerTyRphGluProSerGluAspThrGluGluGluSerMet 60
DB 296 GATTCACACACTCTTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGCGACGATG 355
QY 61 PheSerLeu 63
DB 356 TCCTCTCTC 364

RESULT 137

R14990 416 bp mRNA linear EST 13-APR-1995
LOCUS YG45C11.r1 Soares infant brain IN1B Homo sapiens cDNA clone
DEFINITION IMAGE:35717 5', mRNA sequence.

ACCESSION R14990
VERSION R14990.1 GI:769263
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 416)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Woldmann, P. and
Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Insert Size: 1716
High quality sequence stops: 277 Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert Length: 1716 Std Error: 0.00
Seq primer: M13RP1
High quality sequence stop: 277.

FEATURES
source

Location/Qualifiers
1.416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="DB:408218"
/db_xref="taxon:9606"
/clone="IMAGE:35717"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain IN1B"
/note="Organ: whole brain; Vector: pGEMT; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
AACTGGAAGAAATTCGCGCGCCGAGGAAATTTTTTTTTTTT 3'];
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacia), digested with Not I and directionally cloned
into the Not I and Hind III sites of the lacZid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 2.12e-27 Length: 416
Score: 295.00 Matches: 78
Percent Similarity: 86.8% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 5
Query Match: 65.8% Indels: 8
DB: 8 Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x R14990 (1-416)

QY 1 MetGUArgAlaLeuAnsSerTyRphGluProProValGluGluSerAlaLeuGluArg 20
DB 96 ATGGAAGAGCGCTCTGAACCTCTACTTCGAGCCCTCGGTGAGAGNAGCCCTTGAACGC 154
QY 21 ArgProGluThrIleSerGluProIleThrTyValAspLeuThrAsnGluThrThr 40
DB 155 CGACCTGAAACCATCTCTGAGCCCAAGACCTATGTCTTACCTAACCAATGAGAAACACT 214
QY 41 AspSerThrThrSerTyRphGluProSerGluAspThrGluGluGluSerMet 60
DB 215 GATTCACACACTCTTAAATCAGCCCATCTGAAAGATCTCAGCAAGAAATGCGACGATG 274
QY 60 PheSerLeuIleThrTyRAsnIleAspGlyLeuAsp--LeuAsnLeuSerG 78
DB 275 GTTCTCTCTTCACTTACCTGGAATATTGATGATTAAGATCTTAAACCAATCTGTGAG 334
QY 78 IuArg--AlaArgGlyValCys 84
DB 335 AGGAGGGGAGTCCAGGGGGGTGT 357

RESULT 138

BF243927 751 bp mRNA linear EST 14-NOV-2000
LOCUS BF243927
DEFINITION 601877278P1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105866 5',
mRNA sequence.

ACCESSION BF243927
VERSION BF243927.1 GI:1157869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 751)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM988 row: K column: 19
 High quality sequence stop: 533.

FEATURES

source
 1..751
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4105866"
 /issue_type="from acute myelogenous leukemia"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH_MGC_55"
 /note="Organ: Bone Marrow; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
 (ggccatcggcc); Double stranded cDNA was prepared from
 cell line RNA. 5' and 3' adaptors were used in cloning as
 follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3' and
 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size
 1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained
 inserts by PCR. This library was enriched for full-length
 clones and was constructed by Clontech Laboratories (Palo
 Alto, CA)."

ORIGIN

Alignment Scores:

Pred. No.: 2,326-26 Length: 751
 Score: 28950 Matches: 80
 Percent Similarity: 89.9% Conservative: 0
 Best Local Similarity: 89.9% Mismatches: 7
 Query Match: 94.6% Indels: 7
 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BF243927 (1-751)

Db 1 MetGluArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaGluArg 20
 152 ATGGAAAGGCTCTGAACCTTCACTTCAAGCTCCGTTGAGAGAGAGCCCTTGAAAGCC 211
 Db 21 ArgProGluThrIleSerGluProIleThr-TyrValAspLeuThrAsnGluThrTh 40
 212 CGACT-GAAACCATCTCTAGCCCAAGCCTTATCTTGACCTTAACCAATGAGAAAACT 270
 Db 40 AspSerThrThrSerIleSerProSerGluAspThrGluGluAsnGlySerMe 60
 271 GGAATCCACCAT-TCNNAAATCAG-CCATCTGAAGTCT-CAGCAAGAAAAATGGCAGCT 327
 Db 60 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluVal 80
 328 GTC-TCTCTCATACCTCGAATTTATGATTAAGATCTTAACATCTGTCAAGAGGGCC 386
 Db 80 ArgGlyVal-CysSerTyrLeu 87
 387 TCGAGGGGTGGTCTCTACTTA 409

RESULT 139

LOCUS BG623866 898 bp mRNA linear EST 18-APR-2001
 DEFINITION 60249018F1 NIH_MGC_79 Homo sapiens CDNA clone IMAGE:4770389 5',
 RRNA sequence.

ACCESSION BG623866
 VERSION BG623866.1 GI:13675237
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.

REFERENCE 1 (bases 1 to 898)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: csapbs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM1637 row: d column: 06
 High quality sequence stop: 688.

FEATURES

source

1..898
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4770389"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_id="NIH_MGC_79"
 /note="Organ: placenta; Vector: pDNR-LIB (Clontech);
 Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
 (ggccatcggcc); 5' and 3' adaptors were used in cloning
 as follows: 5' adaptor sequence: 5'-CACGCCATTATGCC-3'
 and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCCGACATG-dt(30)BN-3' (where B = A,
 C, or G and N = A, C, G, or T). Average insert size 1.3
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4,566-26 Length: 898
 Score: 288.00 Matches: 56
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 64.3% Indels: 0
 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x BG623866 (1-898)

Db 32 ValAspLeuThrAsnGluThrThrAspSerThrThrSerIleSerProSerGlu 51
 440 GTTGACCTTAACCAATGAGAAACAACGATTCACCACTTAATAATCAGCCCATCTGAA 499
 Db 52 AspThrGluGluGluAsnGlySerMetPheSerLeuIleThrTyrAsnIleAspGlyLeu 71
 500 GATCTCTAGAGAGAAATGGCGCATGTCTCTCTCAATACCGAATATGATGATTA 559
 Db 72 AspLeuAsnAsnLeuSerGluArgAlaGlyValCysSerTyrLeu 87
 560 GATCTAAACAATCTGTCAAGAGAGGCTCGAGGGGTGGTCTCACTTA 607

RESULT 140

LOCUS BM539358 635 bp mRNA linear EST 20-FEB-2002
 DEFINITION hb08d09.g1 Canis CDNA from testes cells Canis familiaris cDNA
 clone hb08d09 5', mRNA sequence.

ACCESSION BM539358
 VERSION BM539358.1 GI:18821216
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.
 1 (bases 1 to 635)
 O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Ballja,V.,

REFERENCE 1 (bases 1 to 645)
AUTHORS Cogburn, L.A., Morgan, R. and Burnside, J.
TITLE ESTs from Normalized Chicken fat cDNA library-USDA/IFAFS Animal
Genome Project
JOURNAL Unpublished (2002)
COMMENT Contact: Larry A. Cogburn

University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburnudel.edu, www.chickest.udel.edu.

FEATURES

Source
Location/Qualifiers
1..645
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler, Ottawa Research Centre, leghorn"
/db_xref="taxon:9031"
/clone="pGf2n.pK002.c6"
/sex="Male and Female"
/tissue_type="Abdominal Fat"
/dev_stage="Embryonic (d18,d19) ; post-hatch (d1,w3,w7,w9,w16,y1z)"
/lab_host="E. coli EMDH10B"
/clone_lib="Normalized Chicken Abdominal Fat Library (pGf2n)"
/note="Vector: PCMVSPORT6; Library made from equivalent pools of total RNA isolated from each developmental age (across strains); Single pass sequencing from 5'-end"

ORIGIN

Alignment Scores:

Pred. No.: 4,54e-18 Length: 645
Score: 224.00 Matches: 46
Percent Similarity: 70.1% Conservative: 15
Best Local Similarity: 52.9% Mismatches: 24
Query Match: 50.0% Indels: 2
DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BM426270 (1-645)

QY 1 MetGUAArgAlaLeuAnsSerTyRheGluProProValGluGluSerAlaLeuGluArg 20
Db 196 CTGGAGAGGGCGCTGAGCCCTTCAAGCGCGCGATGACAGCGCGCGCGCGCG 255
QY 21 ArgProGluThrIleSerGluProLySerTyRValAspLeuThrAsnGluThr 40
Db 256 GCAGAGAGGGCGCTGCGCGCGCGCTGGAAGCGTGTTTACCTCACACAGATGATCTCA 315
QY 41 AspSerThrSerIleSerProSerGluAspThrGluGluGluAsnGlySerMet 60
Db 316 AGTAATACCGACAGC-----AGTGGTGCAGACCTCCAAAGCAACAAGATGATGACAGCAGC 369
QY 61 PheSerLeuIleThrTPAenIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 80
Db 370 TTCTCGCTGATTAAGCTTGGAACATTGATGGCTGAGCTGGGGAATCTGCACAGCGAGCT 429
QY 81 ArgGlyValCysSerTyRleu 87
Db 430 AAGGTGTCTTCTTACTCG 450

RESULT 143

CN642527 1087 bp mRNA linear EST 12-MAY-2004
LOCUS CN642527
DEFINITION ILUMIGEN MC0 6530 Katze MPMPL2 Macaca mulatta cDNA clone IBUM:4699
5' similar to Bases 1 to 1084 highly similar to human TTRAP
(Hs.210628), mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Macaca mulatta (rhesus monkey)
Macaca mulatta
Bukayorta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.
1 (bases 1 to 1087)
Magness, C.L., Fellin, P.C., Thomas, M.J., Korth, M.J., Agy, M.B.,
Prohl, S.C., Fitzgibbon, M., Scherer, C.A., Miner, D.G., Katze, M.G. and
Iadonato, S.P.

TITLE Analysis of the Macaca mulatta transcriptome and the sequence
JOURNAL divergence between Macaca and human
PUBLISHED Genome Biol. 6 (7), R60 (2005)
1596449
CONTACT: C. Magness
ILLUMIGEN Biosciences Inc. 450, Seattle, WA 98134, USA
2205 Airport Way S, Suite 450
Tel: 2063780408
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2003.12.24. 840 Q20 bases.
PCR PRIMER: CCTGCTAAGAGGAGACAAA
FORMARD: CACTATGCGCGAATTCGCTA
BACKWARD: CACTATGCGCGAATTCGCTA
Insert Length 1087 Std Error: 0.00
Plate: CL000006 Row: D Column: 10
Seq primer: CCTGCTAAGAGGAGACAAA
POLYA-No.

FEATURES

Source
Location/Qualifiers
1..1087
/organism="Macaca mulatta"
/mol_type="mRNA"
/strain="Indian"
/db_xref="taxon:9544"
/clone="IBUM:4699"
/sex="male"
/dev_stage="newborn infant"
/lab_host="E. coli SOLR"
/clone_lib="Katze MPMPL2"
/note="Organ: Placenta; Vector: Uni-ZAP XR; Site 1: Ecor
I; Site 2: Xho I; Created from Strategene ZAP-CDNA
Synthesis Kit (catalog #200400) and ZAP-CDNA GigaPack III
Gold Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.: 2.18e-17 Length: 1087
Score: 221.00 Matches: 43
Percent Similarity: 93.5% Conservative: 0
Best Local Similarity: 93.5% Mismatches: 3
Query Match: 49.3% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CN642527 (1-1087)

QY 42 SerThrSerIleSerProSerGluAspThrGluGluGluAsnGlySerMetPhe 61
Db 2 TCCACCACTTCAAAATCGCCCATCTGAAGATCTCAGCAAGAAATGACGATGTTTC 61
QY 62 SerLeuIleThrTPAenIleAspGlyLeuAspLeuAsnLeuSerGluArgAla 81
Db 62 TGCTTCATTAAGCTTGGAACATTGATGGCTGAGCTGGGGAATCTGCACAGCGAGCT 121
QY 82 GlyValCysSerTyRleu 87
Db 122 GGGGTGTCTTCTTACTTA 139

RESULT 144

Bu471395 625 bp mRNA linear EST 30-NOV-2002
LOCUS Bu471395
DEFINITION 603363114F1 CSEORBN21 Gallus gallus cDNA clone CHEST258k3 5', mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 625)
Boardman, P.E., Sanz-Bzquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445332
COMMENT Contact: Simon Hubbard
Department of Biomedical Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1. 625
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST258K3"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQRBN21"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and EcorI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldi et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 1,41e-17 Length: 625
Score: 220.00 Matches: 45
Percent Similarity: 69.0% Conservative: 15
Best Local Similarity: 51.7% Mismatches: 25
Query Match: 49.1% Indels: 2
DB: 5 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BU471395 (1-625)

QY 1 MetGUARGAlaleuanserTyrPhegluProProValGluGluSerAlaleuGluArg 20
Db 109 CTGGAGAGGGCGCTGAGCGCTACTTGTAGCGCGCATACAGACAGACGGCGGCGG 168
QY 21 ArgProgluThrIleSerGluProlysthrTyrValAspLeuThrAsnGluGluThr 40
Db 169 GCAGAGAGGGCGCTCGCGCGGCTGAGACCTGATGACTCAGACGACATGATGCA 228
QY 41 AspSerThrThrSerIleSerProserGluAspThrGlnGlnGluAsnGlySerMet 60
Db 229 AGTAATACCGAGCAGC-----AGTGTGCGAGCTCCAAAGCAACAGATGATGACGAC 282
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 283 TTCTCGCTGATTAACCTTGAAACATGATGGCTGAGACCTGGGAGATCTGCAGAGCGAGCT 342
QY 81 ArgGlyValCyseSerTyrLeu 87
Db 343 AGAGGTGTCTGTCTTACTCG 363

RESULT 145
LOCUS BI067773 662 bp mRNA linear EST 15-JUN-2001
DEFINITION pgfin.pk007.d9 normalized chicken fat cDNA library Gallus gallus
CDNA clone pgfin.pk007.d9 5' similar to gi11418470

ref|XP_004263.1| TRAF and TNF receptor-associated protein. [Homo
sapiens] emb|CMA1141.1| (AL031775) dJ30W3.3 (novel protein similar
to C. elegans Y63D3A.4) [Homo sapiens] emb|CAB2966.1| (A2269473)
TRAF and TNF receptor associated prote, mRNA sequence.

ACCESSION BI067773.1 GI:14475295
VERSION EST
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 662)
Coburn, L.A., Morgan, R.W. and Burnside, J.
Chicken ESTs from fat
Unpublished (2001)
JOURNAL
COMMENT Contact: Larry A. Coburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: coburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1. 662
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgfin.pk007.d9"
/sex="Male and Female"
/tissue_type="fat"
/lab_host="E.coli BMDH10B"
/clone_lib="normalized chicken fat cDNA library"
/note="Vector: pSPORT1"

ORIGIN

Alignment Scores:
Pred. No.: 1,53e-17 Length: 662
Score: 220.00 Matches: 45
Percent Similarity: 69.0% Conservative: 15
Best Local Similarity: 51.7% Mismatches: 25
Query Match: 49.1% Indels: 2
DB: 2 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BI067773 (1-662)

QY 1 MetGUARGAlaleuanserTyrPhegluProProValGluGluSerAlaleuGluArg 20
Db 118 CTGGAGAGGGCGCTGAGCGCTACTTGTAGCGCGCATACAGACAGACGGCGGCGG 177
QY 21 ArgProgluThrIleSerGluProlysthrTyrValAspLeuThrAsnGluGluThr 40
Db 178 GCAGAGAGGGCGCTCGCGCGGCTGAGACCTGATGACTCAGACGACATGATCTGCA 237
QY 41 AspSerThrThrSerIleSerProserGluAspThrGlnGlnGluAsnGlySerMet 60
Db 228 AGTAATACCGAGCAGC-----AGTGTGCGAGCTCCAAAGCAACAGATGATGACGAC 291
QY 61 PheSerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAla 80
Db 222 TTCTCGCTGATTAACCTTGAAACATGATGGCTGAGACCTGGGAGATCTGCAGAGCGAGCT 351
QY 81 ArgGlyValCyseSerTyrLeu 87
Db 352 AGAGGTGTCTGTCTTACTCG 372

RESULT 146
LOCUS BU468774 946 bp mRNA linear EST 30-NOV-2002
DEFINITION 603571865F1 CSEQRBN20 Gallus gallus cDNA clone CHEST279b17 5', mRNA
sequence.
ACCESSION BU468774
VERSION BU468774.1 GI:25962351
KEYWORDS EST

SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 946)
 REFERENCE Boardman, P.R., Sanz-Exquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 JOURNAL 12445392
 PUBMED
 COMMENT Contact: Simon Hubbard
 Department of Biomedical Sciences
 University of Manchester Institute of Science and Technology
 (UMIST) 1
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 0161206830
 Fax: 01612360403
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 source
 1..946
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Layer and broiler"
 /db_xref="taxon:9031"
 /clone="CHEST2/9b17"
 /sex="Male and female"
 /tissue_type="Chondrocytes isolated from growth plate cartilage"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1fb="CS60RN20"
 /note="Vector: Bluescript II KS(+); Site_1: EcoRI; Site_2: NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylation C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN
 Alignment Scores:
 Pred. No.: 2,82e-17 Length: 946
 Score: 219.50 Matches: 46
 Percent Similarity: 71.3% Conservative: 16
 Best Local Similarity: 52.9% Mismatches: 22
 Query Match: 49.0% Indels: 3
 DB: 5 Gaps: 2
 US-10-757-745-2_COPY_54_140 (1-87) x BU648774 (1-946)
 QY 1 MetGUARGAAlaUeAuSeSerTYrPhGluPProProValGluGluSeRAlaLeuGluAry 20
 Db 60 CTGGAGAGGGCGCTGAGCGCCCTATTGAGCGCGCATGAACGAGCGCGCGCGCGCA 119
 QY 21 ArgProGluThrIleSerGluProLySThrTYrValAspLeuThrAsnGluGluThrThr 40
 Db 120 GGAGGGAGACTCG--GCGGGGCGCTGGAGACTGTATTGACCTCAAGAGATGATATCTGCA 176
 QY 41 AspSerThrThrSerLySileSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 Db 177 AGTATATCAACAGCAC-----AGTGGTGCAAGCTCAAGCAACAAGATGATGACACAC 230
 QY 61 PheSerLeuIleThrTyrPheAlaIleAspGlyLeuAspLeuAsnLeuSeuSerGluAryAla 80
 Db 231 TTCTCGCTGATTAACCTTGAGACATTGATGGCTGAGCTGGGGAAATCTGCAGAGCGAGCT 290

QY 81 ArgGlyValCysSerTyrLeu 87
 Db 291 AGAGGTCTCTGTTCTTACTCTG 311
 RESULT 147
 BI064472
 LOCUS
 DEFINITION B1064472 600 bp mRNA linear EST 15-JUN-2001
 Pffin.pk001.h17 normalized chicken fat cDNA library Gallus gallus
 ref|NP_057698.1| XP_P and YNP receptor-associated protein [Homo sapiens] gb|AF64144.1|AF223469_1 (AF223469) A0022 protein [Homo sapiens] g, mRNA sequence.
 ACCESSION BI064472 GI:14471994
 VERSION
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 600)
 REFERENCE Cogburn, L.A., Morgan, R.W. and Burnside, J.
 Chicken ESTs from fat
 Unpublished (2001)
 CONTACT: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers
 source
 1..600
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="pffin.pk001.h17"
 /sex="Male and female"
 /tissue_type="fat"
 /lab_host="E.coli EMDH10B"
 /clone_1fb="normalized chicken fat cDNA library"
 /note="Vector: pSPORT1"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.8e-17 Length: 600
 Score: 217.50 Matches: 46
 Percent Similarity: 71.3% Conservative: 16
 Best Local Similarity: 52.9% Mismatches: 22
 Query Match: 48.5% Indels: 3
 DB: 2 Gaps: 2
 US-10-757-745-2_COPY_54_140 (1-87) x BI064472 (1-600)
 QY 1 MetGUARGAAlaUeAuSeSerTYrPhGluPProProValGluGluSeRAlaLeuGluAry 20
 Db 65 CTGGAGAGGGCGCTGAGCGCCCTATTGAGCGCGCATGAACGAGCGCGCGCGCA 124
 QY 21 ArgProGluThrIleSerGluProLySThrTYrValAspLeuThrAsnGluGluThrThr 40
 Db 125 GGAGGGAGACTCG--GCGGGGCGCTGGAGACTGTATTGACCTCAAGAGATGATATCTGCA 181
 QY 41 AspSerThrThrSerLySileSerProSerGluAspThrGlnGlnGluAsnGlySerMet 60
 Db 182 AGTATATCAACAGCAC-----AGTGGTGCAAGCTCAAGCAACAAGATGATGACAGCGC 235
 QY 61 PheSerLeuIleThrTyrPheAlaIleAspGlyLeuAspLeuAsnLeuSeuSerGluAryAla 80
 Db 236 TTCTCGCTGATTAACCTTGAGACATTGATGGCTGAGCTGGGGAAATCTGCAGAGCGAGCT 295
 QY 81 ArgGlyValCysSerTyrLeu 87
 Db 296 AGAGGTCTCTGTTCTTACTCTG 316

RESULT 148
BZ858137 577 bp DNA linear GSS 18-MAR-2003
LOCUS CH240_232018.TV CHORI-240 Bos taurus genomic clone CH240_232018,
DEFINITION genomic survey sequence.
ACCESSION BZ858137
VERSION BZ858137.1 GI:29085542
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 577)
Zhao, S., Shetty, U., Shatsman, S., Tseng, G., Geer, K.,
Shvartsbeyn, A., Gebregiorgis, E., Chen, D., Riggs, F., de Jong, P.,
Crawford, A.M. and McEwan, J.C.
Bovine BAC End Sequences from Library CHORI-240
Unpublished (2003)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pjejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by AgResearch Ltd., New Zealand and the
Institute of Genomic Research (TIGR), USA.
Plate: 232 row: 0 column: 18
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
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/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_232018"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARBAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Alignment Scores:
Pred. No.: 3,08e-17 Length: 577
Score: 217.00 Matches: 44
Percent Similarity: 82.8% Conservative: 4
Best Local Similarity: 75.9% Mismatches: 8
Query Match: 48.4% Indels: 2
DB: 9 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BZ858137 (1-577)

QY 32 VALAAPLEUThraAngluThrThraPseThrThraSerlyleSerProSerGu 51
DB 83 GTTGACCTTAACAGAGAAACAAATATTCATTAGTTTAAACCGACATCTGAA 142
QY 52 ACP-----ThgInglIngluAnnglySerMetPheSerLeuileThrTripanileAp 69
DB 143 GATTAAGAGTTCACAGAAAGATGCAAGTATTTCTTTTCATTACCTGGAATATTGAT 202
QY 70 GtyleuApLeuAnleuSerGuArgAlaArglyValCysSerTyrlen 87
|||||.....|

DB 203 GGATTGACATGAACAATCTCTAGAGAGGCTCCAGGGGTGTCTTATTATTA 256
RESULT 149
AM669835 549 bp mRNA linear EST 25-APR-2001
LOCUS 113421.MARC 1BOV Bos taurus cDNA 5', mRNA sequence.
DEFINITION
ACCESSION AM669835
VERSION AM669835.1 GI:7526349
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 549)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Petrea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackendush, J. and Keefe, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -mnscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCATGACCAT
BACKWARD: GTTTCACGACGACGACG
Plate: 108 row: M column: 18
Seq primer: ATTTAGTGACATGATG.
Location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1BOV"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

ORIGIN
Alignment Scores:
Pred. No.: 9.38e-17 Length: 549
Score: 213.00 Matches: 43
Percent Similarity: 82.5% Conservative: 4
Best Local Similarity: 75.4% Mismatches: 8
Query Match: 47.5% Indels: 2
DB: 1 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x AM669835 (1-549)

QY 32 VALAAPLEUThraAngluThrThraPseThrThraSerlyleSerProSerGu 51
DB 312 GTTGACCTTAACAGAGAAACAAATATTCATTAGTTTAAACCGACATCTGAA 371
QY 52 ACP-----ThgInglIngluAnnglySerMetPheSerLeuileThrTripanileAp 69
DB 372 GATTAAGAGTTCACAGAAAGATGCAAGTATTTCTTTTCATTACCTGGAATATTGAT 431
QY 70 GtyleuApLeuAnleuSerGuArgAlaArglyValCysSerTyrlen 86
DB 432 GGATTGACATGAACAATCTCTAGAGAGGCTCCAGGGGTGTCTTATTATTA 482
|||||.....|

Thu Mar 16 10:39:27 2006

us-10-757-745-2_copy_54_140.rst

Page 84

RESULT	150
CN233559	
LOCUS	
DEFINITION	CN233559 531 bp mRNA linear EST 09-APR-2004
ACCESSION	RJ011F02.ab1 RJbrain Gallus gallus cDNA 5' mRNA sequence.
VERSION	CN233559
KEYWORDS	CN233559.1 GI:46337203 -
SOURCE	EST
ORGANISM	Gallus gallus (chicken)
	Gallus gallus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Archaeosauria; Aves; Neognathae; Galliformes; Phasianidae;
	Phasianinae; Gallus
REFERENCE	1 (baes 1 to 531)
AUTHORS	Savolainen,P., Flitzsimmons,C.J., Arvestad,L., Andersson,L. and Lundeberg,J.
TITLE	EST analysis of brain and testis cDNA libraries from white leghorn and Red Jungle Fowl
JOURNAL	Unpublished (2004)
COMMENT	Contact: Peter Savolainen Department of Biotechnology Royal Institute of Technology KTH SE-106 91 Stockholm, SWEDEN Tel.: +46 (0)8 5537 8431 Fax: +46 (0)8 5537 8315 Email: Peter.savolainen@biotech.kth.se Seq primer: M13 reverse primer.

```

FEATURES
  source
    Location/Qualifiers
      1..531
        organism="Gallus gallus"
        mol_type="mRNA"
        strain="Red junglefowl"
        db_xref="taxon:9031"
        sex="female"
        lab_host="ElectroMAX DH10B (Invitrogen)"
        clone_lib="RbBrain"
        note="Organ: brain; Vector: pSPORT-1; Site_1: Hind III
      Site_2: EcoRI; The cDNA libraries were created with the
      Superscript Plasmid System (Invitrogen)."
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Alignment Scores:	1.04e-16	Length:	533
Pred. No.:	21.2	Matches:	45
Score:	51.5	Matched: %:	8.5
Percent Similarity:	12.5	Nonconservative:	17
Percent Conserved:	12.5	Conservative:	13
Query Match:	47.4%	Indels:	1
DB:		Gaps:	2

OY	1	MetGluAlaGluAlaLeuAmSerIyrPheGluProProVal---	GluGluSerAlaLeuGlu	19
DB	123	CTGGAGAGGGCGCTGAGCGCTACTTTGAGCGCCGATGAAGAACAGACAGACGACGCGGG		182
OY	20	ArgArgProGluThrIleSerGluProLysThrTyr-ValAspLeuThrAsnGluIuThr		39
DB	183	GGCGAGAGAGGGCGCTCGCGGGGCTCGAAGCTGATTGACCTCACAGCGAGATGATCT		242
OY	40	ThrAspSerThrThrSerIyrIleSerProSerGluAspThrGluGluAsnGlySer		59
DB	243	GGAAGTATTATCAACAC-----AGTGGTCGACAGCTCCACCAACAGAGATGATGCACG		296
OY	60	MetPheSerLeuIleThrTTPasnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg		79
DB	297	ACCTTCTCGCTGCTAACTTGGAACTGATGGCTGGACCTGGGGAATCTCGAGGACGA		356
OY	80	AlaArgGlyValCysSerTyrLeu		87
DB	357	GCTAGAGGTGCTGTTCTTATCCTG		380
RESULT 151				
BU406549				
LOCUS	BU406549	782 bp	mRNA	linear EST 27-NOV-2002

DEFINITION 603483616f1 CSECHCN59 Gallus gallus cDNA clone CNE57374p3.5, mRNA sequence.

ACCESSION BU406549

VERSION BU406549.1 GI:25775605

KEYWORDS EST.

SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus

REFERENCE Enkaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archaeaula; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 782)

BOARDMAN, P.H., SANZ-EZQUERRO, J., OVELTON, I.M., BURT, D.W., BOSCH, F., FONG, M.T., TICKLE, C., BROWN, R.R.A., MILLIN, S.A. and HUBBARD, S.J. A Comprehensive Collection 1965

Curr. Biol. 12 (22), 1965-1969 (2002)

12445392

COMMENT Contact: Simon Hubbard

Department of Molecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1OD, UK

UK

Tel.: 01612008930

Fax: 01612350403

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1..782

source

FEATURES

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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="cbs374d3"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSEUCHS9"
/notes="Organ: limbs; Vector: pBluescript II KS(+); Site:1:
EcoRI; Site:2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this the first strand reaction, double-stranded cDNA
was bluntend, ligated to NotI adapters, digested with
EcoRI. Size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., FMS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research
6 (1996): 791, except that a significantly longer
reannealing hybridization was used."

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Alignment Scores:	1.73e-16	Length:	782
Pred. No.:	212.50	Matches:	45
Score:	70.5%	Conservative:	17
Percent Similarity:	51.1%	Mismatches:	23
Best Local Similarity:	47.4%	Indels:	3
Query Match:	5	Gaps:	2

US-10-757-745-2_COPY_54_140 (1-87) x BU065549 (1-782)

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OY      1 MetGuaAGaAlaLeuAanSerTYrPheGuaPProPovL---GJugJuseRAlaLeuGJn 19
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Db      165 CTGGAGAGGGCGCTGGAGCGCTACTTTGAGCGGCCGAGCAACGACGACGAGCGCGCG 22
OY      20 ArgAGPProGJutRrThrIleSerGJnPolyRrThrTYrVAlaPLeuThraenGJnUthr 39
      ::::
Db      225 GCGCGAGAGGGGGCGCTCGCGGGGGCCCTGCAACCTGTATTGACCTCAACAGATGATACT 28
OY      40 ThnAaPserTrRrThrSerLyIleSerPProSerGJuaPTrhGJnGJnGJnAenGJySer 59
      ::::
Db      285 GCAAGATATACACACAC-----AGTGGTGAAGCTCCAGCAACAAAGATGATGACAC 33
OY      60 MetPheSerLeuIleTrRrPaaIleIlePajLyLeuAaPLeuAanLeuAanLeuSerGJuaR 79

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QY 1 MetGluArgAlaLeuAnsSerTyrPheGluProProVal---GluGluSerAlaLeuGlu 19
 Db 178 CCGAGAGAGGGGGCGGAGCGCTTCTTGAGGGCGAGTGAACAGACAGCGCGCGC 237
 QY 20 ArgArgProGluThrIleSerGluProIleSerTyrValAspLeuThrAsnGluGluThr 39
 Db 238 GCGGACGAGAGGGCGGCTCGGCGGCGCTGAGACGCTGATGACCTCAAGCAGCATGACT 297
 QY 40 ThrAspSerThrThrSerTyrIleSerProSerGluAspThrGlnGlnGluAsnGlySer 59
 Db 298 GCAGATATATACCGACACG---AGTGGTCGACGCTCCAGACAGACAGATGACACGC 351
 QY 60 MetPheSerLeuIleThrTyrPheIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 79
 Db 352 AGCTTCTGCTGATGATCTTGAAACATTGATGGGCTGACCTGGGGAATCTGCAGAGCGCA 411
 QY 80 AlaArgGlyValCysSerTyrLeu 87
 Db 412 GCTAGAGGTGTCTGTTCTTACCTG 435

RESULT 154
 B1990829 600 bp mRNA linear EST 20-DEC-2001
 LOCUS 4081-88 Mouse E14.5 retina lambda ZAP II library Mus musculus cDNA,
 DEFINITION mRNA sequence.
 ACCESSION B1990829
 KEYWORDS B1990829.1 GI:17961846
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 600)
 AUTHORS Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
 White, R.A., Beremand, P.D., Thomas, T.L., Gan, L., and Klein, W.H.
 TITLE Gene expression in the developing mouse retina by EST sequencing
 JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)
 COMMENT 11812828
 CONTACT: Klein WH
 Department of Biochemistry and Molecular Biology
 University of Texas M.D. Anderson Cancer Center
 Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
 Tel: 713 792 3646
 Fax: 713 790 0329.

FEATURES
 source
 1..600
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
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 /clone_idb="Mouse E14.5 retina lambda ZAP II library"

ORIGIN

Alignment Scores:
 Pred. No.: 1.64e-16 Length: 600
 Score: 211.50 Matches: 45
 Percent Similarity: 66.3% Conservative: 12
 Best Local Similarity: 52.3% Mismatches: 28
 Query Match: 47.2% Indels: 1
 DB: 3 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x B1990829 (1-600)

QY 42 SerThrThrSerIleIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetCpe 61
 Db 349 ACAACCATTTAGAACGACATTCATCT---GGAATCTCTTGAAGATGACGACATATT 405
 QY 62 SerLeuIleThrTyrAsnIleAspGlyLeuAspLeuAsnLeuSerGluAlaArg 81
 Db 406 TCTTTCATTAACCTCGAATATTTGATGATGATGATGATGATGATGATGATGATGATGAT 465

QY 82 GlyValCysSerTyrLeu 87
 Db 466 GGGATGTGTCTCGCTTA 483

RESULT 155
 B1737520 645 bp mRNA linear EST 17-DEC-2002
 LOCUS B1737520 RIKEN full-length enriched, 11 days pregnant adult female
 DEFINITION placenta Mus musculus cDNA clone IS30029B02.5', mRNA sequence.
 ACCESSION B1737520
 KEYWORDS B1737520.1 GI:27150647
 SOURCE EST.
 ORGANISM Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 645)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nishikado, I., Oshio, N., Saito, R., Suuki, H., Yamamaki, T.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., But, C.,
 Hime, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Baisel, K.W., Blake, J.A., Brad, D., Briscoe, V.,
 Chochia, C., Corbani, L.E., Cousins, S., Datta, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gasteier, L.,
 Gariboldi, M., Glasi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gutelnicich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konge, Y.A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Pereira, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Wahnstedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wysshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Hayatsu, N., Hironaka-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arkawa, T., Fukuda, S., Hara, A., Hashizume, W., Imocani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shingawa, A., Yasunishi, A., Yoshino, M., Waterson, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 COMMENT 1246851
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 EMAIL: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, R., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, K., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watanabe, A., Watanabe, M. and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

GIVEN: Interleaved sequence analysis (IRISA) custom. 384 format

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES

source

```
Location/Qualifiers
1. .645
/organism="Mus musculus"
/mol_type="mRNA"
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ORIGIN

Alignment Scores:

Pred. No.:	1.8e-16	Length:	645
Score:	211.50	Matches:	45
Percent Similarity:	66.3%	Conservative:	12
Best Local Similarity:	52.3%	Mismatches:	28
Query Match:	47.2%	Indels:	1
DB:	5	Gaps:	1

US-10-757-745-2_COPY_54_140 (1-87) X BY737520 (1-645)

2 GUAAGAlaLeuAuanserTyrPheGluProProValGluGluseralaleuGluArg 21
 Db 61 CAGAAAGCCCTGAGCGCTACTTGAGCTGCCAGAAAGCAACCAAGGGTGGCCGCGCCAG 12

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QY      22 ProGluThrIleSerGluProLysThrYrValAspLeuThraSngIuGluThrThraSp 41
      ||| ||| :: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     121 CCTCCACGCTCTCAAGTCCGAGGCGCTATGTGATCTAACCAACGAGATGCAATGAT 18

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```

QY      42 SerThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61
      ::||| ::||| ||| |||:: |||
Db      181 ACAACCATTTAGAGACGATCATCT--GGAACCTCCTAGAGATAGCAGCACTATT 23

```

Oy 62 SerLeuIleTnTrpAsnIleaspGlyeuAspIeuAsnAhnLseuSerGIuaRgaIaaArg 81
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
db 238 TCTTCATTACTCGATATTGTAGTAGATGCACATCTGCCCGAGAGGGCTCGA 29

QY	82	GlyValCysSerTyrLeu	87
DB	298	GGGTTGTCTCCCTTA	315

RESULT 156
AW321603

AW321603

LOCUS	AW321603	648 bp	mRNA	linear	EST 25-JAN-2000
DEFINITION	U06060.y1 NCI CGAP Mam6 Mus musculus cdna clone IMAGE:2631539 5'				
ACCESSION	similar to TR:035551.095551 D3J0M3.3 ;, mRNA sequence.				

```

VERSION          AW321603.1  GI:6751147

```

SOURCE	Mus musculus (house mouse)
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100	100

ORGANISM

REFERENCE

Bukayeva-Metzos; Chordata; Crustacea; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Mus.
1 (bases 1 to 648)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

Issue Focused on: Jeffrey Green M.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium
 DNA Sequencing by: Washington University Genome

cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.gov/bdrip/image/image.html

FEATURES

source

Seq primer: -40RP from Gibco
High quality sequence stop: 436.
Location/Qualifiers
1. .648

ORIGIN

Alignment Scores:

Pred. No.:	1,81e-16	Length:	648
Score:	211.50	Matches:	45
Percent Similarity:	66.3%	Conservative:	12
Best Local Similarity:	52.3%	Mismatches:	28
Query Match:	47.2%	Indels:	1
DB:	1	Gaps:	1

US-10-757-745-2_COPY_54_140 (1-87) x AW321603 (1-648)

Db 214 CAGAAAGCCCTGAGCGCCTACTTCCAGCTGCAGAGAACGACCAAGGGTGGCCGCCAC 273

Dh 274 CCTCCACAGCTCTTCAAGTCCGAGGCTAATTGATCTAACCAACGAGATGCAAATGAT 333

Qy 42 SerThrThrSerLysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPhe 61

Db 334 ACAACCATTTAGAGCCAGCTCCATCT---GGAATCCTCTAGAAAGATAGCAGCAGCATATT 390

Db 391 TCTTCAATTACCTGGATATATGATGGATTAGATGCATCTGCCCGAGAGGGCTCGA 450

Q. Now, you're going to tell me that the defendant was not the person who was in the car that was involved in the accident, is that correct?

Qy 82 GlyValCysSerTyrLeu 87
 |||||
Dd 451 GGCGTGTTCCGCTCA 468

RESULT 157

LOCUS	BI648868	691 bp	mRNA	linear	EST 12-SEP-2001
-------	----------	--------	------	--------	-----------------

DEFINITION 603275826F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5316055 5'

QY 82 G1yValCyseTyrleu 87
|||||
Db 425 GGAGTGTCTCCTGCTTA 442

RESULT 159
BF784792 841 bp mRNA linear EST 12-JUN-2001
LOCUS 60211139F1 NCI_CGAP_Kid4 Mus musculus cDNA clone IMAGE:4239537
DEFINITION 5', mRNA sequence.
ACCESSION BF784792
VERSION BF784792.1 GI:12089828
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 841)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM9852 row: n column: 10
High quality sequence stop: 719.
Location/Qualifiers
1. 841
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4239537"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	2,55e-16	Length:	841
Score:	211.50	Matches:	45
Percent Similarity:	66.3%	Conservative:	12
Best Local Similarity:	52.3%	Mismatches:	28
Query Match:	47.2%	Indels:	1
DB:	2	Gaps:	1

US-10-757-745-2_COPY_54_140 (1-87) x BF784792 (1-841)

QY 2 GUATGAlaLeuAnsSerTyRPhGluProProValGluGluSerAlaLeuGluArgArg 21
|||||
Db 236 CAGAAAGCCCTGAGCCCTACTTCCAGTCGCCAGAACAGCAAGGTCGCCGCCAG 295
|||||
QY 22 ProGluThrIleSerGluProIleThrTyRValaPLeuThrAsnGluGluThrThrAap 41
|||||
Db 296 CCTCCACAGTCCTTCAAGTCGAGGCCCTATGTTGATCTTAACCAACAGAGATGCMAATGAT 355
|||||
QY 42 SerThrThrSerIleSerProSerGluAepThrGluGluGluGluSerMetPhe 61
|||||
Db 356 ACAACATTTTAGAACCACTCATCT---GGAACCTCTTAGAAGATAGCAGCACTATT 412
|||||
QY 62 SerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnLeuSerGluArgAlaArg 81
|||||
Db 413 TCTTCATTAACCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 472
|||||

QY 82 G1yValCyseTyrleu 87
|||||
Db 473 GGAGTGTCTCCTGCTTA 490

RESULT 160
BG298330 942 bp mRNA linear EST 21-FEB-2001
LOCUS 602397112F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:4511666 5',
mRNA sequence.
DEFINITION 5', mRNA sequence.
ACCESSION BG298330
VERSION BG298330.1 GI:13062875
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 942)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM10395 row: h column: 03
High quality sequence stop: 715.
Location/Qualifiers
1. 942
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:4511666"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 94"
/note="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally, oligo-dt primed.
Average insert size 3.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	2,96e-16	Length:	942
Score:	211.50	Matches:	45
Percent Similarity:	66.3%	Conservative:	12
Best Local Similarity:	52.3%	Mismatches:	28
Query Match:	47.2%	Indels:	1
DB:	2	Gaps:	1

US-10-757-745-2_COPY_54_140 (1-87) x BG298330 (1-942)

QY 2 GUATGAlaLeuAnsSerTyRPhGluProProValGluGluSerAlaLeuGluArgArg 21
|||||
Db 232 CAGAAAGCCCTGAGCCCTACTTCCAGTCGCCAGAACAGCAAGGTCGCCGCCAG 291
|||||
QY 22 ProGluThrIleSerGluProIleThrTyRValaPLeuThrAsnGluGluThrThrAap 41
|||||
Db 292 CCTCCACAGTCCTTCAAGTCGAGGCCCTATGTTGATCTTAACCAACAGAGATGCMAATGAT 351
|||||
QY 42 SerThrThrSerIleSerProSerGluAepThrGluGluGluGluSerMetPhe 61
|||||
Db 352 ACAACATTTTAGAACCACTCATCT---GGAACCTCTTAGAAGATAGCAGCACTATT 408
|||||
QY 62 SerLeuIleThrTyrAsnIleAapGlyLeuAapLeuAsnLeuSerGluArgAlaArg 81
|||||
Db 409 TCTTCATTAACCTGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 468
|||||

[illegible]

D6		426	CAGAACATTTGAACGCCAGTCATCT--CGAAGCTCCTTAGAAATATGACGACTATT	483
OY		62	SerjeunlelhpThrpansllleapgllyLeuasplLeuasnsRlseScJnkyrphLaryg	81
D6		483	TCTTTCAITACCIGCAATTTGATATGCATTATGATCATGTCCGACAAGGGCTCGA	542
OY		82	GlyValCyseSerTytleu	87
D6		543	GGGGTGTTCTTCGCTTA	560
	RESULT 162			
	LOCUS	CA976386	1046 bp	mRNA linear EST 06-JAN-2000
	DEFINITION	AGENCOURT 8862577 NC1 CGAP Man2 Mus musculus cDNA clone		
	ACCESSION	CA976386		
	VERSION	CA976386.1 GI:27509040		
	KEYWORDS	EST.		
	SOURCE	Mus musculus (house mouse)		
	ORGANISM	Eukaryote; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus. 1 (bases 1 to 1046) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC) unpublished (1999) Contact: Robert Strauszberg, Ph.D. Email: cgaps-remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LHAM3954 row: 1 column: 06 High quality sequence scop: 348.		
	FEATURES			
	source	location/Qualifiers		
		/organism="Mus musculus"		
		/mol_type="mRNA"		
		/strain="FVB/N-3"		
		/db_xref="taxon:10090"		
		/clone="IMAGE:6437549"		
		/tissue.type="tumour, biopsy sample"		
		/dev stage="5 months"		
		/lab_host="DH10B"		
		/clone.lib="NCI CGAP Man2"		
		/notes="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; SalI site; NotI; Cloned unidirectionally; Primer: oligo dt library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"		
	ORIGIN			
	Alignment Scores:			
	Pred. No.: 3,4e+16	Length: 1046		
	Score: 211.50	Matches: 45		
	Percent Similarity: 66.3%	Conservative: 12		
	Best Local Similarity: 52.3%	Mismatches: 28		
	Query Match: 47.2%	Indels: 1		
	D6: 6	Gaps: 1		
	US-10-757-745-2.COPY_54_140 (1-87) x CA976386 (1-1046)			
OY		2	GuarGalaleuansserTyRphegiubProboVaIgInguIsereAlaleuIngArq	21
D6		88	CAGAAGGCCCTGAGCCCTCACTTGAAGGTGCAAGAACAGCACMAAGGTGCGCGCCAG	147
OY		22	ProgIntThrilesexgubProbuShrTyValaspLeuthxangInguIngurThrxAp	41
D6		148	CCTCCACAGTCCTTCAAAGTCGACGACCTATGTGATCTTAACCAACGAGATCCAATGAT	207

QY	42	SeRtThnSerLyIleSerProSerGluAapThrGlnGlnGluAsnGlySerMetPhe	61
DB	208	ACACCATTTTGAAGCCAGTCATCT--GGAATCTCTTGAAGATACGACACTATT	264
QY	62	SeRtThnIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg	81
DB	265	TCTTTCATTACCTGGAAATATTGATGATAGTAGTGAATCTGCCGAGAGGGCTCGA	324
QY	82	GIYValCYSeSerTyrLeu	87
DB	325	GGGGTGTGTCTCGCTCA	342
RESULT 163			
LOCUS	CB579756		
DEFINITION	CB579756	615 bp	mRNA linear EST 03-APR-2003
ACCESSION	AM6NNUC:NRDGI-00175-E9-A	nrldgi (10855)	Rattus norvegicus cDNA clone
VERSION	CB579756		
KEYWORDS	CB579756.1	GI:29523797	
SOURCE	EST.		
ORGANISM	Rattus norvegicus (Norway rat)		
REFERENCE	Rattus norvegicus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;		
JOURNAL	Sciurognathi; Murioidea; Muridae; Murinae; Rattus.		
COMMENT	1 (bases 1 to 615)		
	Amgen EST Program.		
	Amgen Rat EST Program		
	Unpublished (2003)		
	Contact: Dan Fitzpatrick		
	Amgen, Inc		
	One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA		
	Tel: 805 447-4881		
	Plate: 00175 row: e column: 9.		
FEATURES	Location/Qualifiers		
source	1..615		
	/organism="Rattus norvegicus"		
	/mol_type="mRNA"		
	/db_xref="taxon:10116"		
	/clone="nrldgi-00175-e9"		
	/tissue_type="Dorsal Root Ganglia"		
	/clone_lib="nrldgi (10855)"		
	/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat		
	dorsal root ganglia"		
ORIGIN			
Alignment Scores:			
Pred. No.:	2,276-16	Length:	615
Score:	210.50	Matches:	45
Percent Similarity:	67.4%	Conservative:	13
Best Local Similarity:	52.3%	Mismatches:	27
Query Match:	47.0%	Indels:	1.
DB:	6	Gaps:	1
US-10-757-745-2_COPY_54_140 (1-87) x CB579756 (1-615)			
QY	2	GIUArgAlaLeuAsnSerTyrPheGluProProValGluGluSerAlaLeuGluArgArg	21
DB	240	AAAAAGGCTTGAGGGCCTTCTTGACGACGACGAGAACGACCTAGCGGGCTCAGCAG	299
QY	22	ProGluThrIleSerGluProLysThrTyrValAspLeuThrAsnGluGluThrAsp	41
DB	300	CCTCGACATCTCCAAAGTCCGAGACATATGTTGATCTTACCAATGAGAGATGCAATGAT	359
QY	42	SeRtThnIleSerLyIleSerProSerGluAapThrGlnGlnGluAsnGlySerMetPhe	61
DB	360	ACCACATTATTAAGAACCATCTCT---GGAATCTCTTGAAGATACGACACTATC	416
QY	62	SeRtThnIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArg	81
DB	417	TCTTTCATTACCTGGAAATATTGATGATAGTAGTGAATCTGCCGAGAGGGCTCGA	476
QY	82	GIYValCYSeSerTyrLeu	87

[illegible]

DEFINITION AL854676 XGC-egg Xenopus tropicalis cDNA clone TEG9019p19 5', mRNA
 sequence.
 ACCESSION AL854676
 VERSION AL854676.2 GI:38630173
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 640)
 Crounig, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (11.2003)
 JOURNAL Unpublished (2003)
 COMMENT On Sep 15, 2002 this sequence version replaced gi:22874895.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE_ID: TEG9019p19.plksp6
 Sequencing primer: Sp6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from egg
 EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NotI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NotI
 Host: Escherichia coli XL1-blue.
 Location/Qualifiers
 1..640
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TEG9019p19"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NotI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
 Alignment Scores:
 Pred. No.: 3,93e-15 Length: 640
 Score: 201.00 Matches: 44
 Percent Similarity: 61.8% Conservative: 19
 Best Local Similarity: 43.1% Mismatches: 21
 Query Match: 44.9% Indels: 18
 DB: 1 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) X AL854676 (1-640)

QY 1 MetGUARAlAlaleuenseTyrPhegiuPProPovaGlugluSerAlaleuGuarg 20
 |||||
 Db 147 ATGGAAAGGCGCATTAATCTTCTTGAGCCCGGGGTGAGTCAGCTTGCAAAACAAA 206
 |||||
 QY 21 ATGPGGluThrIleSerGluPro-----Lys 29
 |||||
 Db 207 GCTGCAGCTGATATGACATCTTAAAGCAAGACATATGCTGGAACGCTTCGAT 266
 |||||
 QY 30 ThrTYRValAspleuThrAnsluglu-----ThrThraspSerThrThrSer 45
 |||||
 Db 267 TCATGTATTGACCTCACCGCGCATGCTAGTGGTTACCAATTCAGAACCACTACAC 326
 |||||
 QY 46 LysIleSerProSerGluAspThrGlnGlnGluAnslYSerMerPheSerLeuIleThr 65
 |||||
 Db 327 AAT-----TCTCCACACTGTGAGCAAGAAAGATGAAGACATTTCTTCTTGACT 377
 |||||
 QY 66 TTPAsnIleAspGlyLeuAspleuAnslLeuSerGluArgAlaArgIYValCysSer 85
 |||||
 Db 378 TCGAATATATGATGCGCTTGATGAATCAATATGTCGAGAAAGGCTGCTGTGTGTCTCC 437
 |||||

QY 86 Tyrlen 87
 |||||
 Db 438 TATTGG 443

RESULT 168
 CX958091
 LOCUS 842 bp mRNA linear EST 08-FEB-2005
 DEFINITION JGI CAA09595.fwd NIH XGC tropf5 Xenopus tropicalis cDNA clone
 IMAGE:7706138 5', mRNA sequence.
 ACCESSION CX958091
 VERSION CX958091.1 GI:58771618
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 842)
 Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,
 Brokstein, P., and Lindquist, E.A.
 DOE Joint Genome Institute Xenopus tropicalis EST project
 Unpublished (2004)
 Other ESTs: JGI CAA09595.rev
 Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
 University of California, Berkeley)
 http://tropicalis.berkeley.edu/home)
 cDNA Library Preparation: DOE Joint Genome Institute:
 http://www.jgi.doe.gov
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
 Clone Distribution: I.M.A.G.E. Consortium/LLNL:
 http://image.llnl.gov
 Naming Conventions: EST name is generated by the concatenation of
 the JGI Clone id and the direction of sequencing. The suffix 'fwd'
 indicates a forward sequencing read of the insert. It does not
 necessarily reflect the orientation of the insert.
 Plate: CAA0 0097 row: f column: 24
 High quality sequence scop: 821.
 Location/Qualifiers
 1..842
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="IMAGE:7706138"
 /sex="male"
 /tissue_type="Testes"
 /dev_stage="Adult"
 /lab_host="Electromax DH10B"
 /clone_lib="NIH XGC tropf5"
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
 This library was made from dt primed cDNA and cloned into
 Invitrogen pCMVSPORT6 vector. The work was done at DOE
 Joint Genome Institute. Poly A RNA were primed with 5'
 GACTAGTCTGATGCGAG CGGCGCGCTTTTCTTTTCTTTT 3'. cDNA
 were ligated to SalI adapter (5' TCGACCCACGGCTCCG and
 5'CGAGCGCTGGG), digested with NotI, size fractionated in
 1.1% agarose gel electrophoresis and ligated into NotI and
 SalI digested pCMVSPORT6 vector."

ORIGIN
 Alignment Scores:
 Pred. No.: 5.63e-15 Length: 842
 Score: 201.00 Matches: 44
 Percent Similarity: 61.8% Conservative: 19
 Best Local Similarity: 43.1% Mismatches: 21
 Query Match: 44.9% Indels: 18
 DB: 8 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x CX8358091 (1-842)

OY 1 MetGluARGLaleuanserTyrPheGluProProvalGluGluSerAlaLeuGluArg 20
Db 204 ATGGAAGGGCGATTATATCTTTGAGCTGGGGTGAGCCATTCGCAACAA 263
OY 21 ArgProGluThrIleSerGluPro-----Lys 29
Db 264 GCTGCAGCTGATATGACAGATCTTTAAAGCAGAGACTATGTCTGGAACCTGCTCCGAT 323
OY 30 ThrTyValAspLeuThrAsnGluGlu-----ThrThrasperThrThrSer 45
Db 324 TCATGTATTGACCTGACTGCGATGACTTACTGTTACCAATCAGAACCACTACACG 383
OY 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
Db 384 AAC-----TCCCTCCACTGTGAGCAGACAGATGAGCCATTTTCTTCTGACT 434
OY 66 TTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85
Db 435 TGGAAATATGATGAGCTTGATGATCAAAATGTTGCAGAAAGGGCTGTGTGTCTCC 494
OY 86 TyrLeu 87
Db 495 TATTTG 500

RESULT 169

CX843565 866 bp mRNA linear EST 02-FEB-2005
LOCUS JGI CAK11139.Fwd NIH XGC troBm3 Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7661931 5', mRNA sequence.
ACCESSION CX843565
VERSION CX843565.1 GI:58497531
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.
REFERENCE Richardson, P., Lucas, S., Rokhsar, D., Deter, J.C., Ng, D.C.,
AUTHORS Brokstein, P. and Lindquist, E.A.
TITLE DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL Unpublished (2004)
COMMENT Other ESTs: JGI CAK1139.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley, CA)
http://tropicalis.berkeley.edu/home/
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone id and the direction of sequencing. The suffix ".fwd"
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Plate: CAK 0117 row: e column: 1
High quality sequence stop: 795.

FEATURES

1..866
Location/Qualifiers
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8164"
/clone="IMAGE:7661931"
/tissue_type="Brain"

//dev_stage="Adult"
/lab_host="ElectronMAX DH10B"
/clone_lib="NIH XGC troBm3"
/note="Vector: pCMVSPORT6; Site 1: SalI, Site 2: NotI;
This library was made from a primed cDNA and cloned into
Invitrogen pCMVSPORT6 vector. The work was done at DOE
Joint Genome Institute. Poly A RNA was primed with 3'
GACTAGTTCTAGATGCGAG CGGCGCCCTTTTCTTTTCTTTT 3' cDNA
were ligated to SalI adapter (5'-TGCACCAAGCTCGC and
5'-GAGACCGCTGG3'), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested pCMVSPORT6 vector."

ORIGIN

Alignment Scores:
Pred. No.: 5,846-15 Length: 866
Score: 201.00 Matches: 44
Percent Similarity: 61.84 Conservative: 19
Best Local Similarity: 43.14 Mismatches: 21
Query Match: 44.94 Indels: 18
Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x CX843565 (1-866)

OY 1 MetGluARGLaleuanserTyrPheGluProProvalGluGluSerAlaLeuGluArg 20
Db 207 ATGGAAGGGCGATTATATCTTTGAGCTGGGGTGAGCCATTCGCAACAA 266
OY 21 ArgProGluThrIleSerGluPro-----Lys 29
Db 267 GCTGCAGCTGATATGACAGATCTTTAAAGCAGAGACTATGTCTGGAACCTGCTCCGAT 326
OY 30 ThrTyValAspLeuThrAsnGluGlu-----ThrThrasperThrThrSer 45
Db 327 TCATGTATTGACCTGACTGCGGATGACTTACTGTTACCAATCAGAACCACTACACG 386
OY 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerLeuIleThr 65
Db 387 AAT-----TCCCTCCACTGTGAGCAGACAGATGAGCCATTTTCTTCTGACT 437
OY 66 TTPAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85
Db 438 TGGAAATATGATGAGCTTGATGATCAAAATGTTGCAGAAAGGGCTGTGTGTCTCC 497
OY 86 TyrLeu 87
Db 498 TATTTG 503

RESULT 170

CX824886 879 bp mRNA linear EST 01-FEB-2005
LOCUS JGI CAK4320.Fwd NIH XGC troBm3 Xenopus tropicalis cDNA clone
DEFINITION IMAGE:7655281 5', mRNA sequence.

ACCESSION CX824886
VERSION CX824886.1 GI:58402449
KEYWORDS EST.
SOURCE Xenopus tropicalis (western clawed frog)
ORGANISM Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Silurana.

REFERENCE Richardson, P., Lucas, S., Rokhsar, D., Deter, J.C., Ng, D.C.,
AUTHORS Brokstein, P. and Lindquist, E.A.
TITLE DOE Joint Genome Institute Xenopus tropicalis EST project
JOURNAL Unpublished (2004)
COMMENT Other ESTs: JGI CAK4320.rev
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org

Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley):
 http://tropicalis.berkeley.edu/home
 CDNA Library Preparation: DOE Joint Genome Institute:
 http://www.jgi.doe.gov
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
 Clone Distribution: I.M.A.G.E. Consortium/LNL:
 http://image.llnl.gov
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone ID and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: CAK 0045 row: 0 column: 23
 High quality sequence stop: 779.

FEATURES

Source

1. 879

/organism="Xenopus tropicalis"

/mol_type="mRNA"

/db_xref="taxon:8364"

/clone_image="7655281"

/issue_type="Brain"

/dev_stage="Adult"

/lab_host="NIH XGC trophoblast"

/clone_lib="NIH XGC trophoblast"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; This library was made from dt primed cDNA and cloned into Invitrogen pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute. Poly A RNA were primed with 5' GACTGTTCTGATCGCGAG CGGCCGCTTTTCTTTTCTTTT 3'. cDNA were ligated to SalI adapter (5' TCGACCGACGCTCGG and 5' CGGACGCGTGG), digested with NotI, size fractionated in 1.1% agarose gel electrophoresis and ligated into NotI and SalI digested pCMVSPORT6 vector."

ORIGIN

Alignment Scores:

Pred. No.: 5,966-15 Length: 879
 Score: 201.00 Matches: 44
 Percent Similarity: 61.8% Conservative: 19
 Best Local Similarity: 43.1% Mismatches: 21
 Query Match: 44.9% Indels: 18
 DB: 8 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x CK824886 (1-879)

QY 1 MetGUAAGAlaLeuAsnSerTyRheGluProProValGluGluSerAlaLeuGluArg 20
 DB 204 ATGGAAGGGGCGATTAATCTTTTGTAGCCTGGGCGAGTCAAGCTTGCAAAACAA 263
 QY 21 ArgProGluThrIleSerGluPro-----Lys 29
 DB 264 GCTGACGCTGATATAGCAGATCTTTAAAGCAAGACTATGTCGAATCTGCTCGAT 323
 QY 30 ThrTyValAspLeuThrAsnGluGlu-----ThrThrAspSerThrThrSer 45
 DB 334 TCATATATATGACCTACCGGCGATGACTTACGTTACCAATCGAAGCAACTCCAGC 383
 QY 46 LysIleSerProSerGluAspThrGlnGlnGlnGlySerMetPheSerLeuIleThr 65
 DB 384 AAT-----TCTCCACTGTGAAGCAAGAGTGAAGGCAATTTTCTTCTGACT 434
 QY 66 TPAAATLeaSPGLYLeuAspLeuAsnLeuSerGluArgAlaArgGlyValaGlySer 85
 DB 435 TGGATATATAGTGGCTTGATCAATATGCGAGAAAGGCTGAGTGTGTGTTCC 494
 QY 86 TyIleu 87
 DB 495 TATTG 500

RESULT 171
 LOCUS BB609556 712 bp mRNA linear EST 26-OCT-2001
 DEFINITION BB609556 RIKEN full-length enriched, 18 days embryo Mus musculus

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

CDNA clone 1110007K13 5', mRNA sequence.
 BB609556
 BB609556.1 GI:16451282
 EST.
 Mus musculus (house mouse)
 Mus musculus

REFERENCE AUTHORS

1 (bases 1 to 712)
 Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

TITLE JOURNAL COMMENT

Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Saitama-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Ikawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunaga,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Komno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamataka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
 e mouse tissues.

FEATURES source

Location/Qualifiers
 1. 712
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="1110007K13"
 /dev_stage="18 days embryo"
 /lab_host="SOLR"
 /clone_libs="RIKEN full-length enriched, 18 days embryo"
 /note="Site 1: XhoI; Site 2: SacI. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
 GAGGAGAGACGGCCGACCTGAGTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'

ORIGIN

GAGAGAGAGAGATCCAGAGCTCAATTAATTAACCCCGCCCC 3'1.
CDNA was cleaved with XhoI and SclI."

Alignment Scores:

Pred. No.: 7.03e-15 Length: 712
Score: 199.50 Matches: 43
Percent Similarity: 65.18 Conservative: 13
Best Local Similarity: 50.08 Mismatches: 29
Query Match: 44.54 Gaps: 1
DB: 2

US-10-757-745-2_COPY_54_140 (1-87) x BB609556 (1-712)

QY 2 GUUAGAlaleuanserTyrPheGluProProValGluGluSerAlaleuGluArg 21
Db 260 CAGAAAGCCCTGAGCGCTTCTGAGCTCCAGAGACGACCAAGGTGGCGCGCAG 319
QY 22 ProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluThrThra 41
Db 320 CTTCCAGCTCTTCAAGCTCCAGCGCTATGATCTAACCAAGAGATGCAATGAT 379
QY 42 SerThrTherSerIleSerProSerGluAspThrGlnGlnGlnGlnGlnGln 61
Db 380 ACAACCATTTTAAAGCCAGTCATCT--GGAACCTCTCTAGAAAGATGACGACTATT 436
QY 62 SerIleIleThrTyrAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArg 81
Db 437 TCTTCAATTAAGCTGGAATATGATGATGATGATGATGATGATGATGATGATGAT 496
QY 82 GlyValCysSerTyrIleu 87
Db 497 GAGGTGTCTCTGCTCA 514

RESULT 172

CD699206 274 bp mRNA linear EST 25-JUN-2003
LOCUS CD699206 human nasopharynx Homo sapiens cDNA, mRNA sequence.
DEFINITION CD699206
ACCESSION CD699206
VERSION CD699206.1 GI:32228261
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Liu, X.-Q., Zhou, Y., Zhang, L.-J., Xu, H., Chen, H.-K., Pan, Z.-G. and Zeng, Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: Yixin Zeng
Cancer Center
Sun Yat-sen University
651 Dongfeng Road Baot, Guangzhou 510660, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gszums.edu.cn

FEATURES

source

1..274
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_id="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Alignment Scores:

Pred. No.: 2.33e-15 Length: 274
Score: 199.00 Matches: 44
Percent Similarity: 95.9% Conservative: 3

Best Local Similarity: 89.8% Mismatches: 0
Query Match: 44.4% Indels: 2
DB: 6 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87) x CD699206 (1-274)

QY 2 GUUAGAlaleuanserTyrPheGluProProValGluGluSerAlaleuGluArg 21
Db 130 CAGAGGCTCTGAGCTCTTCTGAGCTCCAGAGCGAGAGAGCTGCTTGGAGCGCG 189
QY 21 gProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluThrThra 41
Db 190 ACTGAAACATCTCTGAGCCAGACCTATGACTTAACCAAGTGAAGAAACAATG 249
QY 41 gSerThrTherSerIleSer 48
Db 250 ATTCACCATTTTAAATTCAC 272

RESULT 173

CB728877 475 bp mRNA linear EST 11-APR-2003
LOCUS CB728877
DEFINITION CB728877-00016-D12-A Colon rat 3 (10415) Rattus norvegicus cDNA
ACCESSION CB728877.1 GI:29796001
VERSION CB728877.1
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.
AUTHORS Amgen Inc
TITLES Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00016 row: d column: 12.
location/Qualifiers

FEATURES

source

1..475
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone_id="CB728877-00016-D12-A"
/tissue_type="intestine, fetal"
/clone_id="Colon rat 3 (10415)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; Colon rat 3 fetal rat intestine"

ORIGIN

Alignment Scores:

Pred. No.: 5.55e-15 Length: 475
Score: 198.50 Matches: 43
Percent Similarity: 65.18 Conservative: 13
Best Local Similarity: 50.08 Mismatches: 29
Query Match: 44.1% Indels: 1
DB: 6 Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x CB728877 (1-475)

QY 2 GUUAGAlaleuanserTyrPheGluProProValGluGluSerAlaleuGluArg 21
Db 216 AAAAAGCCTTGAAGCCTTCTTGAAGCGACGACGACGACGACGACGACGACGAC 275
QY 22 ProGluThrIleSerGluProIleThrTyrValAspLeuThrAsnGluThrThra 41
Db 276 CTTCCAGCATCTTCAAGCTCCAGCGCTATGATCTAACCAAGAGATGCAATGAT 335
QY 42 SerThrTherSerIleSerProSerGluAspThrGlnGlnGlnGlnGlnGln 61
Db 336 ACACCATTTTAAAGCCAGTCATCT--GGAACCTCTTAAATATGACGACTATC 392

DB 506 GAGGTGTCTCTGCTCA 523

RESULT 175

BSG00090

LOCUS 2112-54 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.

ACCESSION BSG00090 600 bp mRNA linear EST 20-DEC-2001

VERSION BSG00090.1 GI:117946942

KEYWORDS EST.

SOURCES Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 600)

Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W.,
White, R.A., Beremand, P.D., Thomas, T.L., Gan, L. and Klein, W.H.,
Gene expression in the developing mouse retina by EST sequencing
and microarray analysis

JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)

COMMENT

11812828
Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.

FEATURES

source

1..600

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/tissue_type="neural retina"

/dev_stage="embryonic day 14.5 post-fertilization"

/clone_lib="Mouse E14.5 retina lambda ZAP II Library"

ORIGIN

Alignment Scores:

Pred. No.: 2,45e-14

Score: 194.50

Percent Similarity: 64.4%

Best Local Similarity: 50.6%

Query Match: 43.4%

DB: 2

Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BSG00090 (1-600)

QY 2 GUARGAIAleuAaSerTyPhedGuProProVaIGluSerAlaLeuGUAArg 21

DB 251 CAGAAAGCCCTGACCGCTACTCGAGCGCCAGAGCAAGAGGCGGCCGCCAG 310

QY 22 ProGUThriIleSerGUProLyThTyValaPleuThraEngluGluThThraP 41

DB 311 COTCCACGCTCTCAAGCGCCGAGGCTATGTTGATCTAAACAACGAGATGCAATGAT 370

QY 42 SerThThriSerLyIleSerProSerGUAaPThrGluGluGluGluGluGluGlu 61

DB 371 ACAACCATTTAGAAAGCAGTCCATCT--GGAACCTCTCTAGAAAGATACANCACTATT 427

QY 62 SerLeuIleThThraPleuIleAPGlyLeuAPleuAaAaAaAaAaAaAaAaAaAa 81

DB 428 TCTTTCATTACCTGGAATATTGATGATGATGATGATGATGATGATGATGATGATGAT 487

QY 82 -GlyValCySerTyIleu 87

DB 488 GGGGTGTGTCTGCTCA 506

RESULT 176

BF182465

LOCUS 621 bp mRNA linear EST 31-OCT-2000

DEFINITION 601804232P1 NCI_GAP_Mams Mus musculus cDNA clone IMAGE:4035319 5',

mRNA sequence.

BF182465

VERSION BF182465.1 GI:11060608

KEYWORDS EST.

SOURCES Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 621)

NIH-MGC <http://mgc.nci.nih.gov/>,
National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1992)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Lohar Hemmighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LMNL at:

<http://image.llnl.gov>

Plate: LLN9308 row: p column: 08

High quality sequence stop: 615.

FEATURES

source

1..621

Location/Qualifiers

/organism="Mus musculus"

/mol_type="mRNA"

/strain="mix FVB/N, C57BL/6J"

/db_xref="taxon:10090"

/clone="IMAGE:4035319"

/tissue_type="tumor, gross tissue"

/dev_stage="7 months"

/lab_host="DH10B"

/clone_lib="NCI_GAP_Mams"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1: SalI;
Site: 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lohar Hemmighausen/Robin Humphreys,
NIH"

ORIGIN

Alignment Scores:

Pred. No.: 3.44e-14

Score: 193.50

Percent Similarity: 66.3%

Best Local Similarity: 53.5%

Query Match: 43.2%

DB: 2

Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x BF182465 (1-621)

QY 2 GUARGAIAleuAaSerTyPhedGuProProVaIGluSerAlaLeuGUAArg 21

DB 229 CAGAAAGCCCTGACCGCTACTCGAGCGCCAGAGCAAGAGGCGGCCGCCAG 287

QY 22 ProGUThriIleSerGUProLyThTyValaPleuThraEngluGluThThraP 41

DB 288 COTCCACGCTCTCAAGCGCCGAGGCTATGTTGATCTAAACAACGAGATGCAATGAT 347

QY 42 SerThThriSerLyIleSerProSerGUAaPThrGluGluGluGluGluGluGlu 61

DB 348 ACAACCATTTAGAAAGCAGTCCATCT--GGAACCTCTCTAGAAAGATGACGACATATT 404

QY 62 SerLeuIleThThraPleuIleAPGlyLeuAPleuAaAaAaAaAaAaAaAaAaAa 81

DB 405 TCTTTCATTACCTGGAATATTGATGATGATGATGATGATGATGATGATGATGATGAT 464

QY 82 GlyValCySerTyIleu 87

DB 465 GGGGTGTGTCTGCTCA 482

RESULT 177

AL858410 634 bp mRNA linear EST 02-DEC-2003
 LOCUS AL858410 XCC-egg Xenopus tropicalis cDNA clone TEG9059P03 5'-UTR mRNA
 DEFINITION
 ACCESSION AL858410
 VERSION AL858410.2 GI:38633375
 KEYWORDS
 SOURCE EST.
 ORGANISM Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 634)
 Crothing, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Sep 15, 2002 this sequence version replaced gi:22878591.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE ID: TEG9059P03.plkSP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NciI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NciI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NciI
 Host: Escherichia coli XL1-blue.
 Location/Qualifiers

FEATURES

1..634
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TEG9059P03"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NciI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NciI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NciI at the 3' end"

ORIGIN

Alignment Scores:

Pred. No.: 5.5e-14 Length: 634
 Score: 192.00 Matches: 42
 Percent Similarity: 60.8% Conservative: 20
 Best Local Similarity: 41.2% Mismatches: 22
 Query Match: 42.9% Indels: 18
 DB: 1 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x AL858410 (1-634)

QY 1 MetGUARGAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 :::
 DB 127 GTTCGAGGGCGGATTAATTTCTTTGAGCTGGGGTGAGTCAAGCCTTGCAAAACAA 186
 QY 21 ArgProGluThrIleSerGluPro-----Lys 29
 :::
 DB 187 GGTGAGCTGATATGACATCTTTAAAGCAAGACTATGTGGAACCTGCTCCGAT 246
 QY 30 ThrTyrValAspLeuThrAsnGlu-----ThrThraspSerThrThrSer 45
 :::
 DB 247 TCATGTATTGACCTCAACCGCGCATGCTTAGTGTTACCAATCAAGACATCAACGAC 306
 QY 46 LysIleSerProSerGluAspThrGlnGlnGluAsnGlySerMetPheSerIleuIleThr 65
 307 AAT-----TCTCCACCTGTGAGCAAGAGAGAGACATTTTCTTCTTGACT 357
 QY 66 TrpAsnIleAspGlyLeuAspLeuAsnAsnLeuSerGluArgAlaArgGlyValCysSer 85

DB 358 TCGAATATATGATGCTTGTATGATCAATATGTCGAGAAAGGCTCGTGATGTGTTCC 417
 QY 86 TyrLeu 87
 :::
 DB 418 TATTTG 423

RESULT 178

AL901140 638 bp mRNA linear EST 04-DEC-2003
 LOCUS AL901140 XCC-egg Xenopus tropicalis cDNA clone TEG9077F04 5'-UTR mRNA
 DEFINITION
 ACCESSION AL901140
 VERSION AL901140.2 GI:38699862
 KEYWORDS
 SOURCE EST.
 ORGANISM Xenopus tropicalis (western clawed frog)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 638)
 Crothing, M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Sep 15, 2002 this sequence version replaced gi:22953375.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS_SEQUENCE ID: TEG9077F04.plkSP6
 Sequencing primer: SP6
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NciI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NciI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NciI
 Host: Escherichia coli XL1-blue.
 Location/Qualifiers

1..638
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TEG9077F04"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NciI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NciI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NciI at the 3' end"

FEATURES

1..638
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TEG9077F04"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"
 /note="Vector: pCS107; Site 1: EcoRI; Site 2: NciI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NciI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NciI at the 3' end"

ORIGIN

Alignment Scores:

Pred. No.: 5.5e-14 Length: 638
 Score: 192.00 Matches: 42
 Percent Similarity: 60.8% Conservative: 20
 Best Local Similarity: 41.2% Mismatches: 22
 Query Match: 42.9% Indels: 18
 DB: 1 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x AL901140 (1-638)

QY 1 MetGUARGAlaLeuAnsSerTyrPheGluProProValGluGluSerAlaLeuGluArg 20
 :::
 DB 2 GTTCGAGGGCGGATTAATTTCTTTGAGCTGGGGTGAGTCAAGCCTTGCAAAACAA 61
 QY 21 ArgProGluThrIleSerGluPro-----Lys 29
 :::
 DB 62 GGTGAGCTGATATGACATCTTTAAAGCAAGACTATGTGGAACCTGCTCCGAT 121
 QY 30 ThrTyrValAspLeuThrAsnGlu-----ThrThraspSerThrThrSer 45

DB 122 TCATGTTATGACCTCAGCGGCGATGCTTACTGCTTACCAATGAGAGCACTACACAGC 181
QY 46 LysileserProSerGluAspThrGlnGlnGluValSerMetPheSerLeuIleThr 65
DB 182 AAT-----TCTCCACTGTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 232
QY 66 TTPAATLleAPGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSer 85
DB 233 TCGAATATGATGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 292
QY 86 Tyrlleu 87
DB 293 TATTGTG 298

RESULT 179
AL895081 654 bp mRNA linear EST 04-DEC-2003
LOCUS AL895081 XGC-egg Xenopus tropicalis cDNA clone TEG9074a05 5', mRNA
DEFINITION
ACCESSION AL895081.2 GI:38695207
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 654)
REFERENCE Crothing,M.D.R., Ashmure,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
AUTHORS Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL Unpublished (2003)
COMMENT On Sep 16, 2002 this sequence version replaced gi:22947314.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE_ID: TEG9074a05.plkSP6v
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..654
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEG9074a05"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_1lb="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Alignment Scores:
Pred. No.: 5.73e-14 Length: 654
Score: 192.00 Matches: 42
Percent Similarity: 60.8% Conservative: 20
Best Local Similarity: 41.2% Mismatches: 22
Query Match: 42.9% Indels: 18
DB: 1 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x AL895081 (1-654)
QY 1 MetGUAAGAlaLeuAenSerTYrPheGluProValGluGluSerAlaLeuGuaArg 20

DB 32 GTTGGAGAGGCGCAATATATCTTCTTGAAGCTGGAGGTGAGATCAGCTTGCAGAAACAA 91
QY 21 ArgProGluThrIleSerGluPro-----Lys 29
DB 92 GCTGCAGCTGATATAGCAATCTTTAAAGCAAGACATATGTCTGAACTCTCCGAT 151
QY 30 ThrTYValAspLeuThrAsnGlu-----ThrThrAspSerThrThrSer 45
DB 152 TCATGTTATGACCTCAGCGGCGATGCTTACTGCTTACCAATGAGAGCACTACACAGC 211
QY 46 LysileserProSerGluAspThrGlnGlnGluValSerMetPheSerLeuIleThr 65
DB 212 AAT-----TCTCCACTGTGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 262
QY 66 TTPAATLleAPGlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSer 85
DB 263 TCGAATATGATGCGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 322
QY 86 Tyrlleu 87
DB 323 TATTGTG 328

RESULT 180
B622975 671 bp mRNA linear EST 01-OCT-2003
LOCUS B622975 N18B Mochii normalized Xenopus early gastrula library
DEFINITION
ACCESSION B622975.1 GI:37265119
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 671)
REFERENCE Kohata,Y.
AUTHORS Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadaeu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yatae, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
1..671
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL202p03"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_1lb="N18B Mochii normalized Xenopus early gastrula
library"

ORIGIN
Alignment Scores:
Pred. No.: 1.43e-13 Length: 671
Score: 189.00 Matches: 42
Percent Similarity: 63.0% Conservative: 21
Best Local Similarity: 42.0% Mismatches: 23
Query Match: 42.2% Indels: 14
DB: 3 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x B622975 (1-671)

```

Oy 1 MetGluAaGAlaLeuAsnSerTyzPheGluProProValGIuGIuSerLysLeuGIuArg 20
Db 93 ATGGAAGAGGCGATCAATCTTACTTTAGCCTGGGGT---GATCGACCTTACAAAC 149
Oy 21 ArgProGIuThr--IleSerGIuPro-----Lys 29
Db 150 AAACCTGAGCGATCTAGCACACCTTTAAAGCAAGATGATCAGTACTCCTCGAC 209
Oy 30 ThrTyValAspLeuThrAsnGIuGIuThrThrAspSerThrThSerLysIleSerPro 49
Db 210 GCATGTATTGACTTGACTAGCATGATGCTTGGCGCTACCAATACAGAGCTGTTCACAC 269
Oy 50 SerGIuAspThr-----GlnGlnIuAsnGlySerMetPheSerLeuIleThrTyPasn 67
Db 270 AACCTCCTTACTGTGTAACACAAAGAGATGAGCCATTTTACCTTCTTCATCAGTAAT 329
Oy 68 IleAspGIuLeuAspLeuAsnAsnLeuSerGIuAaGAlaArgGIuValCysSerTyzLeu 87
Db 330 ATGATAGGCTTGATGAATCAACAGCTGAGAGAGGGCTCGTGTGTATGTTCTCGTGTG 389

```

Pred. No.:	1.85e-13	Length:	816
Score:	189.00	Matches:	42
Percent Similarity:	63.08	Conservative:	21
Best Local Similarity:	42.04	Mismatches:	23
Query Match:	42.24	Indels:	14
DB:	7	Gaps:	4

US-10-757-745-2_COPY_54_140 (1-87) x CK806777 (1-816)

QY	1	MetGIuAArgAlaLeuAsnSerTyrPheGIuProProValGIuGIuSerAlaLeuGIuAArg	20
DB	227	ATGGAAAGGGGCGATCAATTTCTTACTTTAGCCTGGGGTG--GATCGACCTTACAAAC	283
QY	21	ArgProGIuThr--IleSerGIuPro-----Lys	29
DB	284	AAACCTGCAGCTGATCTGACAGACCCTTTAAAGCAAGATGCATGCAGTTACTCTGAC	343
QY	30	ThrTyrValAspLeuThrAsnGIuGIuThrIleAspSerThrThnSerIylIleSerPro	49
DB	344	GCATGTATTGACTTCATCAGCAGATCACTTGCGTACCAATCAAGACCTGTCCACAC	403
QY	50	SerGIuAspThr-----GlnGlnGIuAsnGIuSerMetPheSerLeuIleThrTyrAsn	67
DB	404	AACTCCTTACTCTGCAAAACAAACAAAGTAGACCACTTTTAACTTTTACATGAAT	463
QY	68	IleAspGIuLeuAspLeuAsnAsnSerGIuAArgAlaArgGIuValCysSerTyrLeu	87
DB	464	ATAGATGCGCTTGAATCAACAGCTTGACAGAGAGGCTCGTCGTATATCTTCCTTG	523

ORIGIN

Alignment Scores:

The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenihiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sec.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayashizaki, Y., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Machikita, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.

FEATURES

Location/Qualifiers
1. 519
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="G4D0010624"
/cell_type="B cells"
/cell_line="CRL-1669 BCL1 Clone 13.20-3B3"
/clone_1ib="RIKEN full-length enriched, B cells CRL-1669
BCL1 Clone 13.20-3B3 cDNA"

ORIGIN

Alignment Scores:
Pred. No.: 3,33e-13 Length: 519
Score: 185.00 Matches: 44
Percent Similarity: 61.6% Conservative: 9
Best Local Similarity: 51.2% Mismatches: 30
Query Match: 41.3% Indels: 3
Gaps: 2

US-10-757-745-2_COPY_54_140 (1-87) x BB867803 (1-519)

QY 2 GUATGATATLeuanserTyrPhegluProProvalGlu-GluserAlaleuclunarg-- 20
DB 238 CAGAAAGCCCTGACCGCTACTTCGAGCTGCAGACGACGACCAAGGCTGCCGCCA 297
QY 21 -ArgProgluThrIleSerGluProlyrThrTyValaAspLeuThrAsnGluGluThr 40
DB 298 GGGCTCCACGCTCTTCAAGTCCGAGGCCCTATGTGATCTTACCAAGAGATCAAA 357
QY 40 rapserThrThrSerIleSerProserGluapThrngIngluansglyserne 60
DB 358 TGAATACACCATTTTGAAGCAGATCCATCT--GGAATCTCTTGAAGATGACGAC 414
QY 60 rheserLeuIleThrTpaenIleAspGlyLeuAspLeuAsnAspLeuSerGluarg 80
DB 415 TATTTTTCATTAAGTGAATATGATGATGATGATGATGATGATGATGATGATGAT 474
QY 80 aargGlyValCysser 85
DB 475 TCGAGGGGTGTGTCT 490

RESULT 185
LOCUS CB696073 425 bp mRNA linear EST 10-APR-2003
DEFINITION AMGNNUC:NRHY1-00106-D12-A W Rat hypothalamus (10480) Rattus
norvegicus cDNA nrhy1-00106-d12 5', mRNA sequence.

ACCESSION CB696073
VERSION CB696073.1 GI:29753221
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Schizognathus; Muroidea; Muridae; Murinae; Rattus.
JOURNAL 1 (bases 1 to 425)
Unpublished (2003)

COMMENT
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00106 row: d column: 12.

FEATURES

Location/Qualifiers
1. 425
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy1-00106-d12"
/tissue_type="hypothalamus"
/clone_1ib="W Rat hypothalamus (10480)"
/note="Vector: pSPORT1, Site 1: SalI; Site 2: NotI; W Rat
hypothalamus adult female Wistar rat avg. insert size 2.3
kb fraction 6 and 7"

ORIGIN

Alignment Scores:
Pred. No.: 2.97e-13 Length: 425
Score: 184.50 Matches: 42
Percent Similarity: 65.5% Conservative: 15
Best Local Similarity: 48.3% Mismatches: 28
Query Match: 41.2% Indels: 2
Gaps: 1

US-10-757-745-2_COPY_54_140 (1-87) x CB696073 (1-425)

QY 2 GUATGATATLeuanserTyrPhegluProProvalGlu-GluserAlaleuclunarg 21
DB 133 AAAAAGCGTTGAGCGCTCTTTCAGACGACGACCAAGACACTGCGGCTCACCG 192
QY 22 ProgluThrIleSerGluProlyrThrTyValaAspLeuThrAsnGluGluThr 41
DB 193 CCTCGACATCTTCAAGTCCGAGGACATATGTGATCTTACCAATGAGATCAATATG 252
QY 42 SerThrThrSerIleSerProserGluapThrngIngluansglyserne 61
DB 253 ACCACCATTTTGAAGACGATCCATCT--GGAATCTCTTGAAGATGACGACATATC 309
QY 62 SerLeuIleThrTpaenIleAspGlyLeuAspLeuAsnAspLeuSerGluarg 81
DB 310 TCTTTTCATTAAGTGAATATGATGATGATGATGATGATGATGATGATGATGAT 369
QY 81 gGlyValCysserTyrleu 87
DB 370 AMGGGTGTGTCTTCTT 388

RESULT 186
LOCUS AK009089 1289 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2310002D07 product:Traf and Tnf receptor associated
protein, full insert sequence.
ACCESSION AK009089
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

COMMENT Other_ESTs: JGI_CAA05295.rev
Contact: Lindquist, E.A., Richardson, P.

DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:
http://tropicalis.berkeley.edu/home)
cDNA Library Preparation: DOE Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix 'fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Small Insert: Based upon one or more sequencing reads of this clone
where vector sequence was present at both ends, this clone has been
determined to contain a cDNA insert on the order of 600-1000 bases.
Plate: CNAO 0053 row: n column: 4
High quality sequence stop: 778.
Location/Qualifiers
1. 782
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE:7702086"
/sex="male"
/tissue_type="Testes"
/dev_stage="Adult"
/lab_host="Electromax DH10B"
/clone_lib="NIH XCC Croptres5"
/note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into
in vitro transcribed vector. The work was done at DOE
Joint Genome Institute. Poly A RNA was primed with 5'
GACTAGTCTAGATCGCGAG CGAGCGCCCTCTTTTCTTTT 3'. cDNA
were ligated to SalI adapter (5' TCAGCCACGCGCCG and
5' CGAGCGCTGAG), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested PCMVSPORT6 vector."

ORIGIN

Alignment Scores:

Pred. No.: 1.65e-12 Length: 782
Score: 181.00 Matches: 42
Percent Similarity: 61.2% Conservative: 21
Best Local Similarity: 40.8% Mismatches: 21
Query Match: 40.4% Indels: 19
DB: 8 Gaps: 3

US-10-757-745-2_COPY_54_140 (1-87) x CX937111 (1-782)

QY 1 MetGluArgAlaLeuAuaSerTyrPheGluProProValGluGluSerAlaLeuGlu-Ar 20
DB 5 GTTCGAGGCGGATTAATCTTTCTTTGAGCTGCGGAGTGAGCTTTGCCAACAAC 64
QY 20 GAATGAGTATGATTTTCTTTTAAAGCAAGACTATGCTGGAACCTGTTCCGA 29
DB 65 AGCTGACAGTATATACAGATCTTTTAAAGCAAGACTATGCTGGAACCTGTTCCGA 124
QY 29 GTTATGATTAATGATTTTCTTTTAAAGCAAGACTATGCTGGAACCTGTTCCGA 45
DB 125 TTCAATGATTAATGATTTTCTTTTAAAGCAAGACTATGCTGGAACCTGTTCCGA 184
QY 45 TTTATGATTAATGATTTTCTTTTAAAGCAAGACTATGCTGGAACCTGTTCCGA 65
DB 189 CAAC-----TCTCCACAGTGAAGCAAGAGATGAGCCATTTTCTTTCTGAC 235
QY 65 TTATGATTAATGATTTTCTTTTAAAGCAAGACTATGCTGGAACCTGTTCCGA 85
DB 236 TTGGAATTAATGATTTTCTTTTAAAGCAAGACTATGCTGGAACCTGTTCTGTTTC 295

QY 85 rTyrLeu 87
DB 296 CTAATG 302
RESULT 190
LOCUS BX306203 736 bp mRNA linear EST 11-MAY-2004
DEFINITION BX306203 tceay Oncorhynchus mykiss cDNA clone tceay0015b.c.23 5prim,
mRNA sequence.
ACCESSION BX306203 GI:42616188
VERSION BX306203
KEYWORDS EST.
SOURCE Oncorhynchus mykiss (rainbow trout)
ORGANISM Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 736)
Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, *Oncorhynchus mykiss*
Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29586848.
COMMENT
Contact: Guiguen Y
INRA - SCRIBE
Campus de Beaulieu, RENNES cedex, 35042, France
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at sigenaspport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0015 row: c column: 23
Seq primer: M13R.
Location/Qualifiers
1. 736
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tceay0015b.c.23"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tceay"
/note="Vector: pT73D-pac; Rainbow trout multi-clones -
normalized + 1 subtraction (tceay); Clone distribution:
AGENRES Resource centre. Francois PUMI,
Francois.Pumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (URG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

FEATURES

source

1. 736
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tceay0015b.c.23"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tceay"
/note="Vector: pT73D-pac; Rainbow trout multi-clones -
normalized + 1 subtraction (tceay); Clone distribution:
AGENRES Resource centre. Francois PUMI,
Francois.Pumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (URG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, France, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN

Alignment Scores:

Pred. No.: 2.66e-12 Length: 736
Score: 179.50 Matches: 45
Percent Similarity: 53.4% Conservative: 17
Best Local Similarity: 38.8% Mismatches: 25
Query Match: 40.1% Indels: 29
DB: 5 Gaps: 5

US-10-757-745-2_COPY_54_140 (1-87) x BX306203 (1-736)

QY 1 MetGluArgAlaLeuAuaSerTyrPheGluProProValGluGluSerAlaLeuGlu 19
DB 145 ATGAGAGAGAGCTGTAATCTTTTCAAGGCTGACAGGACGAGCTTTTACAGTGGAA 204
QY 20 ATGAGAGAGAGCTGTAATCTTTTCAAGGCTGACAGGACGAGCTTTTACAGTGGAA 30
DB 205 GATTCACCAAGAGAGAGATCAGCCCTTAAGCTTAAAGAGCAAGAAATTGACAAACCA 264

```

OY 31 -----TyrValAspLeuThrAsnGluGluThrThrAspSerThrHiser 45
Db 255 CAGGGGAAATAATGACTGCATTGACTGACCTGACCAAGAAAGACCTGCTGTTCACGACAGC 324
OY 46 -----LysIleSerProSerGluAsp----- 52
Db 325 AGCGCAAGTCAACCAACTCTCCAAAGTCAGGAACCAAGCTGAAGTTAAACCTGC 384
OY 53 ---ThrGlnGlnGluAsnGlySerMetPheSerLeuIleIleThrTyrAsnIleAspGlyLeu 71
Db 385 GGCTGTGAGACAGAGATGCGCGCAAACTGTGCGATCTCTTGGAAATGTAGATGCTCG 444
OY 72 AspleuAsnAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87
Db 445 GACACCGTGAACCTGGAGAGCGCTGCTAGAGCCCTCTGTCTTAATCTG 492

RESULT 191
AG204589 444 bp DNA linear GSS 06-MAR-2000
LOCUS Pan troglodytes DNA, clone: RP43-090B08.TJ, genomic survey
DEFINITION sequence.
ACCESSION AG204589
VERSION AG204589.1 GI:45236764
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
1
REFERENCE
AUTHORS Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
BAC end sequences of library RP-43
Unpublished
2 (bases 1 to 444)
Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
Direct Submission
Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC),
52, Oun-dong, Yuseong-gu, Daejeon 305-333, Korea
(E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kr/bb.re.kr/,
Tel:82-42-866-7181, Fax:82-42-860-4409)
Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the Red process and may have higher chances
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. 444
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-090B08.TJ"
/bex="male"
/cell_type="lymphocytes"
/clone_1ib="RP-43 Chimpanzee Male BAC library"

ORIGIN

Alignment Scores:
Pred. No.: 1,59e-12 Length: 444
Score: 179.00 Matches: 39
Percent Similarity: 95.1% Conservative: 0
Best Local Similarity: 95.1% Mismatches: 1
Query Match: 40.0% Indels: 1
DB: 10 Gaps: 0

US-10-757-745-2_COPY_54_140 (1-87).x AG204589 (1-444)

```

OY		32	ValAapleuthrAngJugUThrThAspSerThrThrSerLySileSerProSeGlu	51
OY		324	GTTAGCCCAACCAATGAAGAACAACGATTTCACCACCTTAAATAACGCCCATCGAA	383
OY		52	AspTrgInglngIuaEngLySerMetPhe-SerLeuIlenthTrpAsnIleAepGlYle	71
DB		384	GATACTCAGCAAGAAATGGCAGCATGTCTCTCTATTACCTGCATATNTGATGATT	443
OY		71 u 71		
Db		444 A 444		
		RESULT 192		
		B1444674		
		LOCUS		
		DEFINITION	B1444674	581 bp mRNA linear EST 21-AUG-2001
			de27dd10.y3 Wellcome CRC pBN3 oocyte Xenopus laevis cDNA clone	
			IMAGE:3472962 5' similar to TR:095551 095551 BJJ0M3.3 ;, mRNA	
			sequence.	
		ACCESSION	B1444674	
		VERSION	B1444674.1	GI:15269381
		KEYWORDS	EST.	
		SOURCE	Xenopus laevis (African clawed frog)	
		ORGANISM	Xenopus laevis	
		REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		AUTHORS	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;	
			Xenopodinae; Xenopus; Xenopus.	
		TITLE	1 (bases 1 to 581)	
		JOURNAL	Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,	
		COMMENT	Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,	
			Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,	
			Waterson,R. and Wilson,R.	
			Washu Xenopus EST project, 1999	
			Unpublished (1999)	
			Contact: Sandy Clifton, Ph.D.	
			Washu Xenopus EST project, 1999	
			Washington University School of Medicine	
			4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA	
			Tel: 314 286 1800	
			Fax: 314 286 1810	
			Email: est@watson.wustl.edu	
			Library constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B.	
			Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington	
			University Genome Sequencing Center	
			Clone distribution: Xenopus clones from this library are available	
			through the I.M.A.G.E. Consortium/LNL at: info@image.jiml.gov	
			High quality sequence stop: 403.	
		FEATURES	Location/Qualifiers	
		source	1..581	
			/organism="Xenopus laevis"	
			/mol_type="mRNA"	
			/db_xref="taxon:8355"	
			/clone_image="IMAGE:3472962"	
			/tissue_type="oocyte"	
			/lab_host="DH10B (phage-resistanc)"	
			/clone_lib="Wellcome CRC pBN3 oocyte"	
			/note="vector: pBSR3; Site_1_NotI; Site_2_EcoRI; CDNAS	
			were oligo-dT primed and directionally cloned. Steging	
			according to Nieuwkoop and Faber. Library was constructed	
			by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon	
			(Wellcome/CRC Institute)." "	
		ORIGIN		
		Alignment Scores:		
		Pred. No.: 2.26e-12	Length: 581	
		Score: 179.00	Matches: 40	
		Percent Similarity: 62.2%	Conservative: 21	
		Best local Similarity: 40.8%	Mismatches: 23	
		Query Match: 40.0%	Indels: 14	
		DB: 3	Gaps: 4	
		US-10-757-745-2_COPY_54_140 (1-87) x B1444674 (1-581)		

QY 3 AGAAlaLeuAnuSerTyrPheGluProValGlnIleuSerAlaLeuGluAlaArgGArgPro 22
 Db 30 AGGCGGATCAATTTACTTTGAGCCTGGGTG---GAGTCGACCTTACAAAACAAACCT 86
 QY 23 GlnThr---IleSerGluPro-----LysThrTyr 31
 Db 87 GCAGGTGATCTAGAGACCTTTAAAGCAAGATGATGACGTACTACTGCAGCGATGT 146
 QY 32 ValAlaPleuThrAngGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
 Db 147 ATTGACTTGACTAGCGATGACTGTGGCTACCAAAATCGAAGACGTCTTACAGCAACTCC 206
 QY 52 AspThr-----GlnGlnGluAnGlySerMetPheSerLeuIleThrTrpAnIleAsp 69
 Db 207 TCTACTGAAAACAACAAGATAGAGATGAGCGCATTTTACCTTCTTACATGAAATATAGAT 266
 QY 70 GlyLeuAspLeuAnuSerGluAnuSerGluAlaArgGlyValCysSerTyrLeu 87
 Db 267 GGCCTTATGATCAACCTGCACAGAGGCGCTGCTGTATATGTTCCCTGTGG 320

ORIGIN

Alignment Scores:

Pred. No.: 3,61e-12 Length: 831
Score: 179.00 Matches: 40
Percent Similarity: 62.2% Conservative: 21
Best Local Similarity: 40.8% Mismatches: 23
Query Match: 40.0% Indels: 14
DB: 6 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x CA981008 (1-831)

QY 3 ArgAlaLeuAenSerTyPheGluProValGluGluSerAlaLeuGluArgPro 22
DB 25 AGGGCGATCAATCTTACTTGAGCCTGGGGTG---GAGTCGACCTTACAAACAACT 81
QY 23 GluThr---IleSerGluPro-----LysThrTyr 31
DB 82 GCAGCTGATCTAGACGACCTTTAAAGCAAGATGATGATGATGATGATGAT 141
QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
DB 142 ATTGACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 201
QY 52 AspThr-----GlnGlnGluAsnGlySerMetPheSerLeuIleThrTPAnIleAsp 69
DB 202 TCTACTGTGAAACAAACAAAGATGATGATGATGATGATGATGATGATGATGAT 261
QY 70 GlyLeuAspLeuAenAenLeuSerGluArgAlaArgGlyValCysSerTyLeu 87
DB 262 GGCCTTGATGATCAACACGTTGAGAGAGGCTCGTGTGATGATGATGATGATGAT 315

RESULT 197

CK797649 879 bp mRNA linear EST 25-FEB-2004
LOCUS CK797649.1
DEFINITION IMAGE:7201410 5', mRNA sequence.
ACCESSION CK797649
VERSION CK797649.1 GI:42809645
KEYWORDS EST
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE

NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 879)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: g9apbs-remail.nih.gov
Tissue Procurement: Igor B. David
cDNA Library Preparation: Express Genomics
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNI at:
http://image.llnl.gov
Plate: LHAM15083 row: m column: 16
High quality sequence stop: 730.
Location/Qualifiers

FEATURES

Source

1..879
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone_image="720410"
/tissue_type="Pooled samples from 6 adult male testis"
/lab_host="DH10B T0MA"
/clone_id="NICHD_XGC_Te2N"
/note="Organ: testis; Vector: pExpress-1; Site:1. EcorV;
Location/Qualifiers

ORIGIN

Alignment Scores:

Pred. No.: 3,88e-12 Length: 879
Score: 179.00 Matches: 40
Percent Similarity: 62.2% Conservative: 21
Best Local Similarity: 40.8% Mismatches: 23
Query Match: 40.0% Indels: 14
DB: 7 Gaps: 4

US-10-757-745-2_COPY_54_140 (1-87) x CK797649 (1-879)

QY 3 ArgAlaLeuAenSerTyPheGluProValGluGluSerAlaLeuGluArgPro 22
DB 12 AGGGCGATCAATCTTACTTGAGCCTGGGGTG---GAGTCGACCTTACAAACAACT 68
QY 23 GluThr---IleSerGluPro-----LysThrTyr 31
DB 69 GCAGCTGATCTAGACGACCTTTAAAGCAAGATGATGATGATGATGATGAT 128
QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51
DB 129 ATTGACTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
QY 52 AspThr-----GlnGlnGluAsnGlySerMetPheSerLeuIleThrTPAnIleAsp 69
DB 189 TCTACTGTGAAACAAACAAAGATGATGATGATGATGATGATGATGATGATGAT 248
QY 70 GlyLeuAspLeuAenAenLeuSerGluArgAlaArgGlyValCysSerTyLeu 87
DB 249 GGCCTTGATGATCAACACGTTGAGAGGCTCGTGTGATGATGATGATGATGAT 302

RESULT 198

CA971409 896 bp mRNA linear EST 27-FEB-2003
LOCUS CA971409
DEFINITION IMAGE:632803 5', mRNA sequence.
ACCESSION CA971409
VERSION CA971409.1 GI:27504063
KEYWORDS EST
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.

REFERENCE

NIH-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
1 (bases 1 to 896)
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: g9apbs-remail.nih.gov
Tissue Procurement: N. Garret, P. Lemaire, A.M. Zorn, and J.B.
Gordon (Wellcome/CRC Institute)
cDNA Library Preparation: N. Garret, P. Lemaire, A.M. Zorn, and
J.B. Gordon (Wellcome/CRC Institute)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNI at:
http://image.llnl.gov
Plate: LHAM13764 row: p column: 04
High quality sequence stop: 611.
Location/Qualifiers

FEATURES

Location/Qualifiers

source

1. 896

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:632803"

/tissue_type="egg"

/lab_host="DH10B (phage-resistant)"

/note="Vector: pBluescript SK-; Site 1: NotI; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Library was constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute). Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:

Pred. No.:	3,986-12	Length:	896
Score:	179.00	Matches:	40
Percent Similarity:	62.2%	Conservative:	21
Best Local Similarity:	40.8%	Mismatches:	23
Query Match:	40.0%	Indels:	14
DB:	6	Gaps:	4

US-10-757-745-2_COPY_54_140 (1-87) x CA971409 (1-896)

QY 3 ArgAlaLeuAsnSerTyrPheGluProProValGluSerAlaLeuGluArgPro 22

DB 24 AGGGGATCAATCTTACTTGTAGCTGGGGTG---GAGTGCACCTTCAAAACAACCT 80

QY 23 GluThr---IleSerGluPro-----LysThrTyr 31

DB 81 GCAGCTGATCTAGACAGACCTTTAAAGCAAGATGCATGCATTAACCTTCAGCAGCAT 140

QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51

DB 141 ATTGACTGACTAGCAGATGACTTGGTGGCTACCAATCAGAGCTGTATACCAAGCACTCC 200

QY 52 AspThr-----GlnGlnGluAsnGlySerMetPheSerLeuIleThrThrAsnIleLeu 69

DB 201 TCTACTGTGAACAACAAGAGATAGAGCCATTATACCTTTCTTACATGAGAAATATAGAT 260

QY 70 GlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87

DB 261 GGCCTTGATGATCAACAGCTTGCAGAGAGGCTCGTGTATGTTCCTGTTTG 314

RESULT 199

CA982823 909 bp mRNA linear EST 27-FEB-2003

LOCUS AGENCOURT 11280235 Wellcome CRC psk egg Xenopus laevis cDNA clone

DEFINITION IMAGE:6870288 5', mRNA sequence.

CA982823

VERSION CA982823.1 GI:27515477

EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 909)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-remail.nih.gov

TISSUE Procurement: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)

CDNA Library Preparation: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: XGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: L14M14500 row: 9 column: 23

High quality sequence start: 6

High quality sequence stop: 708.

Location/Qualifiers

source

1. 909

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:6870288"

/tissue_type="egg"

/lab_host="DH10B (phage-resistant)"

/note="Vector: pBluescript SK-; Site 1: NotI; Site 2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Library was constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute). Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:

Pred. No.:	4,066-12	Length:	909
Score:	179.00	Matches:	40
Percent Similarity:	62.2%	Conservative:	21
Best Local Similarity:	40.8%	Mismatches:	23
Query Match:	40.0%	Indels:	14
DB:	6	Gaps:	4

US-10-757-745-2_COPY_54_140 (1-87) x CA982823 (1-909)

QY 3 ArgAlaLeuAsnSerTyrPheGluProProValGluSerAlaLeuGluArgPro 22

DB 24 AGGGGATCAATCTTACTTGTAGCTGGGGTG---GAGTGCACCTTCAAAACAACCT 80

QY 23 GluThr---IleSerGluPro-----LysThrTyr 31

DB 81 GCAGCTGATCTAGACAGACCTTTAAAGCAAGATGCATGCATTAACCTTCAGCAGCAT 140

QY 32 ValAspLeuThrAsnGluGluThrThrAspSerThrThrSerLysIleSerProSerGlu 51

DB 141 ATTGACTGACTAGCAGATGACTTGGTGGCTACCAATCAGAGCTGTATACCAAGCACTCC 200

QY 52 AspThr-----GlnGlnGluAsnGlySerMetPheSerLeuIleThrThrAsnIleLeu 69

DB 201 TCTACTGTGAACAACAAGAGATAGAGCCATTATACCTTTCTTACATGAGAAATATAGAT 260

QY 70 GlyLeuAspLeuAsnLeuSerGluArgAlaArgGlyValCysSerTyrLeu 87

DB 261 GGCCTTGATGATCAACAGCTTGCAGAGAGGCTCGTGTATGTTCCTGTTTG 314

RESULT 200

CA973696 919 bp mRNA linear EST 27-FEB-2003

LOCUS AGENCOURT 10802116 Wellcome CRC psk egg Xenopus laevis cDNA clone

DEFINITION IMAGE:6326013 5', mRNA sequence.

CA973696

VERSION CA973696.1 GI:27506350

EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 919)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

COMMENT Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

EMAIL: cgapbs-remail.nih.gov

TISSUE Procurement: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)

CDNA Library Preparation: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)

J.B. Gurdon (Wellcome/CRC Institute)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L14M13773 row: e column: 22
High quality sequence stop: 698.
Location/Qualifiers

FEATURES
source

1..919
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6326013"
/issue_type="egg"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC psk egg"
/note="Vector: pBluescript SK-; Site_1: NotI; Site_2:
EcoRI; cDNAs were oligo-dT primed and directionally
cloned. Library was constructed by N. Garrett, P. Lemaire,
A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).
Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

Alignment Scores:

Pred. No.:	4.12e-12	Length:	919
Score:	179.00	Matches:	40
Percent Similarity:	62.2%	Conservative:	21
Best Local Similarity:	40.8%	Mismatches:	23
Query Match:	40.0%	Indels:	14
DB:	6	Gaps:	4

US-10-757-745-2_COPY_54_140 (1-87) x CA973696 (1-919)

QY	3	ArgAlaLeuAenSerTYrPheGluProValGluGluSerAlaLeuGluArgPro	22
DB	23	AGGGGATCAATCTTCTTGGCTGGGGTG--GAGTCGACCTTACAAACAAACCT	79
QY	23	GluThr--IleSerGluPro-----LysThrTyr	31
DB	80	GCAGCTCATCTAGCAGACCTTAAAGCAAGATGATGACGATTAACCTCTGACGATGT	139
QY	32	ValAspLeuThrAenGluGluThrThrAepSerThrThrSerTyIleSerProSerGlu	51
DB	140	ATTGACTGCTAGCTAGCATGACTGTGGCTCAATCAGAAAGCTGTTACCAAGCAACTCC	199
QY	52	AspThr-----GingGluAenGlySerMetPheSerLeuIleThrTyrAenIleAsp	69
DB	200	TCTACTGTGAACAAACAAAGATGAGACCATTTTACCTTTCATCATGATATATAGAT	259
QY	70	GlyLeuAspLeuAenLeuSerGluArgAlaArgGlyValCysSerTyrLeu	87
DB	260	GGCCTTGATGATCAACAGTTGACAGAGGCTCGTGTGATGTTCCTGTTTG	313

Search completed: March 16, 2006, 04:56:59
Job time : 6904.46 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 16, 2006, 00:29:49 | Search time 549.738 Seconds
(without alignments)
595.756 Million cell updates/sec

Title: US-10-757-745-2_COPY_115_121

Perfect score: 38

Sequence: 1 SLITMNI 7

Scoring table:

BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 1000 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-O/abses/ABSSMB.spool/US10757745/runat.15032006.165652.3610/app.query.fasta_1
-DB=EST -QFMT=fasta -SUFFIX=rest -MINMATCH=0.1 -LOOPT=0 -LOOPT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000
-DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=200 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAVISIDE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs802h
-USER=US10757745 @CCN 1.1 8148 @runat.15032006.165652.3610 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPELOCK=100 -LOGLOG -DEV TIMEOUT=120
-NARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:.*
1: gb_est1:.*
2: gb_est2:.*
3: gb_est3:.*
4: gb_est4:.*
5: gb_est5:.*
6: gb_est6:.*
7: gb_est7:.*
8: gb_est8:.*
9: gb_est9:.*
10: gb_est10:.*
11: gb_est11:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	100.0	216	11	CR196611 Forward s
2	38	100.0	221	11	CR404572 Arabidops
3	38	100.0	227	11	CR094068 Forward s
4	38	100.0	246	10	CNS000VFS
5	38	100.0	289	1	BI125347 Arabidops
6	38	100.0	310	8	T26956 1id155proj
7	38	100.0	347	5	BU070378 im09c09.x

8	38	100.0	352	5	BQ787387
9	38	100.0	368	2	BE694706
10	38	100.0	394	1	AV661333
11	38	100.0	429	5	BO582059
12	38	100.0	457	11	CR404571
13	38	100.0	463	8	DN851594
14	38	100.0	471	7	CR543841
15	38	100.0	473	6	CB120234
16	38	100.0	480	1	AI750554
17	38	100.0	485	1	AA486032
18	38	100.0	511	5	BU659432
19	38	100.0	518	9	CC153114
20	38	100.0	530	3	BM466221
21	38	100.0	531	7	CN233559
22	38	100.0	554	3	BP220985
23	38	100.0	558	10	BK997515
24	38	100.0	565	3	BP226620
25	38	100.0	566	3	BP220508
26	38	100.0	568	3	BP257211
27	38	100.0	570	3	BM172060
28	38	100.0	570	3	BU397611
29	38	100.0	572	3	BP262485
30	38	100.0	573	1	AU279894
31	38	100.0	573	3	BP221260
32	38	100.0	573	3	BP261500
33	38	100.0	576	3	BP262642
34	38	100.0	577	7	CN298919
35	38	100.0	580	3	BP261787
36	38	100.0	580	3	BP274368
37	38	100.0	581	1	AV1717253
38	38	100.0	581	3	BP199948
39	38	100.0	581	3	BP207751
40	38	100.0	581	3	BP225088
41	38	100.0	581	3	BP262638
42	38	100.0	581	3	BP264149
43	38	100.0	581	3	BP270744
44	38	100.0	581	3	BP279936
45	38	100.0	581	3	BP279659
46	38	100.0	582	3	BM507091
47	38	100.0	582	3	BP197940
48	38	100.0	582	3	BP233592
49	38	100.0	582	3	BP234218
50	38	100.0	582	3	BP261141
51	38	100.0	582	3	BP263516
52	38	100.0	582	3	BP270415
53	38	100.0	582	3	BP275810
54	38	100.0	583	3	BP195721
55	38	100.0	583	3	BP262103
56	38	100.0	583	3	BP262741
57	38	100.0	583	3	BP319548
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59	38	100.0	583	5	BU783229
60	38	100.0	584	3	BP263059
61	38	100.0	584	3	BP274942
62	38	100.0	584	3	BP348623
63	38	100.0	588	3	BP236074
64	38	100.0	588	3	BP348796
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66	38	100.0	602	1	AL703449
67	38	100.0	604	11	AV730762
68	38	100.0	618	1	CR163431
69	38	100.0	621	6	CB069952
70	38	100.0	625	5	BU471395
71	38	100.0	634	6	CB157906
72	38	100.0	634	7	CV023369
73	38	100.0	644	3	BI333830
74	38	100.0	644	9	AZ360347
75	38	100.0	645	3	BM426270
76	38	100.0	652	7	CR753214
77	38	100.0	657	2	CN298920
78	38	100.0	662	2	BI067773
79	38	100.0	678	2	BG719113
80	38	100.0	701	7	CR767236

Thu Mar 16 10:39:26 2006

us-10-757-745-2 copy 115 121.rst

Page 2

81	38	100.0	704.5	B134820	602989939	C 154	37	97.4	393	4	AK136958
82	38	100.0	710.5	B161472	5172611.2	C 155	37	97.4	394	6	CB776775
83	38	100.0	711.7	CN298822	170060000	C 156	37	97.4	404	6	CB413283
84	38	100.0	720.10	CN800X2P		C 157	37	97.4	427	9	B2202954
85	38	100.0	729.7	CN298822	170060000	C 158	37	97.4	440	1	AA477219
86	38	100.0	739.7	CN298822	170060000	C 159	37	97.4	445	4	AA477219
87	38	100.0	751.8	CX760857	AGENCOURT	C 160	37	97.4	455	2	BB361716
88	38	100.0	757.11	CX170843	FCOMWIDE	C 161	37	97.4	471	6	BB415942
89	38	100.0	759.7	CR91801	DNF2P68U	C 162	37	97.4	501	2	BB125943
90	38	100.0	761.2	BP43821	601871278	C 163	37	97.4	504	1	AA517886
91	38	100.0	767.1	AU123327		C 164	37	97.4	545	3	BB177896
92	38	100.0	767.2	B1758848	603044763	C 165	37	97.4	545	3	BB177896
93	38	100.0	770.2	BQ3911395	B1288488	C 166	37	97.4	585	10	CN865005
94	38	100.0	774.3	BQ3911395	B1288488	C 167	37	97.4	603	7	BB619120
95	38	100.0	774.3	BQ3911395	B1288488	C 168	37	97.4	615	8	DR441373
96	38	100.0	780.5	BK3754579	BK3754579	C 169	37	97.4	649	2	BB611775
97	38	100.0	782.5	BK406549	603483616	C 170	37	97.4	656	2	BB485402
98	38	100.0	783.5	BK65835	BK65835	C 171	37	97.4	657	5	BY740567
99	38	100.0	786.2	BK719977	602691335	C 172	37	97.4	657	5	BY740567
100	38	100.0	789.10	AA597426	ArbIdOps	C 173	37	97.4	660	2	BB616066
101	38	100.0	793.2	BG533717	602562373	C 174	37	97.4	661	9	BB660102
102	38	100.0	799.8	CX166424	AGENCOURT	C 175	37	97.4	661	9	CC432105
103	38	100.0	810.8	CX166335	HESQ2_39	C 176	37	97.4	669	3	BB684350
104	38	100.0	817.10	BUI11103	603127011	C 177	37	97.4	669	3	BB684350
105	38	100.0	818.10	CN953332	265164_10	C 178	37	97.4	688	5	DR665880
106	38	100.0	838.2	B1908925	603067028	C 179	37	97.4	688	5	DR665880
107	38	100.0	846.7	CR765451	DNF2P695E	C 180	37	97.4	694	5	BY748935
108	38	100.0	853.2	BB784416	601473891	C 181	37	97.4	702	3	BQ179160
109	38	100.0	858.3	B1553412	603193358	C 182	37	97.4	712	5	BB053419
110	38	100.0	870.2	BG740396	602634171	C 183	37	97.4	713	5	BY741565
111	38	100.0	870.5	BUI59911	AGENCOURT	C 184	37	97.4	715	6	CF533524
112	38	100.0	883.5	BUI69945	AGENCOURT	C 185	37	97.4	716	6	CF533524
113	38	100.0	883.5	BUI79107	AGENCOURT	C 186	37	97.4	718	4	CNS0B51
114	38	100.0	889.2	BG57046	602565130	C 187	37	97.4	730	5	BQ745578
115	38	100.0	889.11	CR213336	Forward	C 188	37	97.4	737	6	CF749729
116	38	100.0	894.2	BG623866	602649018	C 189	37	97.4	741	7	CR296636
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957 34 89.5 442 8 R28391
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ALIGNMENTS

```

RESULT 1
LOCUS CRI96611/c 216 bp DNA linear GSS 06-JUL-2004
DEFINITION chromosome engineering clone MHPN168n23, genomic survey sequence.
ACCESSION CRI96611.1 GI:49975460
VERSION GSS: genome survey sequence: MTCER.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE
AUTHORS Mammalia, Eutheria, Eumarchontoglires, Glires, Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Murinae;
1 (bases 1 to 216)
ADAMS, D. J., BIGGS, P. J., COX, A. V., DAVIES, R. M., VAN DER WEYDEN, L.,
JONES, J., SMITH, J., PLUMB, R. W., TAYLOR, R. G., NISHIJIMA, I., YU, Y.,
ROGERS, J., and BRADLEY, A.
JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CH10 1SA, UK. http://www.sanger.ac.uk/MTCER
FEATURES
source
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

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/clone="MHPN168n23"
/clone_11b="MHPN"

ORIGIN
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Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CRI96611 (1-216)

QY
1 SerleuileThrTrpAsnIle 7
|||||
191 TCATTATATACCTGGATATATC 171

DB
191 TCATTATATACCTGGATATATC 171

RESULT 2
LOCUS CR404572 221 bp DNA linear GSS 02-MAY-2004
DEFINITION genomic survey sequence.
ACCESSION CR404572.1 GI:46945300
VERSION CR404572.1
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Welschhar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
14756321
JOURNAL
PUBMED 14756321
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
Welschhar, B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
14682050
4 (bases 1 to 221)
Strizhov, N., Li, Y., Rosso, M.G. and Welschhar, B.
Submitted (01-MAY-2004) Welschhar, B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
MYF24. Details on the protocols used for generation of the sequence
are described in References 1-3. The sequences are generated at the
MPI for Plant Breeding Research in the context of the GABI-Kat
project. GABI-Kat is part of the German Plant Genomics program
designated 'GABI'. Information on line availability can be found
at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
location/Qualifiers
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/ecotype="Col-0"

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/note="PCR was performed on DNA from *Arabidopsis thaliana* plants (11) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ37514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Alignment Scores:

Pred. No.:	1.32e+03	Length:	221
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR0404572 (1-221)

QY 1 Serleuilethrttppanille 7

Db 161 AGTTGATTAAGTGGACATTA 181

RESULT 3

CR094068/c

LOCUS Forward strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN414109, genomic survey sequence.

DEFINITION

CR094068 227 bp DNA linear GSS 05-JUN-2004

ACCESSION CR094068

VERSION CR094068.1 GI:49827897

KEYWORDS GSS: genome survey sequence; MICR.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J., and Bradley, A.

TITLE Direct Submission

JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>

FEATURES

source location/Qualifiers

1..227

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/clone_11b="MHPN"

ORIGIN

Alignment Scores:

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Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR094068 (1-227)

QY 1 Serleuilethrttppanille 7

Db 202 TCATTATTAACCTGGAATATC 182

RESULT 4

CNS00VFS/c

LOCUS Arabidopsis thaliana genome survey sequence Sp6 end of BAC T9H2 of TAMU library from strain Columbia of *Arabidopsis thaliana*, genomic survey sequence.

DEFINITION

CNS00VFS 246 bp DNA linear GSS 28-JUN-1999

ACCESSION AL092207

VERSION AL092207.1 GI:5293361

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsia.

AUTHORS

Salamounbat, M., Choisme, N., Artiguenave, F., Brotilier, P., Wincker, P., Samson, D., Saurin, W., Weissenbach, J. and Querier, F.

JOURNAL

Unpublished

AUTHORS

Genoscope.

TITLE

Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

JOURNAL

Direct Submission

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

FEATURES

source location/Qualifiers

1..246

/organism="Arabidopsis thaliana"

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/db_xref="taxon:3702"

/clone="T9H2"

/clone_11b="TAMU"

/ecotype="Columbia"

/note="end : Sp6"

ORIGIN

Alignment Scores:

Pred. No.:	1.5e+03	Length:	246
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CNS00VFS (1-246)

QY 1 Serleuilethrttppanille 7

Db 111 AGTTGATTAAGTGGACATTA 91

RESULT 5

BBI25347/c

LOCUS BBI25347 RIKEN full-length enriched, 16 days neonate cerebellum Mus musculus cDNA clone 963004K16.3' similar to AF046001 Homo sapiens zinc finger transcription factor (ZNF207) mRNA, mRNA sequence.

DEFINITION

BBI25347.1 GI:8779673

VERSION

EST.

KEYWORDS

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 289)

AUTHORS

Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Iehi, Y., Iehikawa, J., Iehikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, T., Komodo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsumura, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toyota, T., Tsunoda, Y., Watabiki, A., Watanabe, S., Yamamura, T., Yamane, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE RIKEN Mouse ESTs (Komno, H., et al.)

JOURNAL

Unpublished (2000)

COMMENT Contact: Yoshitake Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

Email: genome-research.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagao, S.,
Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.,
Thermolabile and thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kikunishi, T., Akiyama, U., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.riken.go.jp) for
further details.

FEATURES

source

Location/Qualifiers

1..289
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9630004K16"
/cissue_type="cerebellum"
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/lab_host="DH10B"
/clone_id="RIKEN full-length enriched, 16 days neonate
cerebellum"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 370.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCCAGTAAATTAATTCCTCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pluscript KS(+) after bulk excision from lambda
phage I."

ORIGIN

Alignment Scores:

Pred. No.: 1,82e+03 Length: 289
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Percent Similarity: 100.0% Conservative: 0
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Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BB125347 (1-289)

QY 1 Serleu1ethrTTPAen1le 7

DB 83 TCTCTAATTAACCTGGAATATTC 63

RESULT 6

LOCUS T26956 310 bp mRNA linear EST 12-JUN-1996
DEFINITION sapiens cDNA clone 11d155, mRNA sequence.
ACCESSION T26956 T27254
VERSION T26956.1 GI:575899

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 310)
Bouilland, F.
Study of expressed sequences tags in adipose tissue 1994
Unpublished (1994)
On Nov 17, 1994 this sequence version replaced gi:624970.
Contact: Frederic Bouilland
Centre de Recherche sur l'Endocrinologie moleculaire et le
Developpement
CNRS
9, Rue Jules Hetzel, Meudon Bellevue, 92190 France
Tel: 33 1 45 07 52 97
Fax: 33 1 45 07 58 90
Email: bouilland@bioingen.fr
Southern blot human DNA Ecoli : 2 major bande 3.1, 2.3 Kb and 2
weak : 4.2 and 1.9 Kb (wash 0.5XSSC).
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
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/note="Vector: lambda g10; Site 1: EcoRI;
dev_stage=adult; tissue_type=adipose tissue;
lab_host=Bacteriophage lambda; first strand priming with
random and poly-d(T) oligonucleotides."

ORIGIN

Alignment Scores:
Pred. No.: 1,98e+03 Length: 310
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x T26956 (1-310)

QY 1 Serleu1ethrTTPAen1le 7

DB 239 TCTCTAATTAACCTGGAATATTC 259

RESULT 7

LOCUS BU070378/c 347 bp mRNA linear EST 27-AUG-2002
DEFINITION im9c09.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:6034553
3' similar to TR:095551 095551 DJ30M3.3 ;, mRNA sequence.
ACCESSION BU070378
VERSION BU070378.1 GI:22511567
KEYWORDS EST.
SOURCES Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo
1 (bases 1 to 347)
Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blaisdell, A.,
Schmidt, A., Theising, B., Rittler, E., Ronko, I., Bennett, J.,
Cordenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: im09c09.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.

FEATURES

source

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/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda Zapri system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	2.26e+03	Length:	347
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU070378 (1-347)

QY 1 SerLeuIleHnTTPaSnIle 7
|||||
Db 51 TCTCTCATTACCTGGATATAT 31

RESULT 8
BQ787387 352 bp mRNA linear EST 26-JUL-2002
LOCUS BQ787387
DEFINITION im09c03.y1 Human Insulinoma Homo sapiens cDNA clone IMAGE:6034553
ACCESSION BQ787387
VERSION BQ787387.1 GI:2195859
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 352)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemisha, I., Scarse, M., Bresnelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Warr, M., Page, D., Wylie, T., Martin, J., Blistein, A.,
Schmitt, A., Theising, B., Rutter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V.,
Williams, T., Jackson, Y., and Bowers, Y.
Unpublished (2000)
Endocrine Pancreas Consortium
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Harvard University, Howard Hughes Medical Institute

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu

Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco.

FEATURES

source

1..352
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6034553"
/tissue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human Insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site 1:
XhoI; Site 2: EcoRI; Constructed with lambda Zapri system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	2.3e+03	Length:	352
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BQ787387 (1-352)

QY 1 SerLeuIleHnTTPaSnIle 7
|||||
Db 298 TCTCTCATTACCTGGATATAT 318

RESULT 9
BE694706 368 bp mRNA linear EST 11-SEP-2000
LOCUS BE694706
DEFINITION PMO-BT0757-140800-006-d10 BT0757 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE694706
VERSION BE694706.1 GI:10081866
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 368)
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsumura, A., Bata, G.S., Simpson, D.H.,
Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brennan, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2707002
Fax: +55-11-2707001
Email: aaimp@iudwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.iudwig.org.br/scripte/gethtml2.pl?cl=et2=PMO-BT0757-140
800-006-d10et3-2000-08-14et4=1)
Seq primer: puc 18 forward
High quality sequence start: 37
High quality sequence stop: 368.
Location/Qualifiers
1..368
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_1lb="BT0757"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini library was made by cloning products derived from ORESTES PCR (U.S. Patents Patent Application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 2.43e+03 Length: 368
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BB694706 (1-368)

QY 1 SerLeuilethrtTpaanlle 7

DB 266 TCTCTATTACTGGAAATATT 246

RESULT 10
LOCUS AV661333 394 bp mRNA linear EST 16-JAN-2002
DEFINITION AV661333 GLC Homo sapiens cDNA clone GLCGRD01 3', mRNA sequence.
ACCESSION AV661333
VERSION AV661333.1 GI:9882347
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 394)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)

JOURNAL PUBLISHED
COMMENT CONTACT: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzge@chc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..394

FEATURES
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GLCGRD01"
/issue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SQR"
/clone_1lb="GLC"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:
Pred. No.: 2.63e+03 Length: 394
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AV661333 (1-394)

QY 1 SerLeuilethrtTpaanlle 7

DB 131 TCTCTATTACTGGAAATATT 151

RESULT 11
LOCUS B0582059 429 bp mRNA linear EST 20-JUN-2002
DEFINITION B0582059 Human insulinoma Homo sapiens cDNA clone IMAGE:6029589
5' similar to TR:095551 095551 D030M3.3', mRNA sequence.
ACCESSION B0582059
VERSION B0582059.1 GI:21494955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 429)
Wetton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K.,
Lemstra,I., Pearce,M., Breckall,J., Gradowl,G., Clifton,S.,
Hiller,U., Marie,M., Pape,D., Wylie,T., Martin,J., Bliscain,A.,
Schmitt,A., Theising,E., Nitter,B., Goto,I., Bennett,J.,
Cardenas,W., Gibbons,M., McEann,R., Cole,K., Teagarshtvill,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 1112c11.x1
Contact: Douglas Wetton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dwetton@biolup.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Glibco.
Location/Qualifiers
1..429

FEATURES
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6029589"
/issue_type="insulinoma"
/lab_host="PH10B (phage-restant)"
/clone_1lb="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
XhoI; Site_2: EcoRI; Constructed with lambda ZAPRI system

1..429

(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permut Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN

Alignment Scores:

Pred. No.:	2,91e+03	Length:	429
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B0582059 (1-429)

Qy 1 Serleu1eThrTPAsn1le 7

Db 286 TCTCTCATTAACCTGGAATATT 306

RESULT 12

LOCUS

CR404571 457 bp DNA linear GSS 02-MAY-2004
Arabidopsis thaliana T-DNA flanking sequence GK-872B08-026084,
genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

COMMENT

FEATURES

source

1. 457
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-872B08-026084"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/ecctype="col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Alignment Scores:

Pred. No.:	3,14e+03	Length:	457
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	11	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CR404571 (1-457)

Qy 1 Serleu1eThrTPAsn1le 7

Db 103 AGTTTGATTAACCTGGAACATA 123

RESULT 13

LOCUS

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

COMMENT

FEATURES

1. 463
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="leghorn and broiler"
/db_xref="taxon:9031"
/clone="3GAL_45109"
/lab_host="DH5alpha"
/clone_lib="BARC 3GAL chicken mixed tissue"
/note="Vector: pBluescript SK+, Stratagene; Site 1: NotI; Site 2: EcoRI; Normalized library of pooled RNA isolated

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.txt

Page 14

from whole brain, ultimobranthial gland, parathyroid gland, cecal tonsil and primordial germ cells Multiple"

ORIGIN

Alignment Scores:

Score: 3.19e+03 Length: 463
Percent Similarity: 39.00 Matches: 7
Percent Similarity: 100.04 Conservative: 0
Best Local Similarity: 100.04 Mismatches: 0
Query Match: 100.04 Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x DN851694 (1-463)

QY 1 Serleu1etHrTPaAm1le 7

Db 155 TCCTCATTTACTCGAATATT 175

RESULT 14

CR543841 471 bp mRNA linear EST 07-JUN-2004
LOCUS DKFZP45900742.F1 459 (synonym: Pongo pygmaeus CDNA clone
DEFINITION DKFZP45900742 5', mRNA sequence.
ACCESSION CR543841
VERSION CR543841.1 GI:49895253
KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)
ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pongo.
1 (bases 1 to 471)
Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Well, B., Amid, C.,
Ossanger, A., Fobz, G., Han, W. and Wiemann, S.
Pongo pygmaeus mRNA (Bloecker, H., Boecher, M., Brandt, P., et al.)
Unpublished (2004)
COMMENT MIPB

REFERENCE
AUTHORS Ingolbaedter Landstr. 1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wiemann@dkfz-heidelberg.de, sequenced by GPF (National
Research Centre for Biotechnology Ltd., Braunschweig/Germany).
Within the cDNA sequencing consortium of the German Genome Project.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/projects/cdna/.

FEATURES

source
1..471
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZP45900742"
/tissue_type="cortex"
/dev_stage="adult"
/lab_host="DH10B"
/clone_id="459 (synonym: pcor1)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiIA; Site_2: SfiIB"

ORIGIN

Alignment Scores:

Score: 3.26e+03 Length: 471
Percent Similarity: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR543841 (1-471)

QY 1 Serleu1etHrTPaAm1le 7

Db 344 TCTTCATTTACTCGAATATT 364

RESULT 15

CR120234 473 bp mRNA linear EST 28-JAN-2003
LOCUS K-EST0167337 LB8CKO Homo sapiens CDNA clone LB8CKO-29-F06 5', mRNA
DEFINITION sequence.
ACCESSION CR120234
VERSION CR120234.1 GI:27946036
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 473)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
CONTACT: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krrib.re.kr
Plate: 29 row: F column: 06
High quality sequence stop: 473.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source
1..473
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LB8CKO-29-F06"
/sex="M"
/cell_line="SCK"
/lab_host="Trop10F"
/clone_lib="LB8CKO"
/note="Organ: Liver; Vector: pT7T3-Pac; Site 1: EcoRI;
Site 2: NotI; The library was constructed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
culture."

ORIGIN

Alignment Scores: 3.27e+03 Length: 473
Score: 39.06 Matches: 7
Percent Similarity: 100.04 Conservative: 0
Best Local Similarity: 100.04 Mismatches: 0
Query Match: 100.04 Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR120234 (1-473)

QY 1 Serleu1etHrTPaAm1le 7

Db 292 TCTTCATTTACTCGAATATT 312

RESULT 16

AT150554 480 bp mRNA linear EST 20-JUN-2002
LOCUS cno4a01.y1 Normal Human Trabecular Bone Cells Homo sapiens CDNA
DEFINITION cno4a01.y1 Normal Human Trabecular Bone Cells Homo sapiens CDNA
sequence.
ACCESSION AT150554
VERSION AT150554.1 GI:5128818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 480)
Jia, J.B., Young, M.F., Touchman, J.W., Bouffard, G.G., Beckstrom-Sterberg, S.M., Green, E.D., Powell, J.I., Yang, L.M., Robey, P.G., Hotchkiss, R.N. and Francomano, C.A.
SGAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
COMMENT
Contact: libin.jia
Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
Email: libin@helix.nih.gov

TITLE
JOURNAL

Genomic sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).
plate: 04 row: a column: 01
Seq primer: M13Rpl reverse primer (ABI).
Location/Qualifiers

FEATURES
source

1..480
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NHTRC_c004a01"
/sex="Female"
/tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
/clone_lib="Normal Human Trabecular Bone Cells"
/note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI; Library constructed by Dr. Marian Young and Dr. Pamela Gehron Robey (NIDCR)"

ORIGIN

Alignment Scores:

Pred. No.: 3.33e+03 Length: 480
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AT50554 (1-480)

QY 1 SerLeuileThrTyrAsnile 7
|||||
333 TCTCTCATTAACCTGGAATATT 357

Db 337 TCTCTCATTAACCTGGAATATT 357

RESULT 17
LOCUS AA486032 485 bp mRNA linear EST 06-MAR-1998
DEFINITION ab40b10.r1 StrataGene Hela cell s3 937216 Homo sapiens cDNA clone
IMAGE:843259 5', mRNA sequence.

ACCESSION AA486032

VERSION AA486032.1 GI:2216248

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 485)

AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,

Kritman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGS Consortium (info@image.lnl.gov) for further information.
Insert Length: 1913 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence scop: 444.
Location/Qualifiers

FEATURES
source

1..485
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:843259"
/sex="Female"
/dev_stage="Hela S3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene Hela cell s3 937216"
/note="Vector: pBluescript SK-; Site_1: EcoRI, Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Hela S3 epithelioid carcinoma cells grown to semi-confluency without induction. Average insert size: 1.5 kb; Uni-ZAP XR Vector. ~5' adaptor sequence: 5' GAATTCGACGACG 3' ~3' adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Alignment Scores:

Pred. No.: 3.37e+03 Length: 485
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AA486032 (1-485)

QY 1 SerLeuileThrTyrAsnile 7
|||||
333 TCTCTCATTAACCTGGAATATT 353

Db 333 TCTCTCATTAACCTGGAATATT 353

RESULT 18
LOCUS BU659432/c 511 bp mRNA linear EST 30-SEP-2002
DEFINITION c147f06.z1 Hembase; Erythroid Precursor Cells (UCB-cl library) Homo
sapiens cDNA clone c147f06 5', mRNA sequence.

ACCESSION BU659432

VERSION BU659432.1 GI:23371614

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 511)

AUTHORS Gubin, A.N., Lee, Y.T., Bouffard, G.G. and Miller, J.L.

Gene Expression in Human Erythroid Precursor Cells

Unpublished (2002)

CONTACT: Jeffery L. Miller

Laboratory of Chemical Biology

National Institute of Diabetes and Digestive and Kidney Diseases

Building 10, Room 9B17, National Institutes of Health, Bethesda, MD

20892, USA

Tel: 301 402 2373

Fax: 301 435 5148

Email: jlm7@nih.gov

The 'cl' library was constructed by Alexander Gubin, Ph.D. in the

laboratory of Chemical Biology, NIDDK, NIH. DNA sequencing and/or

analysis by National Institutes of Health Intramural Sequencing

Center (NISC). More information available at:

http://hembase.nidk.nih.gov

Plate: 47 row: f column: 06

Seq primer: 5' lambda-Triplex2 Sequencing Primer.

Location/Qualifiers

source

1. .511

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c147606"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Precursor Cells"
/cell_line="Primary Culture of Peripheral Blood Mononuclear Cells"
/dev_stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
/clone_1lb="Hembase; Erythroid Precursor Cells (LCB:cl library)"
/notes="Organ: blood; Vector: pTriplex2; Site 1: SfiI; Site 2: SfiI; A complementary DNA (cDNA) library from human erythroid precursor cells was constructed using SMART PCR (polymerase chain reaction) cDNA library Construction Kit (Clontech, Palo Alto, CA) according to the manufacturer's directions, but with slight modifications. Briefly, reverse transcription was performed in the presence of 1 umol/l peptide nucleic acid (PNA) oligos (N-terminal)-biotin-GTC-CAC-CCG-AGG-CTT-G-(C-terminal) and (N-terminal)-biotin-C(T/C)-T-GAA-GTT-AGG-A-(C-terminal). Synthesized cDNA was digested with SfiI and size selected on a 1% agarose gel (>800bp). Large-scale sequencing of the library was performed by the NIH Intramural Sequencing Center (NISC; Http://www.nisc.nih.gov/)."

```

ORIGIN

Alignment Scores:

Pred. No.: 3.59e+03 Length: 511

Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU659432 (1-511)

QY 1 Serleu1ethrTrypanile 7

DB 30 TCATGATCACTCGAATTA 10

RESULT 19

CC153114

LOCUS

DEFINITION

CSU-K34-128K7.SP6 CSU-K34 Aedes aegypti genomic clone

CC153114

CC153114.1 GI:30106410

CSG

CC153114.1

518 bp DNA linear

SSS

25-APR-2003

VERSION

CC153114

KEYWORDS

CSU-K34-128K7

GENOMIC SURVEY SEQUENCE.

ORGANISM

Aedes aegypti (yellow fever mosquito)

REFERENCE

1 (bases 1 to 518)

Knudson, D. and Severson, D.

BAC end sequencing of Aedes aegypti

Unpublished (2003)

Other_GSS: CSU-K34_128K7.T7

Contact: Brendan Lotz

Department of Eukaryotic Genomics

712 Medical Center Drive, Rockville, MD 20850, USA

TEL: 301-838-3543

FAX: 301-838-0208

Email: bseverson@gsf.org

Library was provided by Susan Brown and Dennis Knudson at Colorado State University.

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .518

source

/organism="Aedes aegypti"

/mol_type="genomic DNA"

/db_xref="taxon:7159"

/clone="CSU-K34-128K7"

/clone_1lb="CSU-K34"

/notes="Vector: pBAC63.6; Site 1: EcoRI; Source DNA: Aedes aegypti; strain unknown (derived from freshly hatched larvae at the Virus Research Centre, Poona, India. Reference: SINGH, K. R. P., 1967 Cell cultures derived from larvae of Aedes albopictus (Skuse) and Aedes aegypti (L.). Current Science 36: 506-508); ATC-10 cell line ATCC CCL-125"

ORIGIN

Alignment Scores:

Pred. No.: 3.65e+03 Length: 518

Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 9 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CC153114 (1-518)

QY 1 Serleu1ethrTrypanile 7

DB 167 TCCTCATACCTCGAACAT 187

RESULT 20

BM646221

LOCUS

DEFINITION

K-EST0125204 S13KMS5 Homo sapiens cDNA clone S13KMS5-59-C04 5', mRNA sequence.

BM646221

BM646221.1 GI:19202620

EST

VERSION

BM646221

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 530)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Kim, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea

TEL: +82-42-860-4470

FAX: +82-42-860-4409

Email: yongseung@mail.kr

Plate: 59 row C column: 04

High quality sequence stop: 530.

Location/Qualifiers

1 530

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S13KMS5-59-C04"

/tissue_type="myeloma"

/cell_line="RMS-5"

/lab_host="TOP10F"

/clone_1lb="S13KMS5"

/notes="Vector: PCNS; Site 1: BcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deacapped with tobacco acid

pyrophosphatase (TAP). The deprotected intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoR I which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Alignment Scores:

Pred. No.:	3.75e+03	Length:	530
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BM646221 (1-530)

QY 1 SerLeu11eThrTrpAsn11e 7
DB 347 TCTCTCATTAACCTGGAAATATT 367

RESULT 21

CN233559 531 bp mRNA linear EST 09-APR-2004
DEFINITION RJA113F02.ab1 Rbubrain Gallus gallus cDNA 5', mRNA sequence.
ACCESSION CN233559
VERSION CN233559.1 GI:46337303
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
1 (bases 1 to 531)
Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and Lundberg, U.
EST analysis of brain and testis cDNA libraries from White Leghorn and Red Jungle Fowl
Unpublished (2004)
Contact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5537 8481
Fax: +46 (0)8 5537 8335
Email: Peter.Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.

FEATURES
Location/Qualifiers
1..531
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Red junglefowl"
/db_xref="taxon:9031"
/sex="female"
/lab_host="ElectromAX DH10B (Invitrogen)"
/clone_lib="Rbubrain"
/note="Organ: brain; Vector: pSPORT-1; Site 1: Hind III, Site 2: EcoRI; The cDNA libraries were created with the Superscript Plasmid System (Invitrogen)."

JOURNAL
COMMENT

ORIGIN

Alignment Scores:

Pred. No.:	3.76e+03	Length:	531
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0

Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CN233559 (1-531)

QY 1 SerLeu11eThrTrpAsn11e 7
DB 303 TCGCTGATTAACCTGGAAACATT 323

RESULT 22

BP220985 554 bp mRNA linear EST 15-SEP-2004
DEFINITION BP220985 Sugano cDNA library, colon Homo sapiens cDNA clone
ACCESSION BP220985
VERSION BP220985.1 GI:52093890
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo
1 (bases 1 to 554)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanebaidai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
Location/Qualifiers
1..554
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL06450"
/tissue_type="colon"
/clone_lib="Sugano cDNA library, colon"

JOURNAL
COMMENT

ORIGIN

Alignment Scores:

Pred. No.:	3.95e+03	Length:	554
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BP220985 (1-554)

QY 1 SerLeu11eThrTrpAsn11e 7
DB 252 TCTCTCATTAACCTGGAAATATT 272

RESULT 23

BX997515/c 558 bp DNA linear GSS 05-UTL-2004
DEFINITION Forward strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone WHP34112, genomic survey sequence.
ACCESSION BX997515
VERSION BX997515.1 GI:49728973
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
1 (bases 1 to 558)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

```

AUTHORS      Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
              Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
              Rogers,J. and Bradley,A.
TITLE        Direct Submision
JOURNAL      Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
              CB10 1SA, UK. http://www.sanger.ac.uk/MICER
FEATURES
SOURCE
1..558
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone_lib="MHP341112"
/clone_lib="MHP"

ORIGIN
Alignment Scores:
Pred. No.:      3,996+03      Length:      558
Score:          38.00         Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%         Indels:      0
DB:             10            Gaps:         0

US-10-757-745-2_COPY_115_121 (1-7) x BX997515 (1-558)
QY
1 Serleu1eThrTpAsn1le 7
Db
472 TCCTCATTAACCTTGGAATATT 452

RESULT 24
BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
LOCUS      BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
DEFINITION BP226620 Sugano cDNA library, dermoid cancer Homo sapiens cDNA
ACCESSION  BP226620
VERSION    BP226620.1 GI:52099525
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 565)
            Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
            Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
            Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL    PUBMED
COMMENT    Contact: Yutaka Suzuki
            Department of Virology
            Institute of Medical Science, University of Tokyo
            4-6-1, Shirokane-dai, Minato-ku, Tokyo 108-8639, Japan
            Email: yusuzuki@ims.u-tokyo.ac.jp.
            Location/Qualifiers
FEATURES
SOURCE
1..565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="DMC03190"
/clone_lib="Sugano cDNA library, dermoid cancer"
/note="dermoid cancer"

ORIGIN
Alignment Scores:
Pred. No.:      4,056+03      Length:      565
Score:          38.00         Matches:      7
Percent Similarity: 100.0%      Conservative: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%         Indels:      0
DB:             3            Gaps:         0

US-10-757-745-2_COPY_115_121 (1-7) x BP226620 (1-565)
US-10-757-745-2_COPY_115_121 (1-7) x BP220508 (1-566)
QY
1 Serleu1eThrTpAsn1le 7
Db
262 TCCTCATTAACCTTGGAATATT 282

RESULT 26
BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
LOCUS      BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
DEFINITION BP257211 Sugano cDNA library, heart Homo sapiens cDNA clone
ACCESSION  BP257211
VERSION    BP257211.1 GI:52172441
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homiidae; Homo.
            1 (bases 1 to 568)
            Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
            Mizushima-Sugano,J., Nakai,K. and Sugano,S.
            Sequence comparison of human and mouse genes reveals a homologous
            block structure in the promoter regions
            Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL

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PUBMED 15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. 568
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HRT00430"
/tissue_type="heart"
/clone_lib="Sugano cDNA library, heart"

ORIGIN
Alignment Scores:
Pred. No.: 4.07e+03 Length: 568
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP257211 (1-568)

QY 1 SerLeu1leThrTTPAsn1le 7
Db 313 TCTCTCATTTACTGGAATATT 333

RESULT 27
LOCUS BM172060 570 bp mRNA linear EST 04-DEC-2001
DEFINITION IMAGEC_3_2001/sm1293bdf41.xl NIH_MGC_76 Homo sapiens cDNA clone
IMAGE:4700059 5', mRNA sequence.
BM172060 GI:17311623
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 570)
Kale, P.I., Harsch, T.J., Folta, P.A., Nelson, D.O., Sanders, C.G. and
Prange, C.K.
The I.M.A.G.E. Consortium quality control effort: clone
Unpublished (2001)
Other ESTs: BG533717
Contact: Prange CK
The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
Livermore, CA, USA
Email: help@image.llnl.gov
This read has been verified (found to hit its original self in the
correct orientation), as part of the I.M.A.G.E. Consortium quality
control effort. High quality sequence is defined as having 100 or
more base pairs with a phred quality value of 20 or greater, where
a sliding window of 4 base pairs with a phred quality value of 15
or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
info@image.llnl.gov.
Plate: LCM1533 Row: a Column: 20
Seq primer: -21m13
High quality sequence stop: 570.
Location/Qualifiers
1. 570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4700059"
/lab_host="DH10B (T1 phage-resistant)"

FEATURES
source

/clone_lib="NIH_MGC_76"
/note="Organ: liver; Vector: pDNR-L1B (Clontech); Site 1:
SfiI (ggcgctcgcc); Site 2: SfiI (ggccatcagcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCGCATTTATGCCC-3' and 3' adaptor sequence:
5'-ATTCTAAGAGCGGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 4.09e+03 Length: 570
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BM172060 (1-570)

QY 1 SerLeu1leThrTTPAsn1le 7
Db 195 TCTCTCATTTACTGGAATATT 215

RESULT 28
LOCUS BP221518 570 bp mRNA linear EST 15-SEP-2004
DEFINITION BP221518 Sugano cDNA library, colon Homo sapiens cDNA clone
COL09203, mRNA sequence.
BP221518
BP221518.1 GI:52094423
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 570)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. 570
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL09203"
/tissue_type="colon"
/clone_lib="Sugano cDNA library, colon"

ORIGIN
Alignment Scores:
Pred. No.: 4.09e+03 Length: 570
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP221518 (1-570)

QY 1 SerLeu1leThrTTPAsn1le 7

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.fst

Page 20

DB 251 TCTCATTAACCTGGAAATATT 271

RESULT 29
LOCUS BU397611
DEFINITION BU397611 570 bp mRNA linear EST 27-NOV-2002
603534313F1 CSEQCCHN58 Gallus gallus cDNA clone CHST49314 5', mRNA
sequence.
ACCESSION BU397611
VERSION BU397611
KEYWORDS GI:25766654
SOURCE EST.
ORGANISM Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 570)
Boardman, P. R., Sanz-Bizquerro, J., Overton, I. M., Burt, D. W., Bosch, E.,
Fong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..570
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHST49314"
/sex="Female"
/day_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCCHN58"
/note="Organ. Small intestine; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction,
following this first strand reaction, double-stranded cDNA
was blunt-ended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1984) 81:9228-9232 and Boudado et al. Genome Research 6
(1996) 191, except that a significantly longer
reaminging hybridization was used."

ORIGIN
Alignment Scores:
Pred. No.: 4.09e+03 Length: 570
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU397611 (1-570)

OY 1 SerLeuIIeRnTPaenIIe 7
DB 80 TCGGTGATTAACCTGGAAATATT 100

RESULT 30
BP262485

LOCUS BP262485 572 bp mRNA linear EST 16-SEP-2004
DEFINITION BP262485 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS107111, mRNA sequence.
ACCESSION BP262485
VERSION BP262485.1 GI:52177716
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 572)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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/db_xref="taxon:9606"
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Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP262485 (1-572)

OY 1 SerLeuIIeRnTPaenIIe 7
DB 299 TCTCATTAACCTGGAAATATT 319

RESULT 31
LOCUS AU279894 573 bp mRNA linear EST 31-JUL-2003
DEFINITION AU279894 CHONS2 Homo sapiens cDNA clone CHONS2002038 5', mRNA
sequence.
ACCESSION AU279894
VERSION AU279894.1 GI:28299121
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 573)
Imabayashi, H., Mori, T., Gojo, S., Kiyono, T., Sugiyama, T., Irie, R.,
Isogai, T., Hara, J., Tomoya, Y. and Umezawa, A.
Redifferentiation of dedifferentiated chondrocytes and
chondrogenesis of human bone marrow stromal cells via chondrosphere
formation with expression profiling by large-scale cDNA analysis
Exp. Cell Res. 288 (1), 35-50 (2003)
12878157
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975

Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA Project, Sugiyama, T.; Wakamatsu, A.; Irie, R.;
 Umezawa, A.; Fukuma, M.; Kuwakari, S.; Hata, J.; Ishii, S.; Yamamoto, J.;
 Isono, Y.; Saito, K.; Nakamura, Y.; Masuko, Y.; Nagai, K.; Isogai, T.
 HRI human cDNA Project: cDNA library construction & 5'-end one
 pass sequencing: Helix Research Institute.

FEATURES

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US-10-757-745-2_COPY_115_121 (1-7) x AU279894 (1-573)

Qy 1 SerLeuileThrTrpAsnile 7

Db 380 TCTCTCATTAACCTGGAAATATT 400

RESULT 32
 BP221260 573 bp mRNA linear EST 15-SEP-2004
 LOCUS BP221260 Sugano cDNA library, colon Homo sapiens cDNA clone
 DEFINITION COL08083, mRNA sequence.
 ACCESSION BP221260
 VERSION BP221260.1 GI:52094165
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 573)
 Score: 4.12e+03
 Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)

REFERENCE
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions

JOURNAL
 PUBMED 15342556
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

COMMENT

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ORIGIN

Alignment Scores:

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Best Local Similarity:	100.0%	Mismatches:	0
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DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP221260 (1-573)

Qy 1 SerLeuileThrTrpAsnile 7

Db 265 TCTCTCATTAACCTGGAAATATT 285

RESULT 33
 BP261500 573 bp mRNA linear EST 16-SEP-2004
 LOCUS BP261500 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION clone HS103816, mRNA sequence.
 ACCESSION BP261500
 VERSION BP261500.1 GI:52176731
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 573)
 Score: 4.12e+03
 Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)

REFERENCE
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
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JOURNAL
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 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

COMMENT

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ORIGIN

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Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BP261500 (1-573)

Qy 1 SerLeuileThrTrpAsnile 7

Db 249 TCTCTCATTAACCTGGAAATATT 269

RESULT 34
 BP262642 576 bp mRNA linear EST 16-SEP-2004
 LOCUS BP262642 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION clone HS107584, mRNA sequence.
 ACCESSION BP262642
 VERSION BP262642.1 GI:52177873
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
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 Score: 4.12e+03
 Percent Similarity: 100.0%
 Best Local Similarity: 100.0%
 Query Match: 100.0%
 block structure in the promoter regions
 Genome Res. 14 (9), 1711-1718 (2004)

REFERENCE
 AUTHORS Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

Page 22

TITLE
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

JOURNAL
Genome Res. 14 (9), 1711-1718 (2004)

PUBMED
15342556

COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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Query Match: 100.0% Indels: 0
DB: Gaps: 3

US-10-757-745-2_COPY_115_121 (1-7) x BP262642 (1-576)

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267 TCTCATTACCTGGATATT 287

RESULT 35
CN298919 577 bp mRNA linear EST 16-MAY-2004
LOCUS
17000600175228 GRN_PRRHP Homo sapiens cDNA 5', mRNA sequence.
CN298919
VERSION
CN298919.1 GI:47315333
KEYWORDS
EST
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 577)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, J., and Standon, L.
Lebowitz, J. and Standon, L.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
CONTACT: Brandenberger R
151619
Regenerative Medicine
Gen Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 9658
Fax: 650 473 7760
Email: rbrandenberger@gen.com
Insert Length: 577 Std Error: 0.00.
Location/Qualifiers
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from DMSO-treated hES cell line H9 (p2) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 4.15e+03 Length: 577
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Query Match: 100.0% Indels: 0
DB: Gaps: 3

US-10-757-745-2_COPY_115_121 (1-7) x CN298919 (1-577)

QY
1 SerLeuIeThrTPaenIle 7
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343 TCTCATTACCTGGATATT 363

RESULT 36
BP261787 580 bp mRNA linear EST 16-SEP-2004
LOCUS
BP261787 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION
BP261787 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS105008, mRNA sequence.
BP261787
VERSION
BP261787.1 GI:52177018
KEYWORDS
EST
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 580)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
CONTACT: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Location/Qualifiers
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ORIGIN

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Query Match: 100.0% Indels: 0
DB: Gaps: 3

US-10-757-745-2_COPY_115_121 (1-7) x BP261787 (1-580)

QY
1 SerLeuIeThrTPaenIle 7
|||||
278 TCTCATTACCTGGATATT 298

RESULT 37
BP274368 580 bp mRNA linear EST 16-SEP-2004
LOCUS
BP274368 Sugano cDNA library, kidney Homo sapiens cDNA clone
DEFINITION
BP274368 Sugano cDNA library, kidney Homo sapiens cDNA clone
KDN00894, mRNA sequence.
BP274368
VERSION
BP274368.1 GI:52188100
KEYWORDS
EST
SOURCE
Homo sapiens (human)


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ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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              Homiidae; Homo.
AUTHORS       1 (bases 1 to 580)
              Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
              Mizushima-Sugano,S., Nakai,K. and Sugano,S.
TITLE         Sequence comparison of human and mouse genes reveals a homologous
              block structure in the promoter regions
JOURNAL       Genome Res. 14 (9), 1711-1718 (2004)
PUBMED        15342556
COMMENT       Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES      Location/Qualifiers
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US-10-757-745-2_COPY_115_121 (1-7) x BP274368 (1-580)
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Db      363 TCTCTCATTTACCTGGAAATATT 383

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LOCUS        AV1717253
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ACCESSION    AV1717253
VERSION      AV1717253.1 GI:10814405
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
              1 (bases 1 to 581)
              Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J.,
              Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X.,
              Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
              Lu,G., Cheng,Z., and Han,Z.
              Homo sapiens cDNA DCB clones
              Unpublished (2000)
              Contact: Zeguang Han
              Chinese National Human Genome Center at Shanghai
              351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
              201203, P. R. China
              Tel: 86-21-50801919 (ex.45)
              Fax: 86-21-50801922
              Email: hanzg@chgc.sh.cn
              This clone is available at CHGC in Shanghai.
FEATURES      Location/Qualifiers
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               /db_xref="taxon:9606"
               /clone="DCBMA04"

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Pred. No.:      4.18e+03      Length:      581
Score:          38.00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:             1           Gaps:        0

US-10-757-745-2_COPY_115_121 (1-7) x AV1717253 (1-581)
QY      1 SerLeuileThrTPAsnIle 7
Db      186 TCTCTCATTTACCTGGAAATATT 206

RESULT 39      581 bp      mRNA      linear      EST 14-SEP-2004
LOCUS        BP199948
DEFINITION   BP199948 Sugano cDNA library, amygdala Homo sapiens cDNA clone
              AMR00446, mRNA sequence.
ACCESSION    BP199948
VERSION      BP199948.1 GI:52048428
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homiidae; Homo.
              1 (bases 1 to 581)
              Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
              Mizushima-Sugano,S., Nakai,K. and Sugano,S.
              Sequence comparison of human and mouse genes reveals a homologous
              block structure in the promoter regions
              Genome Res. 14 (9), 1711-1718 (2004)
              Contact: Yutaka Suzuki
              Department of Virology
              Institute of Medical Science, University of Tokyo
              4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
              Email: yusuzuki@ims.u-tokyo.ac.jp.
FEATURES      Location/Qualifiers
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Pred. No.:      4.18e+03      Length:      581
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Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
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DB:             3           Gaps:        0

US-10-757-745-2_COPY_115_121 (1-7) x BP199948 (1-581)
QY      1 SerLeuileThrTPAsnIle 7
Db      379 TCTCTCATTTACCTGGAAATATT 399

RESULT 40      581 bp      mRNA      linear      EST 14-SEP-2004
LOCUS        BP207751

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DEFINITION BP207751 Sugano cDNA library, coronary artery smooth muscle cell
ACCESSION BP207751
VERSION BP207751.1 GI:52064157
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
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block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

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Pred. No.: 4.18e+03 Length: 581
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Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
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Db 251 TCTCTCATTTACCTGGAAATATT 271

RESULT 41
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LOCUS BP225088
DEFINITION cl225 DAT05184, mRNA sequence.
ACCESSION BP225088
VERSION BP225088.1 GI:52097993
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
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block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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/note="Burkitt's lymphoma"

ORIGIN
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Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
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Db 364 TCTCTCATTTACCTGGAAATATT 384

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LOCUS BP262638
DEFINITION clone HS107576, mRNA sequence.
ACCESSION BP262638
VERSION BP262638.1 GI:52177869
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp

FEATURES
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/clone="HS107576"
/tissue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN
Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BP262638 (1-581)
QY 1 SerleuileThrTpAsnIle 7
Db 111 TCTCTCATTTACCTGGAAATATT 111

Db 260 TCTCTCATTTACTCGGATATT 280

RESULT 43
LOCUS BP264149
DEFINITION BP264149 Sugano cDNA library, small intestine Homo sapiens CDNA clone HS114850, mRNA sequence.
ACCESSION BP264149.1 GI:52179380
VERSION BP264149.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
source
1. 581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS114850"
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/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP264149 (1-581)

QY 1 SerLeuIleThrTrpAsnIle 7
|||||
Db 309 TCTCTCATTTACTCGGATATT 329

RESULT 44
LOCUS BP270744
DEFINITION BP270744 Sugano cDNA library, small intestine Homo sapiens CDNA clone KAR05146, mRNA sequence.
ACCESSION BP270744
VERSION BP270744.1 GI:52220093
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology

FEATURES
source
1. 581
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KAR05146"
/issue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP270744 (1-581)

QY 1 SerLeuIleThrTrpAsnIle 7
|||||
Db 251 TCTCTCATTTACTCGGATATT 271

RESULT 45
LOCUS BP349936
DEFINITION BP349936 Sugano cDNA library, brain Homo sapiens CDNA clone SZR06923, mRNA sequence.
ACCESSION BP349936
VERSION BP349936.1 GI:52279921
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 581)
Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers

FEATURES
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1. 581
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZR06923"
/issue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP349936 (1-581)

QY 1 SerLeuIleThrTrpAsnIle 7

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DB      120  TCTCTCATTTACCTGGAAATATT 140
RESULT 46
BP379659 581 bp  mRNA  linear  EST 21-SEP-2004
LOCUS    WMD06642. mRNA sequence.
DEFINITION BP379659.1 GI:52412762
ACCESSION BP379659
VERSION   BP379659.1 GI:52412762
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 581)
Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,
Mizushima-Sugano J., Nakai K. and Sugano S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL  15342556
PUBMED   Contact: Yutaka Suzuki
COMMENT  Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanebashi, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzaki@im.s.u-tokyo.ac.jp.
FEATURES
    source
        1..581 sm="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="WMD06642"
        /tissue_type="uterus"
        /clone_lib="Sugano cDNA library, uterus"

ORIGIN
Alignment Scores:
Pred. No.: 4.18e+03 Length: 581
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 3
DB: 3

US-10-757-745-2_COPY_115_121 (1-7) x BP379659 (1-581)
QY      1 SerLeuIleThrTPanille 7
DB      252  TCTCTCATTTACCTGGAAATATT 272

RESULT 47
BP507091 582 bp  mRNA  linear  EST 15-FEB-2002
LOCUS    1h24h01.y1 Human Insulinoma Homo sapiens cDNA 5' similar to
DEFINITION TR:095551 O95551 D030M3.3 ;, mRNA Sequence.
ACCESSION BP507091
VERSION   BP507091.1 GI:18678234
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 582)
Melton D., Brown J., Kenty G., Permutt A., Lee C., Kaestner K.,
Lemishka L., Scaer M., Brestelli J., Gradwohl G., Clifton S.,
Hillier L., Maria M., Pape D., Wylie T., Martin J., Birstein A.,
Schmitt A., Theising B., Ritzer E., Ronko T., Bennett J.,
Cardenas M., Gibbons M., McCann R., Cole R., Tsagarisvili R.,
Williams T., Jackson Y. and Bowers Y.
Endocrine Pancreas Consortium
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

```

```

JOURNAL  Unpublished (2000)
COMMENT  Other ESTs: 1h24h01.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biochem.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University genome sequencing center for information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 269.
FEATURES
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        1..582
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        /db_xref="taxon:9606"
        /tissue_type="Insulinoma"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="Human Insulinoma"
        /notes="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
XhoI; Site 2: EcoRI; Constructed with lambda ZAPIT system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN
Alignment Scores:
Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 3
DB: 3

US-10-757-745-2_COPY_115_121 (1-7) x BP507091 (1-582)
QY      1 SerLeuIleThrTPanille 7
DB      145  TCTCTCATTTACCTGGAAATATT 165

RESULT 48
BP219740 582 bp  mRNA  linear  EST 15-SEP-2004
LOCUS    BP219740 Sugano cDNA library, caudate nucleus Homo sapiens cDNA
DEFINITION clone CNR08985, mRNA sequence.
ACCESSION BP219740
VERSION   BP219740.1 GI:52092643
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 582)
Suzuki Y., Yamashita R., Shiota M., Sakakibara Y., Chiba J.,
Mizushima-Sugano J., Nakai K. and Sugano S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)

JOURNAL  15342556
PUBMED   Contact: Yutaka Suzuki
COMMENT  Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanebashi, Minato-ku, Tokyo 108-8639, Japan
Email: yusuzaki@im.s.u-tokyo.ac.jp.

```

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source

1.582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NC08985"
/cissue_type="caudate nucleus"
/clone_lib="Sugano cDNA library, caudate nucleus"

ORIGIN

Alignment Scores:

Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP219740 (1-582)

QY 1 SerLeuIleThrTrpAsnIle 7

DB 358 TCTCTCATTAACCTGGAAATATT 378

RESULT 49
BP233592

LOCUS BP233592 582 bp mRNA linear EST 15-SEP-2004
DEFINITION BP233592 Sugano cDNA library, coronary artery endothelial cell Homo
sapiens cDNA clone HCR00774, mRNA sequence.

ACCESSION BP233592 GI:52106502
VERSION BP233592.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
1 (bases 1 to 582)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Homniidae; Homo.
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.

TITLE
JOURNAL Mizushima-Sugano,J., Nakai,K. and Sugano,S.
PUBMED Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source

1.582
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HCR00774"
/cissue_type="coronary artery"
/cell_type="endothelial cell"
/clone_lib="Sugano cDNA library, coronary artery
endothelial cell"

ORIGIN

Alignment Scores:

Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP233592 (1-582)

QY 1 SerLeuIleThrTrpAsnIle 7
DB 358 TCTCTCATTAACCTGGAAATATT 378

RESULT 50
BP234218

LOCUS BP234218 582 bp mRNA linear EST 15-SEP-2004
DEFINITION BP234218 Sugano cDNA library, coronary artery endothelial cell Homo
sapiens cDNA clone HCR02378, mRNA sequence.

ACCESSION BP234218 GI:52107128
VERSION BP234218.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
1 (bases 1 to 582)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Homniidae; Homo.
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.

TITLE
JOURNAL Mizushima-Sugano,J., Nakai,K. and Sugano,S.
PUBMED Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
15342556

COMMENT

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source

1.582
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="HCR02378"
/cissue_type="coronary artery"
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endothelial cell"

ORIGIN

Alignment Scores:

Pred. No.: 4.19e+03 Length: 582
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP234218 (1-582)

QY 1 SerLeuIleThrTrpAsnIle 7

DB 370 TCTCTCATTAACCTGGAAATATT 390

RESULT 51
BP261141

LOCUS BP261141 582 bp mRNA linear EST 16-SEP-2004
DEFINITION BP261141 Sugano cDNA library, small intestine Homo sapiens cDNA
clone HS102606, mRNA sequence.

ACCESSION BP261141 GI:52176372
VERSION BP261141.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
1 (bases 1 to 582)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Homniidae; Homo.
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.

TITLE
JOURNAL Mizushima-Sugano,J., Nakai,K. and Sugano,S.
PUBMED Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

block structure in the promoter regions
 JOURNAL
 Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED
 15342556
 COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 /clone="HS102606"
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ORIGIN
 Alignment Scores:
 Prod. No.: 4.19e+03 Length: 582
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP261141 (1-582)

Qy 1 SerleuilethTrpAnille 7
 |||||
 Db 249 TCTCTCATTACCTGGAAATTT 269

RESULT 52
 BP263516 582 bp mRNA linear EST 16-SEP-2004
 LOCUS
 BP263516 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION
 clone HS111929, mRNA sequence.
 ACCESSION
 BP263516
 VERSION
 BP263516.1 GI:52178747
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 582)
 Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL
 Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED
 15342556
 COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 /clone="HS111929"
 /cissue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN
 Alignment Scores:
 Prod. No.: 4.19e+03 Length: 582
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP263516 (1-582)

Qy 1 SerleuilethTrpAnille 7
 |||||
 Db 309 TCTCTCATTACCTGGAAATTT 329

RESULT 53
 BP270415 582 bp mRNA linear EST 17-SEP-2004
 LOCUS
 BP270415 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION
 clone KAR02166, mRNA sequence.
 ACCESSION
 BP270415
 VERSION
 BP270415.1 GI:52219764
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 582)
 Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL
 Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED
 15342556
 COMMENT
 Contact: Yutaka Suzuki
 Department of Virology
 Institute of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 1..582
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 /db_xref="taxon:9606"
 /clone="KAR02166"
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 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN
 Alignment Scores:
 Prod. No.: 4.19e+03 Length: 582
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP270415 (1-582)

Qy 1 SerleuilethTrpAnille 7
 |||||
 Db 341 TCTCTCATTACCTGGAAATTT 361

RESULT 54
 BP275810 582 bp mRNA linear EST 16-SEP-2004
 LOCUS
 BP275810 Sugano cDNA library, kidney Homo sapiens cDNA clone
 DEFINITION
 KDN04583, mRNA sequence.
 ACCESSION
 BP275810
 VERSION
 BP275810.1 GI:52189542
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 1 (bases 1 to 582)
 Suzuki,Y., Yamashita,R., Shiota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.

TITLE Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

JOURNAL Genome Res. 14 (9), 1711-1718 (2004)

PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1. 582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="KDN04583"
/issue_type="kidney"
/clone_lib="Sugano cDNA library, kidney"

ORIGIN

Alignment Scores:

Pred. No.:	4.19e+03	Length:	582
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BP275810 (1-582)

Qy 1 SerleuileThrTrypsinile 7
|||||
Db 332 TCTCTCATTTACTGGAATATT 352

RESULT 55
BP195721 583 bp mRNA linear EST 14-SEP-2004
LOCUS BP195721 Sugano cDNA library, brain Homo sapiens cDNA clone
DEFINITION ADB08961, mRNA sequence.
ACCESSION BP195721
VERSION BP195721.1 GI:52039998
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ADB08961"
/issue_type="brain"
/clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:

Pred. No.:	4.2e+03	Length:	583
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BP275810 (1-582)

Qy 1 SerleuileThrTrypsinile 7
|||||
Db 277 TCTCTCATTTACTGGAATATT 297

RESULT 57
BP262741 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP262741, mRNA sequence.
ACCESSION BP262741
VERSION BP262741.1 GI:52177972
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP195721 (1-583)

Qy 1 SerleuileThrTrypsinile 7
|||||
Db 400 TCTCTCATTTACTGGAATATT 420

RESULT 56
BP262103 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP262103 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP262103, mRNA sequence.
ACCESSION BP262103
VERSION BP262103.1 GI:52177334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
1. 583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HS105902"
/issue_type="small intestine"
/clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:

Pred. No.:	4.2e+03	Length:	583
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BP262103 (1-583)

Qy 1 SerleuileThrTrypsinile 7
|||||
Db 277 TCTCTCATTTACTGGAATATT 297

RESULT 57
BP262741 583 bp mRNA linear EST 16-SEP-2004
LOCUS BP262741 Sugano cDNA library, small intestine Homo sapiens cDNA
DEFINITION BP262741, mRNA sequence.
ACCESSION BP262741
VERSION BP262741.1 GI:52177972
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 583)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

TITLE Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1716 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PCD1128"
/issue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"

ORIGIN
Alignment Scores:
Pred. No.: 4.2e+03 Length: 583
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0
DB: 3

US-10-757-745-2_COPY_115_121 (1-7) x BP262741 (1-583)

QY 1 SerLeuIleTTPaenlle 7
DB 213 TCTCTACTTACCTGGAAATATT 233

RESULT 58
LOCUS BP319548 583 bp mRNA linear EST 17-SEP-2004
DEFINITION BP319548 Sugano cDNA library, pericardium Homo sapiens cDNA clone
PCD1128, mRNA sequence.
ACCESSION BP319548.1 GI:52248523
VERSION BP319548.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo (583)
1 (bases 1 to 583)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
JOURNAL Genome Res. 14 (9), 1711-1716 (2004)
PUBMED 15342556
COMMENT Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
source
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PCD1128"
/issue_type="pericardium"
/clone_lib="Sugano cDNA library, pericardium"

ORIGIN
Alignment Scores:
Pred. No.: 4.2e+03 Length: 583
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP319548 (1-583)

QY 1 SerLeuIleTTPaenlle 7
DB 392 TCTCTACTTACCTGGAAATATT 412

RESULT 59
LOCUS BU783229 583 bp mRNA linear EST 11-OCT-2002
DEFINITION BU783229 Human insulinoma Homo sapiens cDNA clone IMAGE:6123158
5' similar to TR:095551 O95551 DJ30M3.3 ;, mRNA sequence.
ACCESSION BU783229
VERSION BU783229.1 GI:23827207
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 583)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scaerac,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Maria,M., Pape,D., Wylie,T., Martin,J., Bliscan,A.,
Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: in01a08.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@hchp.harvard.edu
Library was constructed by Dr. J. Ferrer in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 410.
Location/Qualifiers
1..583
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6123158"
/issue_type="insulinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Human insulinoma"
/note="Organ: pancreas; Vector: pBluescript SK-; Site: 1;
XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol.sheml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."

ORIGIN
Alignment Scores:
Pred. No.: 4.2e+03 Length: 583
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0%
 Query Match: 100.0%
 Db: 5
 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU783229 (1-583)

Qy 1 SerleulleThrTpsanlle 7
 Db 341 TCTCTCATTCCTGGAATATT 361

RESULT 60
 BP263059
 LOCUS BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA
 DEFINITION BP263059 Sugano cDNA library, small intestine Homo sapiens cDNA
 ACCESSION BP263059
 VERSION BP263059.1 GI:52178290
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki Y., Yamashita R., Shirota M., Sakakibara Y., Chiba J.,
 1 (bases 1 to 584)
 TITLE Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source
 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HS110591"
 /tissue_type="small intestine"
 /clone_lib="Sugano cDNA library, small intestine"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Db: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP263059 (1-584)

Qy 1 SerleulleThrTpsanlle 7
 Db 266 TCTCTCATTCCTGGAATATT 286

RESULT 61
 BP274942
 LOCUS BP274942 Sugano cDNA library, kidney Homo sapiens cDNA clone
 DEFINITION BP274942 Sugano cDNA library, kidney Homo sapiens cDNA clone
 ACCESSION BP274942
 VERSION BP274942.1 GI:52186674
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki Y., Yamashita R., Shirota M., Sakakibara Y., Chiba J.,
 1 (bases 1 to 584)
 TITLE Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source
 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SZR01143"
 /tissue_type="brain"
 /clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7

AUTHORS Suzuki Y., Yamashita R., Shirota M., Sakakibara Y., Chiba J.,
 Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
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 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KDN02414"
 /tissue_type="kidney"
 /clone_lib="Sugano cDNA library, kidney"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7

Qy 1 SerleulleThrTpsanlle 7
 Db 310 TCTCTCATTCCTGGAATATT 330

RESULT 62
 BP348623
 LOCUS BP348623 Sugano cDNA library, brain Homo sapiens cDNA clone
 DEFINITION BP348623 Sugano cDNA library, brain Homo sapiens cDNA clone
 ACCESSION BP348623
 VERSION BP348623.1 GI:52278608
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Suzuki Y., Yamashita R., Shirota M., Sakakibara Y., Chiba J.,
 1 (bases 1 to 584)
 TITLE Mizushima-Sugano, J., Nakai, K. and Sugano, S.
 Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556
 COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ims.u-tokyo.ac.jp.

FEATURES
 source
 1..584
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SZR01143"
 /tissue_type="brain"
 /clone_lib="Sugano cDNA library, brain"

ORIGIN

Alignment Scores:
 Pred. No.: 4.21e+03 Length: 584
 Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP348623 (1-584)

QY 1 Serleu1eThrTyrPsn1le 7
 |||||
 DB 373 TCTCTCATTAAGCTGGATATT 393

RESULT 63 BP236074 588 bp mRNA linear EST 15-SEP-2004
 LOCUS BP236074 Sugano cDNA library, coronary artery endothelial cell Homo
 DEFINITION sapiens cDNA clone HCR06784, mRNA sequence.

ACCESSION BP236074 GI:52108984
 VERSION BP236074
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 588)
 AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ms.u-tokyo.ac.jp.

FEATURES
 source
 1..588
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HCR06784"
 /tissue_type="coronary artery"
 /cell_type="endothelial cell"
 /clone_1=b"Sugano cDNA library, coronary artery
 endothelial cell"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.24e+03 Length: 588
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP236074 (1-588)

QY 1 Serleu1eThrTyrPsn1le 7
 |||||
 DB 379 TCTCTCATTAAGCTGGATATT 399

RESULT 64 BP348796 588 bp mRNA linear EST 17-SEP-2004
 LOCUS BP348796 Sugano cDNA library, brain Homo sapiens cDNA clone
 DEFINITION SZR01880, mRNA sequence.

ACCESSION BP348796
 VERSION BP348796.1 GI:52278781
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 588)
 AUTHORS Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
 Mizushima-Sugano,J., Nakai,K. and Sugano,S.
 TITLE Sequence comparison of human and mouse genes reveals a homologous
 block structure in the promoter regions
 JOURNAL Genome Res. 14 (9), 1711-1718 (2004)
 PUBMED 15342556

COMMENT Contact: Yutaka Suzuki
 Department of Medical Science, University of Tokyo
 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
 Email: yusuzuki@ms.u-tokyo.ac.jp.

FEATURES
 source
 1..588
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="SZR01880"
 /tissue_type="brain"
 /clone_1=b"Sugano cDNA library, brain"

ORIGIN
 Alignment Scores:
 Pred. No.: 4.24e+03 Length: 588
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP348796 (1-588)

QY 1 Serleu1eThrTyrPsn1le 7
 |||||
 DB 370 TCTCTCATTAAGCTGGATATT 390

RESULT 65 BI064472 600 bp mRNA linear EST 15-JUN-2001
 LOCUS BI064472 pgfin.pK001.h17 normalized chicken fat cDNA library Gallus gallus
 DEFINITION cDNA clone pgfin.pK001.h17 5', similar to gi17705262
 ref1NF_057678.11 ttxr and tnf receptor-associated protein [Homo
 sapiens] gb|AF061444.1|AF223469_1 (AF223469) AD022 protein [Homo
 sapiens]g, mRNA sequence.

ACCESSION BI064472 GI:14471994
 VERSION BI064472.1 GI:14471994
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 REFERENCE 1 (bases 1 to 600)
 AUTHORS Cogburn,L.A., Morgan,R.W. and Burnside,J.
 TITLE Chicken ESTs from fat
 JOURNAL Unpublished (2001)

COMMENT Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers

FEATURES
 source
 1..600
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="pgfin.pK001.h17"
 /sex="Male and Female"
 /tissue_type="fat"
 /lab_host="E.coli BMDH10B"

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ORIGIN
/clone_11b="normalized chicken fat cdna library"
/note="Vector: pSPORT1"

Alignment Scores:
Pred. No.: 4.35e+03 Length: 600
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1064472 (1-600)

Qy 1 SerleuileThrTyrPasnile 7
Db 239 TCGTGATTAACCTGGAAACATT 259

RESULT 66
LOCUS AL703449 602 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686G0621.r1.686 (synonym: h1cc3) Homo sapiens cdna clone
ACCESSION AL703449
VERSION AL703449.1 GI:19686804
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 602)
Ansoerge,W., Wiktner,U., Mewes,W., Well,B. and Wiemann,S.
EST (Ansoerge,W., Wiktner,U., Mewes,H.W., Well,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cdna sequencing consortium of the
German Genome Project.
No si sequence available.
This clone (DKFZp686G0621) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
source
1..602
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686G0621"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_11b="686 (synonym: h1cc3)"
/note="Vector: pTriplex2; Site_1: SfiI; Site_2: SfiIb;
cdna-collection"

ORIGIN
Alignment Scores:
Pred. No.: 4.37e+03 Length: 602
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AL703449 (1-602)

Qy 1 SerleuileThrTyrPasnile 7
|||||

```

```

Db 344 TCTCTAATCACTGGAAATATT 364

RESULT 67
LOCUS AV730762 604 bp mRNA linear EST 17-OCT-2000
DEFINITION AV730762 HTF Homo sapiens cdna clone HTFA010.5', mRNA sequence.
ACCESSION AV730762
VERSION AV730762.1 GI:10840183
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 604)
Gu,Y., Peng,Y., Song,H., Huang,Q., Yang,Y., Gao,G., Xiao,H., Xu,X.,
Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,
Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cdna HTF clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Gu Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..604
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HTFA010"
/tissue_type="Hypothalamus"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_11b="HTF"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 4.38e+03 Length: 604
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AV730762 (1-604)

Qy 1 SerleuileThrTyrPasnile 7
|||||
Db 385 TCACCTAATCACTGGAAATATT 405

RESULT 68
LOCUS CR163431 618 bp DNA linear GSS 06-JUL-2004
DEFINITION Forward strand read from insert in 5'HPT insertion targeting and
chromosome engineering clone MHPN168d24, genomic survey sequence.
ACCESSION CR163431
VERSION CR163431.1 GI:49942280
KEYWORDS GSS; genome survey sequence; MICR.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 618)
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,

```

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

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TITLE
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER

FEATURES
source
1..618
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="MMPN168d24"
/clone_1lb="MHPN"

ORIGIN
Alignment Scores:
Pred. No.: 4.5e+03 Length: 618
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CRI63431 (1-618)

QY
1 SerLeu1eThrTPaSn1le 7
|||||||
194 TCATTAAATACCTGGATATTC 174

RESULT 69
CB069952 621 bp mRNA linear EST 21-JAN-2003
LOCUS 18310.Y1 HR85 1setc Homo sapiens cDNA clone IMAGE:6554035 5'
DEFINITION similar to TR:095551 095551 DJ0M3.3 ; mRNA sequence.
ACCESSION CB069952
VERSION CB069952.1 GI:27814472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 621)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Bresnelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Biststein,A.,
Schmitt,A., Treising,B., Rifter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvalli,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: 18310.Y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohd.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 476.
Location/Qualifiers
1..621
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6554035"
/issue_type="Purified pancreatic 1setc"
/lab_host="DH10B"
/clone_1lb="HR85 1setc"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Alignment Scores:
Pred. No.: 4.53e+03 Length: 621
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CB069952 (1-621)

QY
1 SerLeu1eThrTPaSn1le 7
|||||||
349 TCCTCATTAACCTGGATATTC 369

RESULT 70
BU471395 625 bp mRNA linear EST 30-NOV-2002
LOCUS 603363114F1 CSEQRBN21 Gallus gallus cDNA clone CHEST258K3 5', mRNA
DEFINITION sequence.
ACCESSION BU471395
VERSION BU471395.1 GI:25964972
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 625)
Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomedical Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1..625
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
/clone="CHEST258K3"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSEQRBN21"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methyated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2

rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Alignment Scores:

Pred. No.:	4.56e+03	Length:	625
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x B0471395 (1-625)

Qy 1 SerLeuileThrTyrPasnile 7
 DB 286 TCGCTGATTAAGTGGACATT 306

RESULT 71

LOCUS CB157906 634 bp mRNA linear EST 29-JAN-2003
 DEFINITION K-EST0217150 L18POOL1n1 Homo sapiens cDNA clone L18POOL1n1-5-F06
 ACCESSION CB157906
 VERSION CB157906.1 GI:28143040
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 634)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

AUTHORS

TITLE 21C Frontier Korean EST Project 2001

JOURNAL Unpublished (2002)

COMMENT

Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 5 row: F column: 06
 High quality sequence stop: 634.

FEATURES

source

Location/Qualifiers
 1..634
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L18POOL1n1-5-F06"
 /cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
 /lab_host="Top10F"
 /clone_11b="L18POOL1n1"
 /note="Organ: liver; Vector: pT73-Pac; Site_1: EcoRI; Site_2: NotI; The library was contributed by the Soares Laboratory and it was constructed as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from harvested cell culture."

ORIGIN

Alignment Scores:

Pred. No.:	4.64e+03	Length:	634
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CB157906 (1-634)
 Qy 1 SerLeuileThrTyrPasnile 7
 DB 295 TCTCTCACTTACTGGAAATTT 315

RESULT 72

LOCUS CV023369 634 bp mRNA linear EST 20-AUG-2004
 DEFINITION 288 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC017553, mRNA sequence.

ACCESSION CV023369
 VERSION CV023369.1 GI:51481130
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 634)
 Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cho,D., Moore,T., Simons,B., Segueria,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C., Vandenhaute,V., Cusick,M.E., Albaladejo,S., Hill,D.E. and Vidal,M.

AUTHORS

Human ORFeome Version 1.1: a Platform for Reverse Proteomics
 Genome Res. (2004) In press
 Contact: Vidal M
 Dana Farber Cancer Institute
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
 Tel: 617 632 5180
 Fax: 617 632 5739
 Email: Marc.Vidal@dfci.harvard.edu

JOURNAL

COMMENT

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF results from a PCR reaction using an MGC full-length cDNA as template DNA and ORF specific primers
 PCR Primers
 FORWARD: ATGAGTTGGAGTTGCTGGA
 BACKWARD: TACATATATATCTAGTTGACAGAG
 Insert Length: 634 Std Error: 32.00
 Plate: 11008 row: 05 column: F
 Seq primer: ACTGCCCTCGTTTACACCTGCTGACTGGGAAAC
 High quality sequence start: 97
 High quality sequence stop: 633
 POLYA=No.

FEATURES

source

Location/Qualifiers
 1..634
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="mixed"
 /clone_11b="Full length cDNA from the Mammalian Gene Collection"
 /note="Vector: mixed. The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDONR223 donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"

ORIGIN

Alignment Scores:

Pred. No.:	4.64e+03	Length:	634
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CV023369 (1-634)

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us-10-757-745-2_copy_115_121.rst

Page 36

Qy 1 SerleuileThrTPAa11le 7
Db 343 TCTCTCATTACTCGAATATT 363

RESULT 73
LOCUS B1333830
DEFINITION 644 bp mRNA linear EST 30-JUL-2001
60299339F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141577 5',
mRNA sequence.
ACCESSION B1333830
VERSION B1333830.1 GI:15018487
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 644)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.jnl.gov
plate: L14M1348 row: n column: 10
High quality sequence stop: 531.
Location/Qualifiers
1..644
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5141577"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
/clone_11b="NIH MGC 12"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN
Alignment Scores:
Pred. No.: 4.73e+03 Length: 644
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1333830 (1-644)

Qy 1 SerleuileThrTPAa11le 7
Db 330 TCTCTCATTACTCGAATATT 350

RESULT 74
LOCUS A2360347
DEFINITION 644 bp DNA linear GSS 02-OCT-2000
1M0103M01R Mouse 10kb plasmid U10C1M library Mus musculus genomic
clone U10C1M0103M01 R, genomic survey sequence.
ACCESSION A2360347
VERSION A2360347.1 GI:10474047
KEYWORDS GSS
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
AUTHORS 1 Sciurognath; Muridae; Muridae; Murine; Mus.
1 (bases 1 to 644)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausen,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0103 row: M column: 01
Seq primer: CACACAGAAACGCTATACAC
Class: plasmid ends
High quality sequence stop: 644.
Location/Qualifiers
1..644
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U10C1M0103M01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_11b="Mouse 10kb plasmid U10C1M library"
/note="Vector: pMD229; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptorized DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD22 (g1|473114|g5|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptorized mouse DNA was annealed to
adaptorized vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Alignment Scores:
Pred. No.: 4.73e+03 Length: 644
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x A2360347 (1-644)

Qy 1 SerleuileThrTPAa11le 7
Db 62 TCATTAATACCTCGAATATC 82

RESULT 75
LOCUS BM426270
DEFINITION 645 bp mRNA linear EST 30-JAN-2002
pgf2n.pk002.c6 Normalized Chicken Abdominal Fat Library (pgf2n)
Gallus gallus cDNA clone pgf2n.pk002.c6 5' similar to g1|1418470
ref|xp_004263.1| TBAF and TNF receptor-associated protein (Homo

sapiens) gi|14747264 ref|XP_041296.1| TRAF and TNF
 receptor-associated protein [Homo sapiens] emb|CAA21141.1|
 (AL031775) dfj30M3.3 (novel protein similar to C. elegans, mRNA
 sequence.
 BM426270.1 GI:18430455
 EST.
 Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.
 1 (bases 1 to 645)
 Cogburn, L.A., Morgan, R. and Burnside, J.
 ESTs from Normalized Chicken Fat cDNA library-USDA/IRAFs Animal
 Genome Project
 Unpublished (2002)
 Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers
 1..645
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Commercial broiler, Ottawa Research Centre,
 leghorn"
 /db_xref="taxon:9031"
 /clone="pgfzn.pk002.c6"
 /sex="Male and Female"
 /tissue_type="Abdominal Fat"
 /dev_stage="Embryonic (d18,d19) ; post-hatch
 (d1,w3,w7,w9,w16,1yr)"
 /lab_host="E. coli EMD10B"
 /clone_lib="Normalized Chicken Abdominal Fat Library
 (pgfzn)"
 /note="Vector: pCMVSPORT6; library made from equivalent
 pools of total RNA isolated from each developmental age
 (across strains); Single pass sequencing from 5'-end"
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.74e+03 Length: 645
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x BM426270 (1-645)
 Oy 1 SerLeuIleThrTTPaSnIle 7
 |||||
 Db 373 TCGCTGATTACTTGGAACATT 393
 |||||
 RESULT 76
 CR753214 652 bp mRNA linear EST 01-SEP-2004
 LOCUS CR753214
 DEFINITION DKFZP4691195.1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
 DKFZP4691195.5, mRNA sequence.
 CR753214
 VERSION CR753214.1 GI:51845629
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Pongo.
 1 (bases 1 to 652)
 Ansoerge, W., Krieger, S., Regiert, T., Rittmueler, C., Schwager, B.,
 Mewes, H.W., Weil, B., Amid, C., Oesanger, A., Fobo, G., Han, M. and

Wiemann, S.
 Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 Unpublished (2004)
 JOURNAL
 COMMENT
 MIPS
 Ingolstaetter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email s.wiemann@dkfz-heidelberg.de; lin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp4691195
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 Location/Qualifiers
 1..652
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9600"
 /clone="DKFZp4691195"
 /tissue_type="Kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="469 (synonym: pkid1)"
 /note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiIb"
 ORIGIN
 Alignment Scores:
 Pred. No.: 4.8e+03 Length: 652
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 7 Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x CR753214 (1-652)
 Oy 1 SerLeuIleThrTTPaSnIle 7
 |||||
 Db 360 TCTCTCAATTAACCTGGAAATATT 380
 |||||
 RESULT 77
 CN298920 657 bp mRNA linear EST 16-MAY-2004
 LOCUS CN298920
 DEFINITION 17000600170525 GRN_PRENUE Homo sapiens cDNA 5', mRNA sequence.
 CN298920
 VERSION CN298920.1 GI:47315334
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominoidea; Homo.
 1 (bases 1 to 657)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandiam, R.,
 Lebkowksi, J. and Stanton, L.W.
 Transcriptome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197
 Contact: Brandenberger R.
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
 Insert Length: 657 Std Error: 0.00.
 Location/Qualifiers
 1..657
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 FEATURES
 source

ORIGIN

/tissue_type="embryonic stem cell, retinoic acid and
mitogen-treated hES cell line H7"
/clone_id="GRR_PRENEM"
/note="Oligo dt primed, full-length enriched cDNA library
from hES cell line H7 (p29) maintained in feeder-free
conditions. Embryoid bodies were generated in the presence
of all-trans retinoic acid and mitogens."

Alignment Scores:

Pred. No.:	4.84e+03	Length:	657
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CN298920 (1-657)

QY 1 SerleuileThrtTpansnile 7

Db 299 TCTCTACTACTGGAATATT 319

RESULT 78

BI067773

LOCUS

BI067773 662 bp mRNA linear EST 15-JUN-2001
pgfin.pk007.d9 normalized chicken fat cDNA library Gallus gallus

DEFINITION

cdna clone pgfin.pk007.d9 5' similar to gi111418470
ref|XP_004263.1| TRAF and TNF receptor-associated protein [Homo
sapiens] emb|CAA2141.1| (AL031775) dj30M3.3 (novel protein similar
to C. elegans Y63D3A.4) [Homo sapiens] emb|CAB92966.1| (AJ269473)
TRAF and TNF receptor associated prote, mRNA sequence.

ACCESSION

BI067773

VERSION

BI067773.1

KEYWORDS

EST

SOURCE

Gallus gallus (chicken)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 662)

AUTHORS

Cogburn, L.A., Morgan, R.W. and Burnside, J.

TITLE

Chicken ESTs from fat

JOURNAL

Unpublished (2001)

COMMENT

Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES

Location/Qualifiers

1..662

/organism="Gallus gallus"

/mol_type="mRNA"

/db_xref="taxon:9031"

/clone="pgfin.pk007.d9"

/sex="Male and Female"

/tissue_type="fat"

/lab_host="E.coli EMDH10B"

/clone_idb="normalized chicken fat cDNA library"

/note="Vector: pSPORT1"

ORIGIN

Alignment Scores:

Pred. No.:	4.89e+03	Length:	662
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BI067773 (1-662)

QY 1 SerleuileThrtTpansnile 7
Db 295 TCTCTACTACTGGAATATT 315

RESULT 79

BS719113

LOCUS

BS719113

DEFINITION

BS719113 678 bp mRNA linear EST 08-MAY-2001
602699045F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4831186 5',
mRNA sequence.

ACCESSION

BS719113

VERSION

BS719113.1

KEYWORDS

EST

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 678)

AUTHORS

NIH-MGC

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabs@remail.nih.gov
Tissue Procurement: Miklos Palkovics, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
CDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM10753 row: 1 column: 11
High quality sequence stop: 672.
Location/Qualifiers

FEATURES

1..678

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4831186"

/lab_host="DH10B"

/clone_idb="NIH_MGC_97"

/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
(GCGAGG); Oligo-dt primed using primer
5'-TTTTTTTTTTTTTVA-3', size-selected for average
insert size 2.2 kb and normalized to R0T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NHGRI/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	5.03e+03	Length:	678
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BS719113 (1-678)

QY

1 SerleuileThrtTpansnile 7

Db

365 TCTCTACTACTGGAATATT 385

RESULT 80

CR767236

LOCUS

CR767236

DEFINITION

CR767236 701 bp mRNA linear EST 23-SEP-2004
DKFZP469E1236 r1 469 (synonym: pkl1) Pongo pygmaeus cDNA clone
DKFZP469E1236 5', mRNA sequence.

ACCESSION

CR767236

VERSION CR767236.1 GI:52609173
 KEYWORDS EST.
 SOURCE Pongo pygmaeus (orangutan)
 ORGANISM Pongo pygmaeus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Pongo.
 REFERENCE 1 (bases 1 to 701)
 AUTHORS Ansoerge, W., Krieger, S., Regiert, T., Rittmuller, C., Schwager, B.,
 Mewes, H.W., Weil, B., Amid, C., Oeanger, A., Fobo, G., Han, M. and
 Wiemann, S.
 TITLE Pongo pygmaeus mRNA (Ansoerge, W., Krieger, S., Regiert, T., et al.)
 JOURNAL Unpublished (2004).
 COMMENT Contact: MIPS
 MIPS
 Ingolstaedter Landstr.1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert. Clone from S. Wiemann,
 Molecular Genome Analysis, German Cancer Research Center (DKFZ);
 Email: s.wiemann@dkfz-heidelberg.de; flin, Germany. Please contact
 RZPD for ordering:
 http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469B1236
 Further information about the clone and the sequencing project is
 available at http://mips.gsf.de/projects/cdna/.
 FEATURES
 source
 location/Qualifiers
 1..701
 /organism="Pongo pygmaeus"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp469B1236"
 /tissue_type="kidney"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_id="469 (synonym: pkidi)"
 /note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiIB"
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.23e+03 Length: 701
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x CR767236 (1-701)
 Oy 1 Serleuilethrrtpaanlle 7
 |||||
 DB 271 TCTCTCATTACTCGAATATT 291
 RESULT 81
 BI334820 704 bp mRNA linear EST 30-JUL-2001
 LOCUS 60298939F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5141193 5',
 DEFINITION mRNA sequence.
 ACCESSION BI334820
 VERSION BI334820.1 GI:15019477
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 704)
 AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rmail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11347 row: n column: 10
 High quality sequence stop: 704.
 FEATURES
 source
 location/Qualifiers
 1..704
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5141193"
 /tissue_type="cervical carcinoma cell line"
 /lab_host="DH10B"
 /clone_id="NIH_MGC_12"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.4 kb. Library prepared by Life
 Technologies."
 ORIGIN
 Alignment Scores:
 Pred. No.: 5.26e+03 Length: 704
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x BI334820 (1-704)
 Oy 1 Serleuilethrrtpaanlle 7
 |||||
 DB 331 TCTCTCATTACTCGAATATT 351
 RESULT 82
 BU661472 710 bp mRNA linear EST 30-SEP-2002
 LOCUS C172d11.21 Hembase, Erythroid Precursor Cells (LCB:c1 library) Homo
 DEFINITION sapiens cDNA clone c172d11 5', mRNA sequence.
 ACCESSION BU661472
 VERSION BU661472.1 GI:23373654
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 710)
 AUTHORS Gubin, A.N., Lee, Y.T., Bouffard, G.G. and Miller, J.L.
 TITLE Gene Expression in Human Erythroid Precursor Cells
 JOURNAL Unpublished (2002)
 COMMENT Contact: Jeffery L. Miller
 Laboratory of Chemical Biology
 National Institute of Diabetes and Digestive and Kidney Diseases
 Building 10, Room 9B17, National Institutes of Health, Bethesda, MD
 20892, USA
 Tel: 301 402 2373
 Fax: 301 435 5148
 Email: jlmf@nih.gov
 The 'c1' library was constructed by Alexander Gubin, Ph.D. in the
 Laboratory of Chemical Biology, NIDDK, NIH. DNA Sequencing and/or
 analyses by National Institutes of Health Intramural Sequencing
 Center (NISC). More information available at:
 http://hembase.nidk.nih.gov
 Plate: 72 row: d column: 11
 Seq primer: 5' lambda-TripLex2 Sequencing Primer.
 FEATURES
 source
 location/Qualifiers
 1..710
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="c172d11"
 /sex="unknown"

ORIGIN

Alignment Scores:

Pred. No.: 5.31e+03 Length: 710
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU61472 (1-710)

QY 1 SerLeu1leThrTPAan1le 7
|||||
DB 259 TCTCTCATTAACCTGGAATATT 279

RESULT 83
CN298923 711 bp mRNA linear EST 16-MAY-2004
LOCUS
DEFINITION
ACCESSION CN298923
VERSION
KEYWORDS
KEYWORDS
EST.
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 711)
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Muraige, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, W.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert length: 711 Std Error: 0.00.
Location/Qualifiers
1..711
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES

source

/tissue_type="blood"
/cell_type="Erythroid Precursor Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Precursor erythroblasts; GPA++"
/lab_host="DH5alpha"
/clone_id="Hembase; Erythroid Precursor Cells (LCB:c1
library)"
/note="Organ: blood; Vector: pTriplex2; Site_1: SfiI;
Site_2: SfiI; A complementary DNA (cDNA) library from
human erythroid precursor cells was constructed using
SMART PCR (polymerase chain reaction) cDNA Library
Construction Kit (Clontech, Palo Alto, CA) according to
the manufacturer's directions, but with slight
modifications. Briefly, reverse transcription was
performed in the presence of 1 umol/L peptide nucleic acid
(PNA) oligos
(N-terminal)-biotin-GTC-CAC-CCG-AAG-CTT-G-(C-terminal) and
(N-terminal)-biotin-CTT/C-T-GAA-GTT-CTC-AGG-A-(C-terminal)
size-selected on a 1% agarose gel (>800bp). Large-scale
sequencing of the library was performed by the NIH
Intramural Sequencing Center (NISC;
Http://www.nisc.nih.gov/)."

/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_id="GRN_PREHERP"
/note="Oligo dt primed, full-length enriched cDNA library
from DMSO-treated hES cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN

Alignment Scores:
Pred. No.: 5.32e+03 Length: 711
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN298923 (1-711)

QY 1 SerLeu1leThrTPAan1le 7
|||||
DB 308 TCTCTCATTAACCTGGAATATT 328

RESULT 84
CN500X2P 720 bp DNA linear GSS 28-JUN-1999
LOCUS
DEFINITION
Arabidopsis thaliana genome survey sequence SP6 end of BAC T13A24
of TMMU library from strain Columbia of Arabidopsis thaliana,
genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
KEYWORDS
GSS.
AL094351.1 GI:5295505
SOURCE
ORGANISM
Arabidopsis thaliana (chale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eustos II; Brassicales; Brassicaceae; Arabidopsid.
1 (bases 1 to 720)
Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
Unpublished
2 (bases 1 to 720)
Genoscope.
Direct Submission
Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
1..720
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_id="T13A24"
/clone_id="TMMU"
/ecotype="Columbia"
/note="end : SP6"

FEATURES

source
1..720
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone_id="T13A24"
/clone_id="TMMU"
/ecotype="Columbia"
/note="end : SP6"

ORIGIN

Alignment Scores:
Pred. No.: 5.4e+03 Length: 720
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN500X2P (1-720)

QY 1 SerLeu1leThrTPAan1le 7
|||||
DB 308 AGTTTATTAACCTGGAACATA 328

RESULT 85
CN298922

LOCUS CN298922 729 bp mRNA linear EST 16-MAY-2004
 DEFINITION 1700060007717 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN298922
 VERSION CN298922.1 GI:47315336
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 729)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebrowski, J. and Stanton, L.W.
 Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 JOURNAL 15146197
 PUBMED
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
 Insert Length: 729 Std Error: 0.00.
 Location/Qualifiers
 1..729
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, DMSO-treated H9 cell line"
 /clone_11b="GRN PREHEP"
 /note="oligo dt primed, full-length enriched cDNA library from DMSO-treated hES cell line H9 (p22) maintained in feeder-free conditions"

ORIGIN
 Alignment Scores:
 Pred. No.: 5.48e+03 Length: 729
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0
 DB: 7

US-10-757-745-2_COPY_115_121 (1-7) x CN298922 (1-729)

QY 1 SerLeuIleHrTpAsnIle 7
 |||||
 Db 335 TCTCTCATTAACCTGGAATATT 355

RESULT 86
 LOCUS CN298924 729 bp mRNA linear EST 16-MAY-2004
 DEFINITION 17000424496911 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
 ACCESSION CN298924
 VERSION CN298924.1 GI:47315338
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 729)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebrowski, J. and Stanton, L.W.
 Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 JOURNAL 15146197
 PUBMED

COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
 Insert Length: 729 Std Error: 0.00.
 Location/Qualifiers
 1..729
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, cell lines H1, H7, and H9"
 /clone_11b="GRN ES"
 /note="oligo dt primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

ORIGIN
 Alignment Scores:
 Pred. No.: 5.48e+03 Length: 729
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 Gaps: 0
 DB: 7

US-10-757-745-2_COPY_115_121 (1-7) x CN298924 (1-729)

QY 1 SerLeuIleHrTpAsnIle 7
 |||||
 Db 277 TCTCTCATTAACCTGGAATATT 297

RESULT 87
 LOCUS CX760857 731 bp mRNA linear EST 24-JAN-2005
 DEFINITION AGENCOURT 40963383 NIH MGC 281 Homo sapiens cDNA clone
 IMAGE:77835600 3', mRNA sequence.
 ACCESSION CX760857
 VERSION CX760857.1 GI:58057513
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 731)
 NIH-MGC http://mgc.ncl.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@bld-1@mail.nih.gov
 Tissue Procurement: Meri Filipo
 cDNA Library Preparation: Express Genomics
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: L14M15944 row: b column: 14
 High quality sequence stop: 574.
 Location/Qualifiers
 1..731
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:77835600"
 /tissue_type="pluripotent cell line derived from

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

blastocyst inner cell mass"
/lab_host="DH10B TONa"
/clone_idb="NIH_MGC_281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site: 1;
EcoRV; Site: 2; NotI; RNA obtained from pluripotent cell
line derived from blastocyst inner cell mass (cell line
HSF-6, NIH Registry designation UC06. Positive for OCT4
expression by RT-PCR, positive for SSEA-3, SSEA-4,
Ttra-1-81, Ttra-1-60 by immunofluorescence. Negative for
SSEA-1 by immunofluorescence Passage 62. cDNA was primed
using oligo-dT primer:
5'-pGACTAGTCTGATCGAGCGCGCCGCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
kb resulted in an average insert size of 2.0 kb. This
primary library is normalized (non-normalized primary
library is NIH_MGC_280) and was constructed by Express
Genomics (Frederick, MD). Note: this is a Mammalian Gene
Collection library."

ORIGIN

Alignment Scores:

Pred. No.: 5.5e+03 Length: 731
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CX760857 (1-731)

QY 1 SerleuileThrTPAnille 7

DB 347 TCTCTATTACCTGGATATAT 367

RESULT 88
LOCUS CR170843/c

DEFINITION Forward strand read from insert in 5'HPT insertion targeting and
chromosome engineering clone MHPN168n24, genomic survey sequence.
ACCESSION CR170843 737 bp DNA linear GSS 06-JUL-2004
VERSION CR170843.1 GI:4949692

KEYWORDS GSS; Genome survey sequence; MICER.

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 5.5e+03 Length: 737
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR170843 (1-737)

QY 1 SerleuileThrTPAnille 7
DB 201 TCTATATATACCTGGATATATC 181

RESULT 89

LOCUS CR791801

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

MIPI

INGOLSTADTER

LANDER

1, D-85764

Neuberberg, Germany

This is the 5' sequence of the clone insert. Clone from S. Wiemann,

Molecular Genome Analysis, German Cancer Research Center (DKFZ),

Heidelberg, Germany. Email: s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix

(Martinsried, Germany) within the cDNA sequencing consortium of the

German Genome Project. This clone (DKFZ468J1522) is available at

the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in

Berlin, Germany. Please contact RZPD for ordering:

http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZ468J1522

Further information about the clone and the sequencing project is

available at http://mips.gsf.de/projects/cdna/.

location/Qualifiers

1. 739

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZ468J1522"

/feature_type="cDS"

/db_xref="taxon:9600"

/clone_idb="DH10B"

ORIGIN
Alignment Scores:
Pred. No.: 5.57e+03 Length: 739
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR791801 (1-739)

QY 1 SerleuileThrTPAnille 7

DB 361 TCTCTATTACCTGGATATAT 381

RESULT 90

LOCUS BF243927

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

Homo sapiens (human)

BF243927 751 bp mRNA linear EST 14-NOV-2000
6018727891 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:410586 5',
mRNA sequence.
BF243927
BF243927.1 GI:1157869
EST.
Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 751)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L16M984 row: k column: 19
High quality sequence stop: 533.
Location/Qualifiers
1..751
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4105866"
/tissue_type="from acute myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 55"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgccgcgcgcgc); Site 2: SfiI
(ggcattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGCCATTTAGCC-3' and
3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.65 kb (range 0.9-4.0 kb). 14/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

Alignment Scores:
Pred. No.: 5.68e+03 Length: 751
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BP243927 (1-751)

Qy 1 SerLeuIeThrTPAsnIle 7
|||||
Db 331 TCTCTCATTACCTGGAATATT 351

RESULT 91
AUI39147 752 bp mRNA linear EST 02-AUG-2002
LOCUS AUI39147 PLACE1 Homo sapiens cDNA clone PLACE1010031 5', mRNA
DEFINITION AUI39147 PLACE1 Homo sapiens cDNA clone PLACE1010031 5', mRNA
sequence.
ACCESSION AUI39147
VERSION AUI39147.1 GI:11000668
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 752)
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saio.K., Kawai.Y.,
Yamamoto.D., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
Isogai.T.

REFERENCE
AUTHORS
Ota.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saio.K., Kawai.Y.,
Yamamoto.D., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and
Isogai.T.

TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
CONTACT Takao Isogai
COMMENT Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1..752
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1010031"
/tissue_type="placenta"
/clone_lib="PLACE1"
/note="Vector: pME18SFL3"

ORIGIN

Alignment Scores:
Pred. No.: 5.69e+03 Length: 752
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AUI39147 (1-752)

Qy 1 SerLeuIeThrTPAsnIle 7
|||||
Db 343 TCTCTCATTACCTGGAATATT 363

RESULT 92
B1760756 757 bp mRNA linear EST 25-SEP-2001
LOCUS B1760756 603044763P1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185334 5',
DEFINITION B1760756 603044763P1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185334 5',
mRNA sequence.
ACCESSION B1760756
VERSION B1760756.1 GI:15752334
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 757)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: L16M1462 row: m column: 15
High quality sequence start: 6
High quality sequence stop: 755.
Location/Qualifiers
1..757
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5185334"

FEATURES
source

/lab host="DH10B"
/clone lib="NIH_MGC_115"
/note="Tissue: Pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 columns, age 26 yo male, 45 yo
female, 71 yo male and 46 yo female kidney, and pool of 2
slightly primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb."
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 5 74e+03 Length: 757
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1760756 (1-757)

QY 1 SerLeuLeThrTyrPheGlu 7

Db 251 TCTCTCATTTACTCGAATATT 271

RESULT 93
LOCUS B1258848 767 bp mRNA linear EST 17-JUL-2001
DEFINITION 60241734.F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:510303 5',
B1258848 sequence.
ACCESSION B1258848.1 GI:14815606
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 767)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@dsr-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: Incyte Genomics, Inc.
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM1268 row: m column: 16
High quality sequence stop: 758.
Location/Qualifiers

FEATURES

source
1..761
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:510303"
/feature_type="cervical carcinoma cell line"
/lab host="DH10B"
/clone lib="NIH_MGC_12"
/note="Tissue: Pooled colon, kidney, stomach; Vector:
PCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.4 kb. Library prepared by Life
Technologies."

ORIGIN

Alignment Scores:

Pred. No.: 5 83e+03 Length: 767
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1258848 (1-767)

QY 1 SerLeuLeThrTyrPheGlu 7

Db 280 TCTCTCATTTACTCGAATATT 300

RESULT 94
LOCUS BG391295 770 bp mRNA linear EST 12-MAR-2001
DEFINITION 60241734.F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:453634 5',
BG391295 mRNA sequence.
ACCESSION BG391295
VERSION BG391295.1 GI:13284743
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo
1 (bases 1 to 770)
REFERENCE NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: rgs@dsr-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM10460 row: h column: 11
High quality sequence stop: 693.
Location/Qualifiers

FEATURES

source
1..770
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:453634"
/feature_type="embryonal carcinoma cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH_MGC_92"
/note="Tissue: testis; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 5 85e+03 Length: 770
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BG391295 (1-770)

QY 1 SerLeuLeThrTyrPheGlu 7

Db 353 TCTCTCATTTACTCGAATATT 373

RESULT 95
B1754101

LOCUS B1754101 774 bp mRNA linear EST 25-SEP-2001
 DEFINITION 603027659F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5197838.5,
 mRNA sequence.
 ACCESSION B1754101
 VERSION B1754101.1 GI:15745679
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 774)
 NIH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing By: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11495 row: f column: 15
 High quality sequence stop: 756.
 Location/Qualifiers
 1..774
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5197838"
 /lab_host="DH10B"
 /clone_1ib="NIH_MGC_114"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
 male brains, age range 23-27 yo. Library is oligo-dT
 primed and directionally cloned (EcoRV site is destroyed
 upon cloning). Average insert size 1.5 kb, insert size
 range 1-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 019. Note:
 this is a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 5.89e+03 Length: 774
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1754101 (1-774)

QY 1 Serleuilethrtprasmile 7
 |||||
 402 TCTTCATTACTCGAATATT 422

RESULT 96
 BX374579 760 bp mRNA linear EST 27-APR-2004
 LOCUS BX374579
 DEFINITION BX374579 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
 cDNA clone CS0DB007YB11 5-PRIME, mRNA sequence.
 ACCESSION BX374579
 VERSION BX374579.2 GI:46618956
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 780)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Poljates, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 8, 2003 this sequence version replaced gi:30452317.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?e=CS0DB007CA06QP1&c=3474.r.
 Location/Qualifiers
 1..780
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DB007YB11"
 /tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
 /clone_1ib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
 Pred. No.: 5.94e+03 Length: 780
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BX374579 (1-780)

QY 1 Serleuilethrtprasmile 7
 |||||
 DB 355 TCTTCATTACTCGAATATT 375

RESULT 97
 BU406549 782 bp mRNA linear EST 27-NOV-2002
 LOCUS BU406549
 DEFINITION 603483616F1 CSEQC59N Gallus gallus cDNA clone CHSRT374p3 5', mRNA
 sequence.
 ACCESSION BU406549
 VERSION BU406549.1 GI:25775605
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianidae; Gallus.
 1 (bases 1 to 782)
 Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 12445392
 Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 Location/Qualifiers
 1..782
 source

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHS1374p3"
/dev_stage="36"
/lab_host="DH10B"
/clone_lib="CSBCHNS9"
/note="Organ: Limbs; Vector: pBluescript II KS(+); Site: 1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Boudado et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 5.96e+03 Length: 782
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 5

US-10-757-745-2_COPY_115_121 (1-7) x BU406549 (1-782)

QY 1 SerLeuLeuThrTyrPheIle 7

Db 345 TCCTGTAACCTGGAAACAT 365

RESULT 98 783 bp mRNA linear EST 08-APR-2004
BX365835
LOCUS BX365835 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens
DEFINITION BX365835 cDNA clone CS0DB007YB11 5-PRIME, mRNA sequence.
ACCESSION BX365835.2 GI:46288859
VERSION BX365835.2
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 783)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30370946.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creteilux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seque@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer, five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/cslDB0022F03QPLKc-3474.r.
Location/Qualifiers

FEATURES
Source
1..783
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

/clone="CS0DB007YB11"
/tissue_type="NEUROBLASTOMA COT 10-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 5.97e+03 Length: 783
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 5

US-10-757-745-2_COPY_115_121 (1-7) x BX365835 (1-783)

QY 1 SerLeuLeuThrTyrPheIle 7

Db 355 TCCTGTAACCTGGAAATATT 375

RESULT 99 786 bp mRNA linear EST 08-MAY-2001
BG719977
LOCUS BG719977 60261335F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4823432 5',
DEFINITION mRNA sequence.
ACCESSION BG719977
VERSION BG719977.1 GI:13999164
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 786)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: CGAPdb-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
DNA Sequencing by: Incyte Genomics, Inc.
DNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM0733 row: F column: 09
High quality sequence stop: 784.
Location/Qualifiers

FEATURES

Source

1..786
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4823432"
/lab_host="DH10B"
/clone_lib="NIH_MGC_97"
/note="Organ: testis; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI
(GTCGAG); Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.2 kb and normalized to R07 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this is
a NIH_MGC library."

ORIGIN

Alignment Scores:

Pred. No.: 6e+03 Length: 786
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BG719977 (1-786)

Qy 1 SerleuilethnTTPAanile 7
 Db 488 TCTCTCATTAAGCTGGAACATT 508

RESULT 100

LOCUS AJ597426 789 bp DNA linear GSS 15-JAN-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 450603, genomic survey sequence.
 ACCESSION AJ597426
 VERSION AJ597426.1 GI:37947054
 KEYWORDS GSS; left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
 AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechold, N., Crnaud, C., Derose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
 PUBMED 12446565
 2 (bases 1 to 789)
 Balzerque, S.
 TITLE Direct Submission
 JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

FEATURES
 source
 1..789
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="450603"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Wassilewskija"
 1..789
 /note="T-DNA flanking sequence left border"

ORIGIN
 Alignment Scores:
 Pred. No.: 6.03e+03 Length: 789
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 10 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AJ597426 (1-789)

Qy 1 SerleuilethnTTPAanile 7
 Db 223 AGTTGATTACTTGGAACATA 243

RESULT 101

LOCUS BG533717 793 bp mRNA linear EST 03-APR-2001
 DEFINITION 602562373P1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4700059 5', mRNA sequence.
 ACCESSION BG533717
 VERSION BG533717.1 GI:13525257
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 793)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONETECH Laboratories, Inc.
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L10CM153 row: a column: 20
 High quality sequence stop: 666.

FEATURES
 source
 1..793
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4700059"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NIH MGC_76"
 /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctatggc); Site 2: SfiI (ggcgctatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGCGCGCGCATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."

ORIGIN
 Alignment Scores:
 Pred. No.: 6.06e+03 Length: 793
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BG533717 (1-793)

Qy 1 SerleuilethnTTPAanile 7
 Db 198 TCTCTCATTAAGCTGGAATATT 218

RESULT 102

LOCUS CX756424 799 bp mRNA linear EST 24-JAN-2005
 DEFINITION AGENCOURT 41337854 NIH_MGC_281 Homo sapiens cDNA clone IMAGE:779791 3', mRNA sequence.
 ACCESSION CX756424
 VERSION CX756424.1 GI:58053080

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

Page 48

[illegible]

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SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
1 (bases 1 to 810)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-remail.nih.gov
Tissue Procurement: BresaGen, Inc.
cDNA Library Preparation: Express Genomics, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Laboratorty for Genomics and Bioinformatics,
University of Georgia
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM15771 row: d column: 17
Seq primer: JENREV (CAGGAACGGTATGAC)
High quality sequence stop: 810.
Location/Qualifiers
1 810
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7469923"
/sex="male"
/issue_type="human embryonic stem cells differentiated to
an early endodermal cell type"
/cell_type="human embryonic stem cells"
/cell_line="BG01"
/lab_host="DH10B-T1 phage-resistant E. coli"
/notes="vector: DEpXpress-1; Site 1: NotI; Site 2: EcoRV;
RNA obtained from human embryonic stem cells isolated from
the inner cell mass of blastocyst stage embryos and
differentiated to an early endodermal cell type. Cell line
4 and NIH Registry. HNP4alpha expression; negative for AFP
expression. Image number 40 cDNA primed using oligo-dT
primer: 5'-GACTGAGTCCTGATCGGACGGCCGCTT)25-3' and
cloned into the EcoRV/NotI sites of DEpXpress-1. This
primary library is 250 normalized (normalized by express
Genomics (Frederick, MD). Sequence ends have been trimmed
to exclude vector and regions below third quality 16.
Three-prime sequences are presented as their reverse
complement and have been trimmed to exclude polyA. Note:
this is a Mammalian Gene Collection library."
ORIGIN
Alignment Scores:
Pred. No.: 6.22e+03 Length: 810
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatch: 0
Query Match: 100.0% Indels: 0
DB: 8 Gaps: 0
US-10-757-745-2.COPY_115_121 (1-7) x CX16635 (1-810)
Qy 1 SerLeuIleThrTyrAsnIle 7
db 300 TCTCTCACTACCTGGAAATATT 320
RESULT 104
BU111103 BU111103 817 bp mRNA linear EST 25-NOV-2002

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DEFINITION 603127011 CSEQCHL13 Gallus gallus cDNA clone CHEST97f3 5', mRNA
sequence.
ACCESSION BU111103
VERSION BU111103.1 GI:25314803
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianine; Gallus.
1 (bases 1 to 817)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1OD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
FEATURES
Source
1..817.
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hixex"
/db_xref="taxon:9031"
/clone="CHEST97f3"
/dev_stage="22"
/lab_host="DH10B"
/clone_1ib="CSEQCHL13"
/note="Organ: limbs; Vector: pluescript II KS(+); Site 1
EcorI; Site 2: NotI; Modification of pluescript II KS(+)"
[Stratagenel vector (construction of uni-directionally
cloned cDNA libraries from messenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pluescript II KS(+) with NotI and EcorI.
Ligate in double stranded adaptor containing BsgI and
BamH sites [5'ggcgcggtgcagcccgatccgaaaaaag]
[5'aattcttttctcgatccgg99ctcgacgc]"
Alignment Scores:
Pred. No.: 6.28e+03 Length: 817
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: Gaps: 5
US-10-757-745-2_COPY_115_121. (1-7) x BU111103 (1-817)
QY 1 SerLeuIleThrTyrAsnIle 7
Db 378 TCCTGTAATTAATTGAAACATT 398
RESULT 105
LOCUS C2953332 818 bp DNA linear GSS 11-AUG-2000
DEFINITION 265164 Tomato ECORI BAC library Lycopersicon esculentum genomic
clone SL_ECOR10056K18 5, genomic survey sequence.
ACCESSION C2953332
VERSION C2953332.1 GI:72298562
KEYWORDS GSS.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

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REFERENCE
AUTHORS      1 (bases 1 to 818)
TITLE        Mueller,L.A., Brels,R.M., Wang,Y., Tanksley,S.D., Giovannoni,J.J.,
JOURNAL      Van Eck,J. and Stack,S.
COMMENT      BAC end sequencing from three Solanum lycopersicon libraries
              Other GSSs: 269931
              Contact: Lukas Mueller
              Tanksley Lab, Dept. of Plant Breeding
              Cornell University
              251 Emerson Hall, Ithaca, NY 14853, USA
              Tel: 607-255-6557
              Fax: 607-255-6683
              Email: sgn-feedback@sgn.cornell.edu
              Plate: 56 row: K column: 18
              Seq primer: T7
              Class: BAC ends
              High quality sequence stop: 579.

FEATURES
Source
Location/Qualifiers
1..818
/organism="Solanum lycopersicon esculentum"
/mol_type="genomic DNA"
/cultivar="Heinz 1706"
/db_xref="taxon:4081"
/clone="SL_ECOR1056K18"
/lab_host="E. coli"
/clone_id="Tomato ECORI BAC Library"
/note="Vector: unk; Site_1: EcorI"

ORIGIN
Alignment Scores:
Pred. No.:      6.29e+03      Length:      818
Score:          38..00        Matches:      7
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches:    0
Query Match:    100.0%        Indels:      0
DB:             10           Gaps:        0

US-10-757-745-2_COPY_115_121 (1-7) x CZ953332 (1-818)
CY      1 SerpuletherrTPanille 7
|||||
|||||
Db      622 AGCTTATTAAGTTGGAACATT 642

RESULT 106
BI908925      838 bp      mRNA      linear      EST 16-OCT-2001
LOCUS        603067028P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5215926 5',
DEFINITION   mRNA sequence.
ACCESSION    BI908925
VERSION      BI908925.1 GI:16172029
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 838)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@dc-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLB)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLB at:
http://image.llnl.gov
Plate: LHAM1542 row: h column: 07
High quality sequence stop: 773.

Location/Qualifiers
1..838

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="IMAGE:5215926"
/tissue_type="leukocyte"
/lab_host="DH10B"
/clone_id="NIH_MGC_118"
/note="Vector: PCMV-SPOK6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (ScoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research genetics tracking code 027. Note: this is a NIH_MGC library."

ORIGIN

Alignment Scores:
Pred. No.: 6.48e+03 Length: 838
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1908925 (1-838)

QY 1 SerLeu1eHrTTPaani1e 7
|||||
Db 344 TCTCTCATTCCTGGAATATT 364

RESULT 107
CR765451 846 bp mRNA linear EST 23-SEP-2004
LOCUS DKFP469E2434.r1.469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DEFINITION DKFP469E2434 5', mRNA sequence.
ACCESSION CR765451
VERSION CR765451
KEYWORDS CR765451.1 GI:52605526
SOURCE EST.
ORGANISM Pongo pygmaeus (orangutan)
Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pongo.
1 (bases 1 to 846)
Ostenwaelder, B.; Obermaier, B.; Deutschenbaur, S.; Schaipp, A.;
Mewes, H.W.; Well, B.; Amlid, C.; Oesinger, A.; Fobo, G.; Han, M. and
Wiemann, S.

REFERENCE

AUTHORS

TITLE Pongo pygmaeus mRNA (Ostenwaelder, B., Obermaier, B.,
Deutschenbaur, S., et al.)
JOURNAL Unpublished (2004)
COMMENT Contact: MIPS

FEATURES
source
MIPS
Ingolstaedter Landstr.1, D-85764 Neuburg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email: s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the cDNA sequencing consortium of the
German Genome Project. This clone (DKFP469E2434) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFP469E2434
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/project/cdna/.
Location/Qualifiers
1..846
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone_id="DKFP469E2434"
/tissue_type="kidney"
/dev_stage="adult"

/lab_host="DH10B"
/clone_id="469 (synonym: pkid1)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:
Pred. No.: 6.55e+03 Length: 846
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR765451 (1-846)

QY 1 SerLeu1eHrTTPaani1e 7
|||||
Db 246 TCTCTCATTCCTGGAATATT 266

RESULT 108
BE784416 853 bp mRNA linear EST 20-OCT-2000
LOCUS BE784416 601473891F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876862 5',
DEFINITION mRNA sequence.
ACCESSION BE784416
VERSION BE784416.1 GI:10205614
KEYWORDS EST.
SOURCE Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 853)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: ILAMB638 row: e column: 23
High quality sequence stop: 660.
Location/Qualifiers
1..853
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="IMAGE:3876862"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_68"
/note="Organ: Lung; Vector: PCMV-SPOK6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

REFERENCE

AUTHORS

TITLE NIH-MGC
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: ILAMB638 row: e column: 23
High quality sequence stop: 660.
Location/Qualifiers

FEATURES

source

1..853
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="IMAGE:3876862"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_68"
/note="Organ: Lung; Vector: PCMV-SPOK6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 6.61e+03 Length: 853
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BE784416 (1-853)

QY 1 SerLeu1eHrTTPaani1e 7

Db 347 TCTTCATTAACCTGGAAATTT 367

RESULT 109
BI553412 858 bp mRNA linear EST 05-SEP-2001
LOCUS 603193558P1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5264582 5',
DEFINITION mRNA sequence.
ACCESSION BI553412
VERSION BI553412.1 GI:15440724
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 858)
AUTHORS NIH-MGC Consortium of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: Miklos Palcovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1667 row: C column: 15
High quality sequence stop: 829.
Location/Qualifiers
1. 858
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5264582"
/issue_type="hippocampus"
/lab_host="DH10B"
/clone.lib="NIH_MGC_95"
/note="Organ: Brain; Vector: pBluescript (modified
pBluescript KS+); Site 1: BamHI, Site 2: SalI-XhoI
(gtcgag); Oligo-dT primed using primer
5'-TTTTTTTCTTTT-3', size-selected for average
insert size 2.5 kb and normalized to RGT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	6.66e+03	Length:	858
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BI553412 (1-858)

OY 1 SerLeuIleThrTyrPasnIle 7
|||||
Db 363 TCTTCATTAACCTGGAAATTT 383

RESULT 110
BG740396 870 bp mRNA linear EST 15-MAY-2001
LOCUS 602634171P1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4779449 5',
DEFINITION mRNA sequence.
ACCESSION BG740396

VERSION BG740396.1 GI:14051049
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 870)
AUTHORS NIH-MGC Consortium of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10636 row: m column: 18
High quality sequence stop: 826.
Location/Qualifiers
1. 870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4779449"
/lab_host="DH10B (T1 phage-resistant)"
/clone.lib="NCI_CGAP_Skn3"
/note="Organ: SKIN; Vector: pCMV-SPORT6; Site 1: NCI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

ORIGIN

Alignment Scores:

Pred. No.:	6.77e+03	Length:	870
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG740396 (1-870)

OY 1 SerLeuIleThrTyrPasnIle 7
|||||
Db 254 TCTTCATTAACCTGGAAATTT 274

RESULT 111
BU159911 870 bp mRNA linear EST 04-SEP-2002
LOCUS 60159911T1 AGENCOURT_7933863 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6144208
DEFINITION 5', mRNA sequence.
ACCESSION BU159911
VERSION BU159911.1 GI:22673821
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homniidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 870)
AUTHORS NIH-MGC Consortium of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LHAM13468 row: n column: 17
High quality sequence stop: 677.
Location/Qualifiers

FEATURES

source

1.870
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6144208"
/issue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Library constructed by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	6.77e+03	Length:	870
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU159911 (1-870)

Qy 1 SerLeu1eThrTPaen1le 7

Db 278 TCTCATTAACCTGGAATATT 298

RESULT 112

LOCUS

BU169945 883 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7913097 NIH_MGC_68 Homo sapiens CDNA clone IMAGE:6024760

DEFINITION

5', mRNA sequence.

ACCESSION

BU169945

VERSION

BU169945.1 GI:22683929

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 883)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LHAM13235 row: m column: 17
High quality sequence stop: 413.
Location/Qualifiers

FEATURES

source

1.883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6024760"
/issue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_68"
/note="Organ: lung; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.8 kb. Library constructed by Life Technologies."

ORIGIN

Alignment Scores:

Pred. No.:	6.89e+03	Length:	883
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU169945 (1-883)

Qy

1 SerLeu1eThrTPaen1le 7

Db 223 TCTCATTAACCTGGAATATT 243

RESULT 113

LOCUS

BU179107 883 bp mRNA linear EST 04-SEP-2002
AGENCOURT 7984768 NIH_MGC_71 Homo sapiens CDNA clone IMAGE:6174938

DEFINITION

5', mRNA sequence.

ACCESSION

BU179107

VERSION

BU179107.1 GI:22693091

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 883)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LHAM13548 row: 0 column: 23
High quality sequence stop: 672.
Location/Qualifiers

FEATURES

source

1.883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6174938"
/issue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."

ORIGIN

Alignment Scores:

Pred. No.:	6.89e+03	Length:	883
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BU179107 (1-883)

Qy

1 SerLeu1eThrTPaen1le 7

Db 201 TCTCATTAACCTGGAATATT 221

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RESULT 114
BG537046      889 bp    mRNA     linear   EST 03-APR-2001
DEFINITION    BG537046 Homo sapiens cDNA clone IMAGE:4689919 5' ,
              mRNA sequence.
ACCESSION     BG537046
VERSION       BG537046.1 GI:13528594
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homidae; Homo.
REFERENCE     1 (bases 1 to 889)
AUTHORS      NIH-MGC http://mgi.mcl.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
               Email: cgabbs-r@mail.nih.gov
               Tissue Procurement: CLONTECH Laboratories, Inc.
               cDNA Library Preparation: CLONTECH Laboratories, Inc.
               cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNLN)
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LNLN at:
               http://image.llnl.gov
               Plate: LNCMI506 row: k column: 08
               High quality sequence stop: 525.
FEATURES
Source
Location/Qualifiers
1..889
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="4689919"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccctgcgsc); Site 2: SfiI (ggcattatgccg); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCATTTGACC-3' and 3' adaptor sequence
5'-ATTCTAGAGGGCCGAGCGCGCAGCAATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb), 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:          6,95e+03      Length:      889
Score:             38.00         Matches:      7
Percent Similarity: 100.0%        Conservative: 0
Best Local Similarity: 100.0%     Mismatches:  0
Query Match:       100.0%         Indels:      0
DB:                2            Gaps:        0

US-10-757-745-2_COPY_115_121 (1-7) x BG537046 (1-889)

Cy      1 SerLeuIIeThTPAaIIIle 7
Db      358 TCCTCATTAACCTGGAAATATT 378

RESULT 115
CR212336/c
LOCUS        CR212336
DEFINITION   Forward strand read from insert in 5'Hprt insertion targeting and
              chromosome engineering clone WHPN238m07, genomic survey sequence.
ACCESSION    CR212336
VERSION      CR212336.1 GI:49991185
KEYWORDS     GSS; genome survey sequence; MICER.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus

```

```

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
SOURCE
ORIGIN
Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
Dn:
US-10-757-745-2_COPY_115_121 (1-7) x CR212336 (1-889)
Cy 1 Serleu1ethrTTpaa11le 7
Db 176 TCATTATTAACCTGGAATATC 156
RESULT 116
Bg623866
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Homo sapiens (human)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 898)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov
Plate: L1CM1637 row: d column: 06
High quality sequence stop: 688.
Location/Qualifiers
1..898
/organism="Homo sapiens"
/mol_type="RNA"
/db_xref="taxon:9606"
/clone="IMAGE:4770389"
/lab_host="DH10B (T1 phage-resistant)"
/clone_1ib="NIH MGC 79"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgctcgggc); Site_2: SfiI
(ggcattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5'-CACGGCCATTATGGCC-3'

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Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

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ORIGIN

and 3' adaptor sequence:
5'-ATTCTAGGCGCCAGCGCCGACAGG-dT (30) EN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC library."

Alignment Scores:

Pred. No.:	7.03e+03	Length:	898
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG623866 (1-898)

OY 1 Serleu1eThrTTPanille 7

Db 530 TCTCTCATCTACCTGGAAATAT 550

RESULT 117

BK422491 904 bp mRNA linear EST 03-MAY-2004
LOCUS BK422491 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM007YE11 5-PRIME, mRNA sequence.
ACCESSION BK422491
VERSION BK422491.2 GI:46955237
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 904)
Li W.B., Gruber C., Jessee J. and Polayes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced GI:3076188.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0DM007AC06Q1&c=3474.r.

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES source

1..904
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DM007YE11"
/tissue_type="FETAL LIVER"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7.03e+03
Score: 38.00
Percent Similarity: 100.0%

Length: 904
Matches: 7
Conservative: 0

Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 5
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BK422491 (1-904)

OY 1 Serleu1eThrTTPanille 7

Db 384 TCTCTCATCTACCTGGAAATAT 404

RESULT 119

CD251503 906 bp mRNA linear EST 22-MAY-2003
LOCUS CD251503
DEFINITION AGENCOURT_14212105 NIH_MGC_179 Homo sapiens cDNA clone
IMAGE:30385385 5', mRNA sequence.
ACCESSION CD251503
VERSION CD251503.1 GI:31011969
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 906)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: NDAM452 row: f column: 18
High quality sequence stop: 588.
Location/Qualifiers
1..906
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30385385"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A" T1 and T5 phage resistance"
/clone_lib="NIH_MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site: 1; EcoRV
(destroyed); Site: 2; NotI; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

Alignment Scores:
Pred. No.: 7.11e+03
Score: 38.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 100.0%
DB: 6
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CD251503 (1-906)

OY 1 Serleu1eThrTTPanille 7

Db 384 TCTCTCATCTACCTGGAAATAT 404

RESULT 119

LOCUS BG391213 908 bp mRNA linear EST 12-MAR-2001
DEFINITION 602417244F1 NIH_MGC_92 Homo sapiens CDNA clone IMAGE:453635 5',
RNA sequence.
ACCESSION BG391213
VERSION BG391213.1 GI:13284661
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 908)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10460 row: h column: 12
High quality sequence stop: 732.
Location/Qualifiers
1..908
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:453635"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

Alignment Scores:
Pred. No.: 7.13e+03 Length: 908
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BG391213 (1-908)

QY 1 SerleuilethrtTPAsnile 7
|||||
Db 346 TCTCTCATTAAGCTGGAATATT 366

RESULT 120
BI915865 915 bp mRNA linear EST 16-OCT-2001
LOCUS BI915865
DEFINITION 603184522F1 NIH_MGC_121 Homo sapiens CDNA clone IMAGE:5248495 5',
RNA sequence.
ACCESSION BI915865
VERSION BI915865.1 GI:16179808
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 915)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10215 row: a column: 24

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM11627 row: e column: 08
High quality sequence stop: 696.
Location/Qualifiers
1..915
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5248495"
/lab_host="DH10B"
/clone_1ib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

Alignment Scores:
Pred. No.: 7.19e+03 Length: 915
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BI915865 (1-915)

QY 1 SerleuilethrtTPAsnile 7
|||||
Db 350 TCTCTCATTAAGCTGGAATATT 370

RESULT 121
BI119064 927 bp mRNA linear EST 30-JAN-2001
LOCUS BI119064
DEFINITION 602347589F1 NIH_MGC_90 Homo sapiens CDNA clone IMAGE:4442399 5',
RNA sequence.
ACCESSION BI119064
VERSION BI119064.1 GI:12612570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 927)
REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10215 row: a column: 24

High quality sequence stop: 676.
Location/Qualifiers

FEATURES

source

1..927
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="A42399"
/clone_type="deletion-resistant"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally, oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	7.3e+03	Length:	927
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG119064 (1-927)

QY 1 SerleuileThrtPpanile 7
DB 175 TCTCTATTACCTGGATATTT 195

RESULT 122

BC740339

LOCUS BC740339 932 bp mRNA linear EST 15-MAY-2001
DEFINITION 602569712F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4780318 5',
RNA sequence.

ACCESSION

BC740339

VERSION BC740339.1 GI:14050992

KEYWORDS

EST

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 932)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: James G. Leaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA
Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clones distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LNCM1639 row: a column: 23
High quality sequence stop: 759.
Location/Qualifiers

1..932
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="4780318"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; NotI; Site 2: SalI; Cloned unidirectionally, primer: oligo-dT. Average insert size 1.5 kb. Library constructed by Life Technologies. Note: this is a NIH-MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	7.35e+03	Length:	932
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG740339 (1-932)

QY 1 SerleuileThrtPpanile 7
DB 174 TCTCTATTACCTGGATATTT 194

RESULT 123

BC541819

LOCUS BC541819 937 bp mRNA linear EST 03-APR-2001
DEFINITION 602569712F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4694066 5',
mRNA sequence.

ACCESSION

BC541819

VERSION BC541819.1 GI:13534052

KEYWORDS

EST

SOURCE

ORGANISM

Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 937)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: CLOWBCH Laboratories, Inc.
CDNA Library Preparation: CLOWBCH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LNCM1517 row: h column: 03
High quality sequence stop: 714.
Location/Qualifiers

1..937
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="4694066"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH MGC 77"
/note="Organ: lung; Vector: pBMR-LIB (Clontech); Site: 1; Site 2: SalI (ggccatcgcc); Site 3: SfiI (ggccatcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGCGC-3' and 3' adaptor sequence: 5'-ATTCTGAGCGCGACGCCGATGAC-3' (where B = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.:	7.4e+03	Length:	937
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BG541819 (1-937)

QY 1 SerleuileThrtPpanile 7

DB 359 TCTCTCATTAAGCTGGAAATATT 379

RESULT 124
BX358707 942 bp mRNA linear EST 08-APR-2004
LOCUS BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION BX358707 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
ACCESSION BX358707
KEYWORDS BX358707.2 GI:46306560
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
1 (bases 1 to 942)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30378261.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequef@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3474.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdnas=CSD01042CPI00P1ec=3474.r.

FEATURES
source
1..942
Location/Qualifiers

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSD01042YL19"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_1lb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7.44e+03 Length: 942
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BX358707 (1-942)

QY 1 SerLeuIIeThTPaenIIe 7

DB 212 TCTCTCATTAAGCTGGAAATATT 232

RESULT 125
BU468774 946 bp mRNA linear EST 30-NOV-2002
LOCUS BU468774
DEFINITION 603371865F1 CSEQRBN20 Gallus gallus cDNA clone CHEST279b17 5', mRNA
sequence.
ACCESSION BU468774
KEYWORDS BU468774.1 GI:25962351
SOURCE EST.
ORGANISM Gallus gallus (chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE
1 (bases 1 to 946)
AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..946
Location/Qualifiers

/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="CHEST279b17"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
cartilage"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSEQRBN20"
/note="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunt-ended, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldi et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

ORIGIN

Alignment Scores:
Pred. No.: 7.48e+03 Length: 946
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU468774 (1-946)

QY 1 SerLeuIIeThTPaenIIe 7

DB 234 TCGCTGATTAAGCTGGAAATATT 254

RESULT 126
CR113807 946 bp DNA linear GSS 05-JUL-2004
LOCUS CR113807
DEFINITION Forward strand read from insert in 5'HPT insertion targeting and
chromosome engineering clone WHPN215K05, genomic survey sequence.
ACCESSION CR113807
KEYWORDS CR113807.1 GI:49861238
MUS musculus (house mouse)
SOURCE GSS; genome survey sequence; MICR.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 946)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

Page 58

Jongers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK <http://www.sanger.ac.uk/MICRR>
FEATURES
SOURCE
1
946
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone_11b="MHPN215X05"
/clone_11b="MHPN"

ORIGIN

Alignment Scores:
Pred. No.: 7.48e+03 Length: 946
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 11 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CR113807 (1-946)

OY 1 SerLeuileThrTPaenile 7
|||||
200 TCATTATACCTGGATATTC 180

RESULT 127 948 bp mRNA linear EST 30-MAR-2004
LOCUS AL555333 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK007YK05 5-PRIME, mRNA sequence.
ACCESSION AL555333
VERSION AL555333.3 GI:45860070
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 948)
La, W.B., Gruber, C., Jessup, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31277141.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of invitrogen. This sequence belongs to sequence cluster
3474.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DK007Afp03Qp1lc=3474.r>.

FEATURES
SOURCE
1
948
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK05"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_11b="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7.5e+03 Length: 948
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 1 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x AL555333 (1-948)

OY 1 SerLeuileThrTPaenile 7
|||||
362 TCCTCATYACCTGGATATTT 382

RESULT 128 952 bp mRNA linear EST 04-MAY-2004
LOCUS BX433489/c Homo sapiens ADULT BRAIN Homo sapiens CDNA clone
DEFINITION CS0DN005YN02 3-PRIME, mRNA sequence.
ACCESSION BX433489
VERSION BX433489.2 GI:47002503
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 952)
La, W.B., Gruber, C., Jessup, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30775195.
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by life technologies, a
division of invitrogen.
This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0BA1056ZD12_CS05372_1lc=3474.r.

FEATURES
SOURCE
1
952
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN005YN02"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_11b="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7.54e+03 Length: 952
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BX433489 (1-952)

OY 1 SerLeuileThrTPaenile 7
|||||

DB 801 TCTCTCATTCCTGGAAATATT 781

RESULT 129

LOCUS B1161201 959 bp mRNA linear EST 05-JUL-2001

DEFINITION 602865659F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:5019639 5',

ACCESSION B1161201

VERSION B1161201.1 GI:14621202

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L16M1835 row: e column: 16
High quality sequence scop: 551.

FEATURES

source

1..959

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5019639"

/tissue_type="epitheloid carcinoma cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library." |"

ORIGIN

Alignment Scores:

Pred. No.: 7.61e+03 Length: 959

Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B1161201 (1-959)

Qy 1 SerLeuileThrTyrPasnile 7

Db 361 TCTCTCATTCCTGGAAATATT 381

RESULT 130

LOCUS BM468826 972 bp mRNA linear EST 05-FEB-2002

DEFINITION AGENCOURT 6445782 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587154

ACCESSION BM468826

VERSION BM468826.1 GI:18517868

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L16M12356 row: d column: 03
High quality sequence scop: 707.

FEATURES

source

1..972

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5587154"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: testis; Vector: pCMV-Sport6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." |"

ORIGIN

Alignment Scores:

Pred. No.: 7.73e+03 Length: 972

Score: 38.00 Matches: 7

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BM468826 (1-972)

Qy 1 SerLeuileThrTyrPasnile 7

Db 238 TCTCTCATTCCTGGAAATATT 258

RESULT 131

LOCUS BX338160 981 bp mRNA linear EST 08-APR-2004

DEFINITION BX338160 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS001056YC3 5-PRIME, mRNA sequence.

ACCESSION BX338160

VERSION BX338160.2 GI:46283046

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

JOURNAL Full-length cDNA libraries and normalization Unpublished (2001)

COMMENT On May 2, 2003 this sequence version replaced gi:30345671.
Genoscope - Centre National de Sequencage
2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r

FEATURES

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSODI056AB12QPI&c=3474.r.

Location/Qualifiers

1..981
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI056YC23"

/issue_type="PLACENTA COT 25-NORMALIZED"

/clone_1ib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:

Pred. No.: 7.81e+03 Length: 981
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BX338160 (1-981)

OY 1 Serleuilethrtipansille 7

DB 356 TCTCTGATTAAGTGAATATT 376

RESULT 132

CC216952

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..992

/organism="Homo sapiens"

/mol_type="genomic DNA"

/strain="Red Jungle Fowl"

/db_xref="taxon:9031"

/clone="CH261-110N21"

/sex="Female"

ordering information: http://www.chori.org/bacpac"

ORIGIN

Alignment Scores:

Pred. No.: 7.92e+03 Length: 992
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 9 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CC216952 (1-992)

OY 1 Serleuilethrtipansille 7

DB 423 TCTCTGATTAAGTGAATATT 443

RESULT 133

BE892886

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..995

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3920790"

/issue_type="melanotic melanoma"

/lab_host="DHI0B (phage-resistant)"

/clone_1ib="NIH MGC_72"

/note="Organ: skin; Vector: pCMV-SPORT6, site 1: NotI, site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."

US-10-757-745-2_COPY_115_121 (1-7) x BE892886 (1-995)

OY 1 Serleuilethrtipansille 7

DB 372 TCTCTGATTAAGTGAATATT 392

RESULT 134
 BX337141
 LOCUS 1018 bp mRNA linear EST 07-APR-2004
 DEFINITION BX337141 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0D1036YJ02 5-PRIME, mRNA sequence.
 ACCESSION BX337141
 VERSION BX337141.2 GI:46271144
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1018)
 L1.W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 2, 2003 this sequence version replaced gi:30337585.
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and cloned into the NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3474.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?cs=CS0D1036DB01QPlc=3474.r.
 FEATURES
 source
 1..1018
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1036YJ02"
 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with NotI and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.17e+03 Length: 1018
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x BX337141 (1-1018)
 QY 1 SerLeulleThrTPAsnIle 7
 Db 333 TCTCTCATTAACCTGGAATATT 353
 RESULT 135
 BU235217
 LOCUS 1030 bp mRNA linear EST 26-NOV-2002
 DEFINITION 603791177F1 GSEQCHN24 Gallus gallus cDNA clone CHEST754J19 5', mRNA sequence.
 ACCESSION BU235217
 VERSION BU235217.1 GI:25480405
 KEYWORDS EST.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 1 (bases 1 to 1030)
 REFERENCE

AUTHORS
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 PUBMED 12445392
 COMMENT Contact: Simon Hubbard
 Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology (UMIST)
 PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.
 FEATURES
 source
 1..1030
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
 /clone="CHEST754J19"
 /dev_stage="22"
 /lab_host="DH10B"
 /clone_lib="GSEQCHN24"
 /note="Organ: heads; Vector: pluescript II KS(+); Site_1: EcoRI; Site_2: NotI. This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.28e+03 Length: 1030
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: Gaps: 0
 US-10-757-745-2_COPY_115_121 (1-7) x BU235217 (1-1030)
 QY 1 SerLeulleThrTPAsnIle 7
 Db 13 TCGCTGATTAACCTGGAACATT 33
 RESULT 136
 BM554324
 LOCUS 1035 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6546794 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742466 5', mRNA sequence.
 ACCESSION BM554324
 VERSION BM554324.1 GI:18793827
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 1035)
 NIH-MGC http://mgi.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@biml.nih.gov
 Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
Plate: LLM12760 row: K column: 11
High quality sequence stop: 738.
Location/Qualifiers

FEATURES

1..1035
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5742466"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"

/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3 kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	8.33e+03	Length:	1035
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BM554324 (1-1035)

QY 1 SerLeuLeTtTTPaenile 7

Db 515 TCTCTCATTAAGTGAATATT 535

RESULT 137

BM926092

LOCUS

DEFINITION

AGENCOURT 6649780 NIH_MGC_114 Homo sapiens CDNA clone IMAGE:5764440

BM926092

VERSION

KEYWORDS

SOURCE

ORGANISM

EST

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 1046)

NIH-MGC <http://mgs.nci.nih.gov/>.

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: csapbs@emall.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

<http://image.jnl.gov>

Plate: LLM12817 row: 0 column: 01

High quality sequence stop: 632.

Location/Qualifiers

1..1046

source

ORIGIN

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5764440"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 013. Note:
this is a NIH_MGC Library."

Pred. No.:	8.43e+03	Length:	1046
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BM926092 (1-1046)

QY 1 SerLeuLeTtTTPaenile 7

Db 216 TCTCTCATTAAGTGAATATT 236

RESULT 138

EX337905

LOCUS

DEFINITION

EX337905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA

clone CS0D1052YN13 5-PRIME, mRNA sequence.

EX337905

VERSION

KEYWORDS

SOURCE

ORGANISM

EST

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

1 (bases 1 to 1067)

L.I.W.B., Gruber, C., Jessee, J., and Polyes, D.

Full-length CDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30339657.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE

Email: sequenc@genoscope.cns.fr, web: www.genoscope.cns.fr

1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand CDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of invitrogen. This sequence belongs to sequence cluster

3474.r

For more information about this cluster, see

<http://www.genoscope.cns.fr/cdna/CS0D1052C00/Plac2474.r>.

Location/Qualifiers

1..1067

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0D1052YN13"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand CDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand CDNA was

digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

Location/Qualifiers

1..1067

source

ORIGIN

Alignment Scores:

Pred. No.:	8.64e+03	Length:	1067
Score:	38.00	Matches:	7
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BX337905 (1-1067)

Qy 1 SerLeuileThrTrpAsnIle 7
 |||||
Db 367 TCTCTCATTTACCTGGAAATATT 387

RESULT 139
PIT1 11073

LOCUS	1077 bp	mRNA	linear	EST 25-NOV-2002
DEFINITION	603116142F1	Gallus gallus	CDNA clone	ChEST70d12 5', mRNA
ACCESSION	U131072			
SEQUENCE				

ACCESSION	BU131072
VERSION	BU131072.1
KEYWORDS	GI:25343002
SOURCE	EST.
COLLECTOR	Cellular collector (shibata)

ORGANISM

REFERENCE
1 (pages 1 to 1077)
Phasianinae; Gallus.
Archosauiria; Aves; Neognathae; Galliformes; Phasianidae;
Eumalyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.

AUTHORS

TITLE
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken Eggs

JOURNAL
PLIMMETS

COMMENT

Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(MRC)

Tel: 0161206930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk

nos

Source

ORIGIN

Alignment Scores:

Pred. No.:	8.73e+03	Length:	1077
Score:	36.00	Matches:	7
Percent Similarity:	100.00	Conservative:	0
Best Local Similarity:	100.00	Mismatches:	0
Query Match:	100.00	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) X BU131072 (1-1077)

```

Oy      1 SerLeuileThrTyrpsnile 7
          |||||
Db      358 TCGCTGATTAAGTGAACATT 378

```

RESULT 140
BX444691

LOCUS	1081 bp	mRNA	linear	EST 0
DEFINITION	BX444691 Homo sapiens ADULT BRAIN Homo sapiens CDNA clone			
DEFINITION	CS0DN005YN02 5-PRIME, mRNA sequence.			
ACCESSION	BX444691			

KEYWORDS
VERSION
BX444691.2
FST
GI:47009162

SOURCE ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
1 (bases 1 to 1081)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Hominidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

Contact: Genoscope

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 3474.r
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?S=CS0DN005DG01QPlc=3474.r>

Source

Source

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN005YN02"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_1ib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

```

ORIGIN

Alignment Scores:

Pred. No.:	8.77e+03
Score:	38.00
Percent Similarity:	100.0%
Best Local Similarity:	100.0%
Query Match:	100.0%
DB:	5
	Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) X BX444691 (1-1081)

QY 1 SerLeu11eThrTrypasn1le 7

Db 369 TCTCTATTACCTGAATAT 389

RESULT 141

LOCUS	DQ049205	1089 bp	DNA	linear	GSS 02-JUN-2005
DEFINITION	Homo sapiens TTRAP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	DQ049205				

VERSION DQ049205.1 GI:66902404
KEYWORDS GSS, sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo

REFERENCE
AUTHORS Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.
1 (bases 1 to 1089)
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES
source
1..1089
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
/gene="TTRAP"
/locus_tag="HC17203"

ORIGIN
1
SerLeuIleTnTPaAnIle 7
|||||
343 TCTCTATTACCTGGATATT 363

Alignment Scores:
Pred. No.: 8.85e+03 Length: 1089
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x DQ049205 (1-1089)

QY 1 SerLeuIleTnTPaAnIle 7
|||||
343 TCTCTATTACCTGGATATT 363

RESULT 142
DQ049206 1089 bp DNA linear GSS 02-JUN-2005
LOCUS Pan troglodytes TTRAP gene, VIRUTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION DQ049206
VERSION DQ049206.1 GI:66902405
KEYWORDS GSS,
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Pan.
1 (bases 1 to 1089)
REFERENCE
AUTHORS Hubisz, M.J., Bustamante, C., Clark, A.G., Gnanowski, S., Sackton, T.B.,
Nielsen, R., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)

JOURNAL
PUBMED 15869325
REFERENCE 2 (bases 1 to 1089)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Gnanowski, S., Sackton, T.B.,

Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Civejlo, D.,
White, T.J., Sniinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.

FEATURES
source
1..1089
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/gene="TTRAP"
/locus_tag="HC17203"

ORIGIN
1
SerLeuIleTnTPaAnIle 7
|||||
343 TCTCTATTACCTGGATATT 363

Alignment Scores:
Pred. No.: 8.85e+03 Length: 1089
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x DQ049206 (1-1089)

QY 1 SerLeuIleTnTPaAnIle 7
|||||
343 TCTCTATTACCTGGATATT 363

RESULT 143
BM555041 1103 bp mRNA linear EST 20-FEB-2002
LOCUS AGENCOURT 6545705 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5737150
5', mRNA sequence.
ACCESSION BM555041
VERSION BM555041.1 GI:18795166
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 1103)
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: LLM12746 row: m column: 23
High quality sequence stop: 678.

FEATURES
source
1..1103
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5737150"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC_88"
/note="Organ: small intestine; Vector: PCMV-SPORE6;
site 1: NotI; site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life

ORIGIN Technologies. Note: this is a NIH_MGC Library."

Alignment Scores:

Pred. No.: 8.99e+03 Length: 1103
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BM555041 (1-1103)

Qy 1 SerLeu1eThrTPAsn1le 7

Db 372 TCTCTCATTAACCTGGAATATT 392

RESULT 144

CR601303 1168 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DN005YN02 of Adult brain of Homo sapiens (human).

ACCESSION CR601303 GI:50482110

VERSION HTC; CNSLT_CDNA.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 1168)

AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue

2 (bases 1 to 1168)

REFERENCE Genoscope.

AUTHORS Direct Submision

TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)

JOURNAL - Web: www.genoscope.cns.fr

REMARK 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES Location/Qualifiers

1..1168

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DN005YN02"

/tissue_type="Adult brain"

/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 9.62e+03 Length: 1168
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR601303 (1-1168)

Qy 1 SerLeu1eThrTPAsn1le 7

Db 368 TCTCTCATTAACCTGGAATATT 388

RESULT 145

BM553049

LOCUS BM553049 1192 bp mRNA linear EST 20-FEB-2002

DEFINITION AGENCOURT 6542413 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742798

ACCESSION BM553049

VERSION BM553049.1 GI:18791437

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo

REFERENCE 1 (bases 1 to 1192)

AUTHORS NIH-MGC http://mgs.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cga@b-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM12761 row: 1 column: 07

High quality sequence stop: 747.

Location/Qualifiers

1..1192

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5742798"

/tissue_type="medulla"

/lab_host="DH10B"

/clone_1ib="NIH_MGC_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 9.86e+03 Length: 1192
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BM553049 (1-1192)

Qy 1 SerLeu1eThrTPAsn1le 7

Db 400 TCTCTCATTAACCTGGAATATT 420

RESULT 146

CR592636 1620 bp mRNA linear HTC 21-JUL-2004

DEFINITION full-length cDNA clone CS0DM007YB1 of Fetal liver of Homo sapiens (human).

ACCESSION CR592636

VERSION CR592636.1 GI:50473443

KEYWORDS HTC; CNSLT_CDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 Homidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@life.techno.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1620)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODM007YE11"
/tissue_type="Fetal liver"
/plasmid="PCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.42e+04 Length: 1620
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CR592636 (1-1620)
QY 1 SerLeuIleThrTPAsnIle 7
Db 286 TCTCTCATTAACCTGGAATATT 306
RESULT 147
CR602029 1743 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1042YL19 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR602029.1 GI:50482836
VERSION HTC; CNGSLT cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1743)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@life.techno.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1743)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.
FEATURES
source
1. 1743
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1042YL19"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="PCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.55e+04 Length: 1743
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CR602029 (1-1743)
QY 1 SerLeuIleThrTPAsnIle 7
Db 212 TCTCTCATTAACCTGGAATATT 232
RESULT 148
CR597293 1894 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODK007YK05 of HeLa cells Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR597293
VERSION CR597293.1 GI:50478100
KEYWORDS HTC; CNGSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1894)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Peng Liang Email : fliang@life.techno.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 1894)
REFERENCE 2 Genoscope.
AUTHORS Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1. 1894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK007YK05"
/tissue_type="HeLa cells Cot 25-normalized"
/plasmid="PCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 1.71e+04 Length: 1894
Score: 38.00 Matches: 7
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CRS97293 (1-1894)

QY 1 SerLeuileThrTyrPasnile 7
 DB 361 TCTTCATTAACCTGGAAATATT 381

RESULT 149
 CRS95644 1909 bp mRNA linear HTC 21-JUL-2004
 full-length cDNA clone CS0D1052YN13 of Placenta Cot 25-normalized
 of Homo sapiens (human)

ACCESSION CRS95644
 VERSION CRS95644.1 GI:50476451
 KEYWORDS HTC; CNSLT_cDNA
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 1909)
 Li, W.B., Gruber, C., Jesse, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact : Peng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Paraday Avenue
 2 (bases 1 to 1909)
 Genoscope.
 Direct Submission
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen

FEATURES
 source
 1..1909
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D1052YN13"
 /issue_type="Placenta Cot 25-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.73e+04 Length: 1909
 Score: 38.00 Matches: 7
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 100.0% Indels: 0
 DB: 4 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CRS95644 (1-1909)

QY 1 SerLeuileThrTyrPasnile 7
 DB 367 TCTTCATTAACCTGGAAATATT 387

RESULT 150
 CN164099 181 bp mRNA linear EST 02-APR-2004
 DEFINITION 994218 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION CN164099
 VERSION CN164099.1 GI:46178529
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;

REFERENCE 1 (bases 1 to 181)
 Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
 Noneman, D.J., Wray, J.E. and Keefe, J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)

JOURNAL
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: TMM8062 row: L column: 14
 Seq primer: GGAATACGACCTGCACTAATGCG.

FEATURES
 source
 1..181
 Location/Qualifiers
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /issue_type="pooled"
 /lab_host="PH10B"
 /clone_lib="MARC 4P1G"
 /note="vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN
 Alignment Scores:
 Pred. No.: 1.64e+03 Length: 181
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN164099 (1-181)

QY 1 SerLeuileThrTyrPasnile 7
 DB 70 AGTTGGTCACCTGGAAATATT 90

RESULT 151
 CN164315 181 bp mRNA linear EST 02-APR-2004
 DEFINITION 994602 MARC 4P1G Sus scrofa cDNA 3', mRNA sequence.
 ACCESSION CN164315
 VERSION CN164315.1 GI:46178745
 KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 Sus.

REFERENCE 1 (bases 1 to 181)
 Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
 Noneman, D.J., Wray, J.E. and Keefe, J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)

JOURNAL
 COMMENT Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
 trimmed with the aid of the trim_alt option. Vector identified with
 cross_match v0.990329.
 Plate: TMM8062 row: L column: 14

FEATURES
Seq primer: TAGAAGCAGCAGTCGAGC.
Location/Qualifiers
1. 181
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_1lb="MARC 4P1G"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

ORIGIN
Alignment Scores:
Pred. No.: 1.64e+03 Length: 181
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 05.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 7 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CN164315 (1-181)

QY
1 SerLeu1eThrTTPaen1le 7
|||||:|||||
DB 112 AGTTGTCCTCGAATATT 92

RESULT 152
AA658041/c 354 bp mRNA linear EST 03-DEC-1997
LOCUS nullf03.e1 NCI CGAP Pr2 Homo sapiens CDNA clone IMAGE:1208093
DEFINITION similar to contains Alu repetitive element; mRNA sequence.
ACCESSION AA658041
VERSION AA658041.1 GI:2594195
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 354)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marsdon Linehan, M.D., Rodrigo Chuagui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Kitzman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
www.bio.lnl.gov/bbrp/image/image.html
Insert Length: 617 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham.
Location/Qualifiers
1. 354
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1208093"
/sex="Male"
/dev stage="45 Years Old"
/lab host="DH10B"
/clone_1lb="NCI CGAP Pr2"
/note="Vector: pAMP10; Site 1: NotI; Site 2: EcoRI; 1st
strand CDNA was primed with oligo(dT)17 on 50 ng of
DNase-treated, total cellular RNA obtained from
5,000-10,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial

neoplasia 2 (PIN2) cells. Double-stranded CDNA was
ligated to EcoRI adaptor, 5 cycles of PCR applied to the
CDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDC-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Kitzman."

ORIGIN
Alignment Scores:
Pred. No.: 3.66e+03 Length: 354
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AA658041 (1-354)

QY
1 SerLeu1eThrTTPaen1le 7
|||||:|||||
DB 200 TCTCTGTATACCTGGAATATT 180

RESULT 153
CR462749 354 bp mRNA linear EST 01-JUL-2004
LOCUS CR462749 Rat pBluescript L10n Rattus norvegicus CDNA clone
DEFINITION L10NP463C02133 3', mRNA sequence.
ACCESSION CR462749
VERSION CR462749.1 GI:49595098
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 354)
Schuette, J., Hermann, J., Kranz, H., Loebbert, R., Schlueter, T.,
Schuette, D., Weindl, M., Heil, O., Ebert, L., Neubert, P., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
Rat ArrayTAG CDNA
Unpublished (2004)
Contact: Inge Axlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD: L10NP463C02133.
RZPDLIB;
Rat ArrayTAG CDNA
http://www.rzpd.de/cgi-
bin/product/showlib.pl.cgi?response?libNo=463 Contact: Inge Axlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTACGAC.
Location/Qualifiers
1. 354
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="L10NP463C02133"
/lab host="DH10B"
/clone_1lb="Rat pBluescript L10n"

ORIGIN
Alignment Scores:
Pred. No.: 3.66e+03 Length: 354
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.fst

Page 70

JOURNAL
COMMENT

Unpublished (2003)
Contact: Longtao Wu
Experimental Marine Biology Laboratory (EMBL)
Institute of Oceanology, Chinese Academy of Science (IOCAS)
7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
Tel: +86-0532-2898552
Email: lshong@eml.ac.cn
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES
source

1..404
/organism="Argopecten irradians"
/mol_type="mRNA"
/db_xref="taxon:11199"
/sex="hermaphrodite"
/tissue_type="whole body"
/dev_stage="maturation phage"
/clone_1ib="Bay scallop Uni-ZAP XR Expression Library"
/note="Organ: whole body; Vector: pBluescript(+/-) ;
Site 1: XhoI; Site 2: EcoRI; Using Stratagene's Uni-ZAP XR
cDNA synthesis kit, we constructed a cDNA library of Bay
scallop. 4975 ESTs were gained."

ORIGIN

Alignment Scores:

Pred. No.: 4.28e+03 Length: 404
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CH413283 (1-404)

QY 1 SerleuileThTPanille 7

DB 85 TCCTTATCAGCTGGAATGTA 105

RESULT 157

BZ202954/c 427 bp DNA linear GSS 11-OCT-2002
LOCUS CH230-399H1.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION CH230-399H1, genomic survey sequence.
ACCESSION BZ202954
VERSION BZ202954.1 GI:23661006
KEYWORDS GSS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Shaying Zhao
Department of Rukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: szhao@igir.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact pletier de Jong (pdejong@eml.ac.cn).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ordering information.htm). BAC end
plates: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Seq primer: T7
Class: BAC ends.

FEATURES
source

Location/Qualifiers
1..427
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNrd/MCv"
/db_xref="taxon:10116"
/clone="CH230-399H1"
/sex="Female"
/cell_type="Brain"
/clone_1ib="CHORI-230 Segment 2"
/note="Vector: pTARBA1.3 Site 1: MhoI; Site 2: MhoI;
CHORI-230 Rat (BN/SsNrd/MCv) BAC library produced by
Pleier de Jong"

ORIGIN

Alignment Scores:

Pred. No.: 4.57e+03 Length: 427
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BZ202954 (1-427)

QY 1 SerleuileThTPanille 7

DB 159 TCACCTGACCTGGAACATC 139

RESULT 158

AA427279/c 440 bp mRNA linear EST 16-OCT-1997
LOCUS V447911.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
DEFINITION IMAGE:803780 5', mRNA sequence.
ACCESSION AA427279
VERSION AA427279.1 GI:2110084
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)
Contact: Maira M/Mouse EST Project
WashU-HMNI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:460124
Seq primer: -40m13 fwd, ET from Amersham.
Location/Qualifiers
1..440
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J x DBA/2J F1"
/db_xref="taxon:10090"
/clone="IMAGE:803780"
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified) ;

Site 1: MluI; Site 2: SalI; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: SalI(dT): 5'-CGATCAGCGTCGACCGTCTTTTCTTT-3'. CDNAS were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

ORIGIN

Alignment Scores:

Pred. No.:	4,74e+03	Length:	440
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	1	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x AA427279 (1-440)

QY 1 SerLeuIeThrTPaSnIle 7

Db 258 TCTTGTGTCACATGGAACATA 238

RESULT 159

A0613212 454 bp DNA linear GSS 15-JUN-1999

LOCUS HS_5133_A1_G02_SPEE_RPC1-11 Human Male BAC library Homo sapiens

ACCESSION A0613212

VERSION A0613212.1 GI:5074488

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Buzary, G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Kellar, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

PUBMED 10449764

COMMENT Contact: Mahairas CG, Wallace JC, Hood L

High Throughput Sequencing Center

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong

pieter@dejong.med.bufileo.edu. Clones may be purchased from BACPAC Resources (http://bacpac.med.bufileo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.hresc.washington.edu

Plate: 709 row: M column: 3

Seq primer: SP6

Classes: BAC ends

High quality sequence stop: 454.

Location/Qualifiers

1..454

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone_id="Plate=709 Col=3 Row=M"

/sex="male"

/clone_lib="RPC1-11 Human Male BAC library"

/note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

ORIGIN

Alignment Scores:

Pred. No.:	4,92e+03	Length:	454
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	9	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x A0613212 (1-454)

QY 1 SerLeuIeThrTPaSnIle 7

Db 203 AGCTTAGTACATGGAATATC 183

RESULT 160

BE836176 455 bp mRNA linear EST 22-SEP-2000

LOCUS PM4-FN0057-100600-001-cl1 FN0057 Homo sapiens CDNA, mRNA sequence.

ACCESSION BE836176

VERSION BE836176.1 GI:10268554

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Buzary, G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Kellar, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPS/PICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM4-FN0057-100600-001-cl1&t3=2000-06-10&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 3

High quality sequence start: 455.

Location/Qualifiers

1..455

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_id="FN0057"

/note="Organ: prostate_normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	4,93e+03	Length:	455
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	9	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x A0613212 (1-454)

QY 1 SerLeuIeThrTPaSnIle 7

Db 203 AGCTTAGTACATGGAATATC 183

RESULT 160

BE836176 455 bp mRNA linear EST 22-SEP-2000

LOCUS PM4-FN0057-100600-001-cl1 FN0057 Homo sapiens CDNA, mRNA sequence.

ACCESSION BE836176

VERSION BE836176.1 GI:10268554

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Buzary, G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Kellar, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the PAPS/PICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=PM4-FN0057-100600-001-cl1&t3=2000-06-10&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 3

High quality sequence start: 455.

Location/Qualifiers

1..455

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_id="FN0057"

/note="Organ: prostate_normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

Thu Mar 16 10:39:26 2006

us-10-757-745-2_copy_115_121.rst

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Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BE836176 (1-455)
QY 1 SerleuileThrtPansille 7
DB 47 TCCTTGTCACATGGAATGTA 27
RESULT 161
CB415942 471 bp mRNA linear EST 01-JAN-2005
LOCUS CB415942
DEFINITION Scap 5865 Bay scallop Uni-ZAP XR Expression Library, Argopecten
irradians cDNA 5' similar to Argopecten irradians similar to
Metridium senile Cam mRNA for calmodulin, partial cds, mRNA
sequence.
ACCESSION CB415942 GI:56937503
VERSION CB415942.1
KEYWORDS EST
SOURCE Argopecten irradians
ORGANISM Argopecten irradians
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
REFERENCE 1 (bases 1 to 471)
AUTHORS Song, L., Xu, W., Li, H., Wu, L., Xiang, J. and Guo, X.
TITLE The construction and EST analysis of cDNA library from bay scallop
Argopecten irradians
JOURNAL Unpublished (2003)
COMMENT Contact: Longtao Wu
Experimental Marine Biology Laboratory (EMBL/C)
Institute of Oceanology, Chinese Academy of Science (IOCAS)
7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
Tel: +86-0532-2898552
Email: lshsongem.qdio.ac.cn
Seq primer: M13 Forward.
FEATURES
source
1..471
Location/Qualifiers
/organism="Argopecten irradians"
/mol_type="mRNA"
/db_xref="taxon:31199"
/sex="hermaphrodite"
/tissue_type="whole body"
/dev_stage="maturation phase"
/clone_lib="Bay scallop Uni-ZAP XR Expression Library"
/note="Organ: whole body; Vector: pBluescript (+/-);
Site 1: XhoI; Site 2: EcoRI; Using Stratagene's Uni-ZAP XR
cDNA synthesis kit, we constructed a cDNA library of Bay
scallop. 4975 ESTs were gained."
ORIGIN
Alignment Scores:
Pred. No.: 5.14e+03 Length: 471
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CB415942 (1-471)
QY 1 SerleuileThrtPansille 7
DB 270 TCCTTATCATCGTGGAATGTA 290
RESULT 162
BI275343 501 bp mRNA linear EST 18-JUL-2001
LOCUS BI275343
DEFINITION UI-R-CXO-bmw-d-04-0-UI-s1 UI-R-CXO Rattus norvegicus cDNA clone
UI-R-CXO-bmw-d-04-0-UI 3', mRNA sequence.
ACCESSION BI275343 GI:14887105
VERSION BI275343.1

KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Carnata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 501)
AUTHORS Bonaldo, M.P., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Gene Res. 6 (9), 791-806 (1996)
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa 4156 MBRF, Iowa City, IA 52242, USA
375 Newcom Road
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized rat placenta pool library cDNA library preparation. M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
source
1..501
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone_lib="UI-R-CXO-bmw-d-04-0-UI"
/dev_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-CXO"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CXO
library is a normalized library constructed from the
following rat placenta tissues: embryonic day 17,
embryonic day 19, embryonic day 21. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratres.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_TISSUE=rat placenta pool
TAG_LIB=UI-R-CXO
TAG_SEQ="TCACGACATG"
ORIGIN
Alignment Scores:
Pred. No.: 5.53e+03 Length: 501
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BI275343 (1-501)
QY 1 SerleuileThrtPansille 7
DB 344 TCCTTGTCACATGGAACATA 364
RESULT 163
AA591859 504 bp mRNA linear EST 16-SEP-1997
LOCUS AA591859/c
DEFINITION VK91h07.s1 Knowles Solter mouse 2 cell Mus musculus cDNA clone
IMAGE:962077 5', mRNA sequence.

ACCESSION AA591859
 VERSION AA591859.1 GI:2405522
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidae; Muridae; Murinae; Mus.
 1 (bases 1 to 504)
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through INM: contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MG1:550869
 High quality sequence stop: 491.

FEATURES
 source Location/Qualifiers
 1..504
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J x DBA/2J F1"
 /db_xref="taxon:10090"
 /clone="IMAGE:962077"
 /issue_type="embryo"
 /dev_stage="2-cell"
 /lab_host="DH10B"
 /clone_lib="Knowles Solter mouse 2 cell"
 /note="Organ: embryo; Vector: plasmid (modified);
 Site 1: MluI; Site 2: SalI; Cloned unidirectionally from
 mRNA prepared from 13,500 2-cell stage embryos. Primer:
 SalI(dT): 5'-CGGTGCGACGCGACGCTTTTCTTTT-3',
 were cloned into the MluI/SalI sites of a modified
 plasmid vector using commercial linkers (NEB).
 Average insert size: 1.2 kb."

ORIGIN
 Alignment Scores:
 Pred. No.: 5.57e+03 Length: 504
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 1 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x AA591859 (1-504)

Qy 1 SerLeuileThrTPasnlle 7
 |||||:|||||
 Db 258 TCTTGTGCATGCAACATA 238

RESULT 164
 LOCUS BE107896 545 bp mRNA linear EST J3-JUN-2000
 DEFINITION UI-R-CAO-awy-a-11-0-UI.s1 UI-R-CAO Rattus norvegicus cDNA clone
 BE107896
 UI-R-CAO-awy-a-11-0-UI 3', mRNA sequence.
 ACCESSION BE107896.1 GI:8500001
 VERSION EST.
 KEYWORDS Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE
 AUTHORS Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
 1 (bases 1 to 545)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 COMMENT 8889548
 CONTACT: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site
 and the oligo-dT track served to identify it as a clone from the
 normalized cerebellum library cDNA library preparation: M.B. Soares
 Lab Clone distribution: clones will be available through Research
 Genetics (www.resgen.com)
 Seg primer: M13 Forward
 POLYA=yes.

FEATURES
 source Location/Qualifiers
 1..545
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CAO-awy-a-11-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="UI-R-CAO"
 /note="Vector: pRT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI. The UI-R-CAO
 library is a subtracted library derived from the following
 tissues: thalamus, cerebellum, hypothalamus, medulla,
 pons, midbrain, cerebral cortex, corpus striatum, testis,
 and hippocampus. For a detailed description of the
 library from which this clone was derived, please visit
 our web site at ratat.eng.uiowa.edu. The subtraction
 has been previously described in (Bonaldo, Lennon and
 Soares, Genome Research 6:791-806, 1996)
 TAG_TISSUE=cerebellum
 TAG_LIB=UI-R-CAO
 TAG_SEQ=CGAAC"

ORIGIN
 Alignment Scores:
 Pred. No.: 6.12e+03 Length: 545
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BE107896 (1-545)

Qy 1 SerLeuileThrTPasnlle 7
 |||||:|||||
 Db 343 TCTTGTGCATGCAACATA 363

RESULT 165
 LOCUS CE565005 585 bp DNA linear GSS 28-SEP-2003
 DEFINITION tigr-gss-dog-17000312704632 dog library Canis familiaris genomic,
 genomic survey sequence.
 ACCESSION CE565005.1 GI:36881786
 VERSION GSS.
 KEYWORDS Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Page 74

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamamoto, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with

/clone_lib="RIKEN full-length enriched, 13 days embryo lung"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCCGACACCTCGAGTTTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGTTCTCGAGTTTAAATTAATATCCCTCCCTCCCTCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda FHC I."

ORIGIN

Alignment Scores:

Pred. No.:	7.63e+03	Length:	656
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BM485402 (1-656)

OY 1 SerLeuileThrTPAnlle 7

DB 332 TCTTGTGCATGACATCA 312

RESULT 171

LOCUS

BY740567 RIKEN full-length enriched, 16 days embryo kidney Mus

DEFINITION

musculus cDNA clone I920089D14 5', mRNA sequence.

ACCESSION

BY740567 GI:27164930

VERSION

BY740567.1

KEYWORDS

MUS MUSCULUS (house mouse)

SOURCE

MUS MUSCULUS

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Scuriongnathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 657)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bulc, C.,

Hune, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chochola, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fleischer, C.F., Forrest, A., Frerzer, K.S., Gaasterland, T.,

Giaroldi, M., Giesi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglocz, D.R.,

Maltais, K., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavani, W.J., Perrea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wyszynski, B., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavalan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Araawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

TITLE
 JOURNAL
 PUBMED
 COMMENT

Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
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 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Komno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watanabe, A., Watanabe, M., and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multichannel sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.

FEATURES

source

Location/Qualifiers
 1..657
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="I920089D14"
 /tissue_type="kidney"
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 /clone_lib="RIKEN full-length enriched, 16 days embryo
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ORIGIN

Alignment Scores:

Pred. No.:	7.64e+03	Length:	657
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BY740567 (1-657)

OY 1 SerLeuileThrTPAnlle 7

DB 582 TCTTGTGCATGACATCA 562

RESULT 172

LOCUS

BY740568 RIKEN full-length enriched, pooled tissues, 16 days

DEFINITION

embryo, etc. Mus musculus cDNA clone I920089C06 5', mRNA sequence.

ACCESSION

BY740568

VERSION

BY740568.1

GI:27164963

10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Aizawa, K., Shingawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Hayashizaki, Y., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.

FEATURES

source
 1. 658
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4931404P18"
 /sex="male"
 /tissue_type="testis"
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 /note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
 GAGAGAGAGAGATTCAGACCTCTTTTCTTTTCTTTTCTTTT 3'}. cDNA was prepared by using triethanolamine thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5].
 GAGAGAGAGAGCGCCGCAATTATCTTCGAGTAAATTAATATCCCCCCCC 3'}. cDNA was cloned into the XhoI and BamHI sites."

ORIGIN

Alignment Scores:

Pred. No.:	7.66e+03	Length:	658
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	2	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BB616066 (1-658)

Qy 1 SerLeuIeThrTPAsnIle 7

DB 611 TTTTGGTCACATGAGACATA 591

RESULT 174

BB660102C

LOCUS

DEFINITION

musculus cDNA clone D430031101 5', mRNA sequence.

ACCESSION

BB660102

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

BB660102 660 bp mRNA linear EST 26-OCT-2001
 BB660102 RIKEN full-length enriched, 13 days embryo lung Mus
 musculus cDNA clone D430031101 5', mRNA sequence.
 BB660102.1 GI:164933923.
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.
 1 (bases 1 to 660)
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Horii, F., Ishii, Y., Ito, M., Kawai, J., Kono, H., Konda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,

TITLE

JOURNAL

COMMENT

Ono, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Saeki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
 Unpublished (2001)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)
 Konno, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., and Hayashizaki, Y.
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
 e mouse tissues.

FEATURES

source

Location/Qualifiers
 1. 660
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="D430031101"
 /tissue_type="lung"
 /tissue_type="lung"
 /dev_stage="13 days embryo"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 13 days embryo lung"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5].
 GAGAGAGAGAGCGCCGCACTGAGTTTCTTTTCTTTTCTTTT 3'}. cDNA was prepared by using triethanolamine thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5].
 GAGAGAGAGATTCGAGTAAATTAATATCTTCGAGTAAATTAATATCCCCCCCC 3'}. cDNA was cleaved with BamHI and XhoI. Vector: a modified Bluescript KS(+) after bulk excision from Lambda PUC I."

ORIGIN

Alignment Scores:

Pred. No.:	7.66e+03	Length:	660
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0

DB: 2 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BB660102 (1-660)

QY 1 Serleu1ethrTPanille 7

DB 517 TCTTGGTCACATGAAACATA 497

RESULT 175

LOCUS CC432105 661 bp DNA linear GSS 20-MAY-2003

DEFINITION PUHQ72TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMB7a453123,

ACCESSION CC432105

VERSION CC432105.1 GI:30927633

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

TITLE 1 (bases 1 to 661)

JOURNAL Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

COMMENT Resnick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and

Benetzen, J.

Maize Genomics Consortium

Unpublished (2003)

Other GSSs: PUHQ72TB

Contact: Cathy Whiteley

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whiteley@tigr.org

Seq primer: TP

DB: Class: sheared ends.

Location/Qualifiers

1..661

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="873"

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ORIGIN

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Percent Similarity: 100.0% Conservative: 1

Best Local Similarity: 85.7% Mismatches: 0

Query Match: 97.4% Indels: 0

DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CC432105 (1-661)

QY 1 Serleu1ethrTPanille 7

DB 361 TCACGATCCTCGAATGTA 381

RESULT 176

LOCUS BI684350 669 bp mRNA linear EST 18-SEP-2001

DEFINITION 603308186F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5344269 5',

ACCESSION BI684350

VERSION BI684350.1 GI:15646978

KEYWORDS EST

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Muridae; Murinae; Mus.

1 (bases 1 to 669)

NH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@bbs-remail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CNA Library Preparation: Life Technologies, Inc.

CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

plate: L1AM1874 row: k column: 22

High quality sequence etop: 669.

FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="mRNA"

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/clone="IMAGE:5344269"

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/tissue_type="infiltrating ductal carcinoma"

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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Library constructed by Life Technologies. Investigator

providing samples: Jeffrey Green, M.D., NIH

ORIGIN

Alignment Scores:

Pred. No.: 7.81e+03 Length: 669

Score: 37.00 Matches: 6

Percent Similarity: 100.0% Conservative: 1

Best Local Similarity: 85.7% Mismatches: 0

Query Match: 97.4% Indels: 0

DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BI684350 (1-669)

QY 1 Serleu1ethrTPanille 7

DB 517 TCTTGGTCACATGAAACATA 497

RESULT 177

LOCUS DE065880

DEFINITION Oryzias latipes DNA, clone: olat-160B09.F, genomic survey sequence.

ACCESSION DE065880

VERSION DE065880.1 GI:62577424

KEYWORDS GSS.

SOURCE Oryzias latipes (Japanese medaka)

ORGANISM Oryzias latipes

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Acanthomorpha; Acanthopterygii; Percormorpha; Atherinomorpha;

Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.

REFERENCE Fujitama, A., Toyoda, A., Kuroki, Y. and Sakaki, Y.

BAC end sequences of Olat Oryzias latipes library

Submitted (12-APR-2005) Asao Fujitama, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC),

1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama, Kanagawa, 230-0045, Japan

(E-mail: afujitama@gsc.riken.jp, URL: http://etc.gsc.riken.jp/)

COMMENT
Tel: 81-3-4212-2558, Fax: 81-3-3556-1916
This work was done in collaboration with Takeda, H. (1), Naruse, K. (2)

Tel: 81-3-4212-2558, Fax: 81-3-3556-1916
This work was done in collaboration with Takeda, H. (1), Naruse, K
(2)

and Narita, T. (3)
(1) Department of Biological Science,
University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, JAPAN
Phone: +81-3-5841-4431

Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the M.M.A.G.E. Consortium/UMD at:
<http://image.lnli.gov>

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cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the M.M.A.G.E. Consortium/UMD at:
<http://image.lnli.gov>

Chochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaeteland, T., Gariboldi, M., Giasi, C., Godzik, A., Gough, J., Grimmond, S., Gustlinich, S., Hitokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagishima, T., Numata, K., Okido, T., Pavani, W.J., Petosa, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takemaki, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Veitard, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Kono, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

1246851

TITLE
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216

JOURNAL
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

COMMENT
Direct Submission
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichipillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES
source
1..694
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630217A16"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clone_lib="RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells"

ORIGIN
Alignment Scores:
Pred. No.: 8.16e+03 Length: 694
Score: 57.00 Matches: 6
Percent Similarity: 100.0% Mismatches: 0
Best Local Similarity: 85.7% Indels: 1
Query Match: 97.4% Gaps: 0
DB: 5
US-10-757-745-2_COPY_115_121 (1-7) x BY48935 (1-694)
OY 1 SerLeuLeuTrpPantle 7
DB 528 TCTTGTGTCACATGAAACATA 508
RESULT 180
BQ179160/c 702 bp mRNA linear EST 30-APR-2002
LOCUS
DEFINITION
UT-M-EMO-bwu-k-23-0-UT-r1 NIH_BMAP_EMO Mus musculus cDNA clone
IMAGE:5703310 5', mRNA sequence.
ACCESSION
BQ179160 GI:20354652
VERSION
BQ179160.1
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 702)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
R18se Procurement: Dr. James Lin, University of Iowa
cDNA library preparation: Dr. M. Bento Soares, University of Iowa
DNA library arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pyx-5.
Location/Qualifiers
1..702
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5703310"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP EMO"
/note="Organ: brain; Vector: pyx-Asc; Site: 1; Ecor I; Site: 2; Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCTGGA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

FEATURES
source
1..702
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5703310"
/tissue_type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP EMO"
/note="Organ: brain; Vector: pyx-Asc; Site: 1; Ecor I; Site: 2; Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I, and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCTGGA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 8,27e+03 Length: 702
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 3 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x B0179160 (1-702)

Qy 1 SerleuilerThrTpasnlle 7
 Db 518 TCTTGTGCATCGACATCA 498

RESULT 181
 BU053419 712 bp mRNA linear EST 26-AUG-2002
 LOCUS BU053419/c
 DEFINITION UI-M-FCO-bzd-k-13-0-UI.r1 NIH BMAP_FCO Mus musculus cDNA clone
 IMAGE:6402180 5', mRNA sequence.

ACCESSION BU053419 GI:22493496
 VERSION BU053419.1
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS NIH-MGC
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/URL at:
 http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

FEATURES
 source location/Qualifiers

1..712
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6402180"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP FCO"
 /note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is TAGAGAGCC. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP): 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 8.41e+03 Length: 712

Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BU053419 (1-712)

Qy 1 SerleuilerThrTpasnlle 7
 Db 525 TCTTGTGCATCGACATCA 505

RESULT 182
 BY741565/c

DEFINITION BY741565 RIKEN full-length enriched, B16 F10Y cells Mus musculus
 cDNA clone G370147H12 5', mRNA sequence.

ACCESSION BY741565
 VERSION BY741565.1 GI:27166545
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS NIH-MGC
 TITLE NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-r@mail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/URL at:
 http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.
 FEATURES
 source location/Qualifiers

1..712
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:6402180"
 /tissue_type="whole brain"
 /dev_stage="embryo 12.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH BMAP FCO"
 /note="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an
 oligo-dT primer containing a Not I site. Double stranded
 cDNA was size selected according to mRNA size fraction,
 ligated with EcoR I adaptor, digested with Not I, and then
 cloned directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA
 tail, is TAGAGAGCC. This library was created for the
 University of Iowa Mouse Brain Molecular Anatomy Project
 (BMAP): 'Gene Discovery in the Developing Mouse Nervous
 System', supported by National Institutes of Mental Health
 (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 8.41e+03 Length: 712

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Cells were provided by Drs. William J Pavan, Stacie Loftus, and Denise Larson (Division of Intramural Research Genetic Disease Research Branch National Human Genome Research Institute, National Institutes of Health (NIH) Building 49, Room 4A82 49 Convent Drive MSC 4472 Bethesda, Maryland U.S.A) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
1..713
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370147H12"
/cell_type="B16 F10Y cells"
/clone_11b="RIKEN full-length enriched, B16 F10Y cells"

ORIGIN

Alignment Scores:

Pred. No.:	8.43e+03	Length:	713
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	5	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BY741565 (1-713)

QY 1 SerLeuileThrTPaenile 7

Db 527 TCTTGGTCACATGGAACATA 507

RESULT 183

CA132027

LOCUS

SCBGR1052C04

DEFINITION

5' mRNA sequence:

ACCESSION

CA132027

VERSION

CA132027.1

KEYWORDS

EST

SOURCE

ORGANISM

Saccharum officinarum

Saccharum officinarum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE

1 (bases 1 to 714)

Vector, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda, P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

FEATURES

source

Email: parvada@unicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcer.unesp.br>
Plate: 052 row: C column: 04
Seq primer: 17 Promoter primer.
Location/Qualifiers
1..714
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCBGR1052C04"
/lab_host="DH10B"
/clone_11b="RT1"
/note="Organ: Root tips (0.3cm-long) from adult plants; Vector: pSport1; Site 1: SalI Site 2: NotI; An unidirectional cDNA library generated from [Root tips (0.3cm-long) from adult plants] cDNA was prepared from poly(A+ mRNA) using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNA were fractionated in a Sepharose CL-2B 40cm-column and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucst.lad.ic.unicamp.br/public>"

ORIGIN

Alignment Scores:

Pred. No.:	8.44e+03	Length:	714
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CA132027 (1-714)

QY 1 SerLeuileThrTPaenile 7

Db 685 AGCTTAATTAACGTGAATGTT 705

RESULT 184

CF533524/C

LOCUS

DEFINITION

IMAGE:3053759 5' mRNA sequence.

ACCESSION

CF533524

VERSION

CF533524.1

KEYWORDS

EST

SOURCE

ORGANISM

Mus musculus

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 715)

NIH-MGC <http://mgc.ncl.nih.gov/>

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mouse1.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5'

Location/Qualifiers

1..715

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:30532759"
 /tissue_type="Whole brain"
 /dev_stage="1, 5, and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_GH0"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was
 size selected according to mRNA size fraction, ligated
 with EcoR I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CGAAGTGAAT. This library was created for the University
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System, supported by National
 Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,
 program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 8.45e+03 Length: 715
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CFS353524 (1-715)

QY 1 SerLeuilethnTPAsnile 7
 |||||:::|||||
 Db 457 TCTTGTGCATGAGACATA 437

RESULT 185

CNS0ES51 718 bp mRNA linear HTC 05-JUL-2005
 LOCUS Tetraodon nigroviridis full-length cDNA.
 ACCESSION CR639168
 VERSION CR639168.2 GI:56240375
 KEYWORDS HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
 SOURCE Tetraodon nigroviridis
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes;
 Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

Jallion, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
 Maucell, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
 Nicud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
 Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
 Casellano, S., Anthouard, V., Ubbin, C., Castell, V., Katinka, M.,
 Vacherie, B., Biemont, C., Skalli, Z., Catolico, L., Poulain, J., De
 Bernardis, V., Cruaud, C., Duprat, S., Broctier, P., Coutanceau, J.P.,
 Gouy, J., Parra, G., Lardier, G., Chappe, C., McKernan, K.J.,
 McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
 Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
 Robinson-Rechavi, M., Lauder, V., Schachter, V., Quetzer, F.,
 Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.,
 and Roest Croolius, H.

TITLE

Genome duplication in the teleost fish Tetraodon nigroviridis
 reveals the early vertebrate proto-karyotype

JOURNAL

PUBMED

AUTHORS

JOURNAL

Nature 431 (2004), 946-957 (2004)
 2 (bases 1 to 718)
 Genoscope.
 Direct Submission
 Submitted (25-Nov-2004) Genoscope - Centre National de Sequencage -

COMMENT

: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 (E-mail : segrete@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 On Dec 3, 2004 this sequence version replaced gi:51135613.
 The sequences are based on single pass reads.
 More information available at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES

source

1..718
 /organism="Tetraodon nigroviridis"
 /mol_type="mRNA"
 /db_xref="taxon:99883"
 /tissue_type="Liver"

ORIGIN

Alignment Scores:

Pred. No.: 8.5e+03 Length: 718
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: 4 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CNS0ES51 (1-718)

QY 1 SerLeuilethnTPAsnile 7
 |||||:::|||||
 Db 358 TCGCTGATTAACCTGGAACGTG 378

RESULT 186

LOCUS B0745578 730 bp mRNA linear EST 17-JUL-2002
 DEFINITION UT-M-EMO-bxh-e-03-0-UT-r1 NIH_BMAP_EMO Mus musculus cDNA clone
 IMAGE:5708138 5', mRNA sequence.
 ACCESSION B0745578
 VERSION B0745578.1 GI:21892365
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Mus.
 1 (bases 1 to 730)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-rcmail.nih.gov
 Tissue Procurement: Dr. James Lin, University of Iowa
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILM at:
 http://image.llnl.gov

REFERENCE

AUTHORS

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)
 Seq primer: pYX-5.
 Location/Qualifiers
 1..730
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:5708138"
 /tissue_type="Whole brain"
 /dev_stage="embryo 15.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_EMO"
 /note="Organ: Brain; Vector: pYX-Asc; Site_1: EcoR I;
 Site_2: Not I; The library was constructed according to
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured mRNA was size fractionated on a 1% agarose
 gel. First strand cDNA synthesis was primed with an

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 8.67e+03 Length: 730
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 5 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BQ745578 (1-730)

QY 1 Serleu1eThrTyrPasn1e 7

DB 123 TCTTGGTCACATGACACATA 103

RESULT 187

CF749729/c

LOCUS

DEFINITION

IMAGE:30627991 5', mRNA sequence.

CF749729

CF749729.1 GI:37646074

EST

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Seq primer: PYX-5.

Location/Qualifiers

1..737

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30627991"

/tissue_type="Upper Head"

/dev_stage="9.5 and 10.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH BMAP HJ0"

/note="Organ: Head; Vector: pyx-asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaïdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned

oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pyx-asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTCGGA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."

ORIGIN

Alignment Scores:

Pred. No.: 8.76e+03 Length: 737
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 6 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CF749729 (1-737)

QY 1 Serleu1eThrTyrPasn1e 7

DB 339 TCTTGGTCACATGACACATA 319

RESULT 188

CR296536/c

LOCUS

DEFINITION

mte1-13C4FM1 BAC end, cultivar Jemalong A17 of Medicago truncatula, genomic survey sequence.

CR296536

CR296536.1 GI:44690539

GSS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..740

/organism="Medicago truncatula"

/mol_type="genomic DNA"

/cultivar="Jemalong A17"

/db_xref="taxon:3880"

/clone_lib="MT1"

/note="Vector: pIndigoBAC; Site 1: EcoRI; Site 2: EcoRI; Debelie F. and Chalhou B. Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

Genoscope sequence ID: mte1-13C4FM1"

directionally into pyx-asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGCTGAAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Alignment Scores:

Pred. No.: 8.81e+03 Length: 740
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 11 Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CR296536 (1-740)

QY 1 Serleu1eThrTyrPasn1e 7

DB 654 AGTTTGATACCTTGGAATATT 634

RESULT 189

CC666503

LOCUS

DEFINITION

OG01Y93TH_ZM_0.7.1.5_KB Zee may genomic clone ZMMBM45Z017, genomic survey sequence.

741 bp DNA linear GSS 19-JUN-2003

ACCESSION CC666503 GI:32070577
 VERSION CC666503.1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 741)
 White, C.A., Quackenbush, J., Van Aken, S., Uteerback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)
 Other_GSSs: OCU7193TV
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: TR
 Class: methylation filtered.
 Location/Qualifiers
 1..741
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZMMB0452017"
 /note="Vector: pBCSK-1 Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN
 Alignment Scores:
 Pred. No.: 8.82e+03 Length: 741
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CC666503 (1-741)

Qy 1 SerleuIIerhTTPasnlle 7
 |||||
 Db 162 TCACGTGATCAGCTGGAATGTA 182

RESULT 190
 CVO73972/c 743 bp mRNA linear EST 25-AUG-2004
 LOCUS CVO73972
 DEFINITION AGENCOURT_31481300 NIH_MGC_251 Rattus norvegicus cDNA clone
 IMAGE:7387175 5', mRNA sequence.
 CVO73972
 CVO73972.1 GI:51541003
 EST.
 Rattus norvegicus (Norway rat)
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Rattus.
 1 (bases 1 to 743)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics / NIH
 National Cancer Institute
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cga@db-remail.nih.gov
 Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

FEATURES
 source
 1..741
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZMMB0452017"
 /note="Vector: pBCSK-1 Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

cdna library Preparation: Open Biosystems
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM1555 row: h column: 21
 High quality sequence stop: 705.
 Location/Qualifiers
 1..743
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="IMAGE:7387175"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC_251"
 /note="Organ: thymus; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
 5'-pGACTAGTCTAGATCGGAGCGGCCGCT-3'
 the EcoRV/NotI sites of pExpress-1 size-selection >1.25kb resulted in an average insert size of 1.6 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_250) and was constructed by Open Biosystems. Note: this is a NIH_MGC library"

ORIGIN
 Alignment Scores:
 Pred. No.: 8.85e+03 Length: 743
 Score: 37.00 Matches: 6
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 85.7% Mismatches: 0
 Query Match: 97.4% Indels: 0
 DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CVO73972 (1-743)

Qy 1 SerleuIIerhTTPasnlle 7
 |||||
 Db 493 TCTTTGTCATGGAACATA 473

RESULT 191
 CVO45302/c 747 bp mRNA linear EST 10-JUN-2004
 LOCUS CVO45302
 DEFINITION UI-M-HQ0-cgp-a-23-0-UI_r1 NIH_BMAP_HQ0 Mus musculus cDNA clone
 IMAGE:30662710 5', mRNA sequence.
 CVO45302
 CVO45302.1 GI:48585456
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 747)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@db-remail.nih.gov
 Tissue Procurement: Dr. James Lin University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mouse1.html
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
 Seq primer: PYX-5.
 Location/Qualifiers
 1..747

FEATURES
 source
 1..747
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone_lib="ZMMB0452017"
 /note="Vector: pBCSK-1 Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30662710"
/rissue_type="Upper Head"
/dev_stage="embryo 9.5 - 10.5 dpc"
/lab_host="NIH RMAP HQ"
/note="Organ: Upper Head; Vector: pYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGACTGAAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Alignment Scores:

Pred. No.:	8.91e+03	Length:	747
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x C0045302 (1-747)

QY 1 SerleuileThrTPanille 7

Db 176 TCTTGGTCACATGGAACATA 156

RESULT 192

BZ993817/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1 location/Qualifiers
1 758
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"

/clone="ZMMBTA360F12"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOP0; Site 1: EcoRI, 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.:	9.06e+03	Length:	758
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	9	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BZ993817 (1-758)

QY 1 SerleuileThrTPanille 7

Db 570 TCACTGATCACCCTGGAATGTA 550

RESULT 193

BZ993822

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1. 764
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA360F12"
/clone_1lb="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOP0; Site 1: EcoRI, 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.:	9.15e+03	Length:	764
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	9	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x BZ993822 (1-764)

QY 1 SerleuileThrTPanille 7

Db 655 TCACTGATCACCCTGGAATGTA 675

RESULT 194
CA327827/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CA327827
UI-M-FY0-ccw-b-15-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:6825232 5', mRNA sequence.
CA327827
GI:24545925
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
1 (bases 1 to 767)
NIH-MGC <http://mgi.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: PYX-5.

FEATURES
source
Location/Qualifiers
1..767
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6825232"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP FY0"
/note="Organ: Brain; Vector: PYX-Asc; Site 1: Bcor I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into PYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN
Alignment Scores:
Pred. No.: 9.19e+03 Length: 767
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x CA327827 (1-767)

OY 1 SerLeuIleThrTTPAsnIle 7
DB 36 TCTTTGGTCACATGAGACATA 16
RESULT 195

BUT58712
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

BUT58712
UI-R-FP0-coy-g-20-0-UI.s1 NCI CGAP_FP0 Rattus norvegicus cDNA clone
UI-R-FP0-coy-g-20-0-UI 3', mRNA sequence.
BUT58712
GI:23721519
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 769)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
Tissue Procurement: Jeff Stevens, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: DISTRIBUTION: Researchers may obtain clones
from Research Genetics (www.resgen.com).
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
Location/Qualifiers
1..769
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="UI-R-FP0-coy-g-20-0-UI"
/tissue_type="Mixed tissues"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1ib="NCI CGAP_FP0"
/note="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site 1: Bcor I; Site 2: Not I; UI-R-FP0 is a
subtracted cDNA library containing the following
tissue(s): Normal cartilage and SR-JWS tumor line. The
subtraction was made according to Bonaldo, Lennon and
Soares, Genome Research, 6:791-806, 1996. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for these libraries are: CTAATGACG,
CATCTTGTA,
TAG_TISSUE-rat SRC-JWS tumor line
TAG_LIB=UI-R-FP0
TAG_SEQ=CATTCTTGTA"

ORIGIN
Alignment Scores:
Pred. No.: 9.22e+03 Length: 769
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: Gaps: 0

US-10-757-745-2_COPY_115_121 (1-7) x BUT58712 (1-769)

OY 1 SerLeuIleThrTTPAsnIle 7
DB 631 TCTTTGGTCACATGAGACATA 651

RESULT 196
BI158794/c 779 bp mRNA linear EST 05-JUL-2001
LOCUS 60292158791 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5062076 5',
DEFINITION mRNA sequence.
ACCESSION BI158794
VERSION BI158794.1 GI:14618795
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL NIH-MGC
COMMENT NIH-MGC
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Lotmar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L14M1167 row: m column: 21
High quality sequence stop: 634.
Location/Qualifiers
1..779
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5062076"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
/clone_idb="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lotmar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
ORIGIN
Alignment Scores:
Pred. No.: 9.36e+03 Length: 779
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 2 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x BI158794 (1-779)
QY 1 SerLeuileThrtPaaenlle 7
DB 491 TCTTGTGTCACATGGAACATA 471
RESULT 197
CA327598/c 781 bp mRNA linear EST 09-JUL-2003
LOCUS 60292158791 NCI_CGAP_Mam3 Mus musculus cDNA clone
DEFINITION IMAGE:6826440 5', mRNA sequence.
ACCESSION CA327598
VERSION CA327598.1 GI:24545696
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL NIH-MGC
COMMENT NIH-MGC
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5
Location/Qualifiers
1..781
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:6826440"
/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 15.5, 16.5, 17.5 dpc"
/lab_host="DH10B (rt, page resistant)"
/clone_idb="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Acc; Site 1: EcoR I;
Site 2: Not I. The library was constructed according
to Bontal, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was self, fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to Bontal, size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Acc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Haimin Chiu, Ph.D.,
program coordinator."
ORIGIN
Alignment Scores:
Pred. No.: 9.39e+03 Length: 781
Score: 37.00 Matches: 6
Percent Similarity: 100.0% Conservative: 1
Best Local Similarity: 85.7% Mismatches: 0
Query Match: 97.4% Indels: 0
DB: 6 Gaps: 0
US-10-757-745-2_COPY_115_121 (1-7) x CA327598 (1-781)
QY 1 SerLeuileThrtPaaenlle 7
DB 536 TCTTGTGTCACATGGAACATA 516
RESULT 198
CX780657/c 785 bp mRNA linear EST 23-FEB-2004
LOCUS 60292158791 NCI_CGAP_Mam3 Mus musculus cDNA clone
DEFINITION UI-M-HDO-Cko-b-24-0-UI-r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:3061319 5', mRNA sequence.
ACCESSION CX780657
VERSION CX780657.1 GI:42746335
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE
AUTHORS NIH-MGC
TITLE NIH-MGC
JOURNAL NIH-MGC
COMMENT NIH-MGC
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5
Location/Qualifiers
1..781
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:6826440"
/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 15.5, 16.5, 17.5 dpc"
/lab_host="DH10B (rt, page resistant)"
/clone_idb="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pYX-Acc; Site 1: EcoR I;
Site 2: Not I. The library was constructed according
to Bontal, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was self, fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to Bontal, size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Acc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAC. This library was created for the University
of Iowa Brain Anatomy Project (BMAP). Gene Discovery in the
Developing Mouse Nervous System, supported by National
Institute of Mental Health (NIMH), Haimin Chiu, Ph.D.,
program coordinator."

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES

source

Seq primer: pyx-5

Location/Qualifiers

1..785
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30613199"
/tissue_type="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1ib="NIH BMAP HD0"
/note="Organ: Eye; Vector: pyx-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pyx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
9.45e+03	37.00	785	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	7	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CK780657 (1-785)

Qy 1 SerLeu1erThrTpAsnIle 7

DB 230 TCTTTGTCACATGGAACATA 270

RESULT 199

CA505075/C

LOCUS UI-R-FU0-cpy-1-21-0-UI-s1 UI-R-FU0 Rattus norvegicus cDNA clone
DEFINITION UI-R-FU0-cpy-1-21-0-UI-3', mRNA sequence.
CA505075

ACCESSION CA505075.1 GI:24996029

VERSION

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.

REFERENCE

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED

COMMENT

8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 101-157, >(CA)n\$Simple_repeat
Seq primer: M13 FORWARD
POLYA=yes.

FEATURES

source

Location/Qualifiers

1..797
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-FU0-cpy-1-21-0-UI"
/tissue_type="embryo"
/dev_stage="embryo"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_1ib="UI-R-FU0"
/note="Vector: pyx-Asc; Site 1: EcoR I; Site 2: Not I; UI-R-FU0 is a cDNA library containing the following tissue(s): rat embryo. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)
TAG_TISUB=rat-embryo
TAG_L1B=UI-R-FU0
TAG_SEQ=CATCTCTACT"

ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
9.62e+03	37.00	797	6
Percent Similarity:	100.0%	Conservative:	1
Best Local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	6	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CA505075 (1-797)

Qy 1 SerLeu1erThrTpAsnIle 7

DB 614 TCTTTGTCACATGGAACATA 594

RESULT 200

CG455947/C

LOCUS CG455947 803 bp DNA linear GSS 17-SEP-2003
DEFINITION PUFYF86TB.1 ZM 0.6 1.0 KB Zea mays genomic clone ZMBRna0753P04,
genomic survey sequence.
CG455947

ACCESSION CG455947.1 GI:34840947

VERSION

KEYWORDS GSS.

SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 803)

REFERENCE
AUTHORS

White, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Benneken, J.

TITLE
JOURNAL

Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUFXP867BP PUFXP867D PUFXP867DB
Contact: Cathy White

COMMENT

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208

Email: white@tigr.org

Seq primer: TR

FEATURES

source

Location/Qualifiers
1..803
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="873"
/db_xref="taxon:4577"
/clone="ZMMBTa0753p04"
/clone_lib="ZM 0.6-1.0 kb"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Alignment Scores:

Prod. No.:	9.71e+03	length:	803
Score:	37.00	Matches:	6
Percent Similarity:	100.0%	Conservative:	1
Best local Similarity:	85.7%	Mismatches:	0
Query Match:	97.4%	Indels:	0
DB:	10	Gaps:	0

US-10-757-745-2_COPY_115_121 (1-7) x CG455947 (1-803)

OY 1 SerLeuIeThrTrpAnIle 7

DB 601 TCCTGATCACTCGAATGTA 581

Search completed: March 16, 2006, 04:55:47
Job time : 616.738 secs